

Exhibit A

**results of BLAST****BLASTP 2.2.10 [Oct-19-2004]****Reference:**

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1113831716-2827-42556718445.BLASTQ4

Query=

(720 letters)

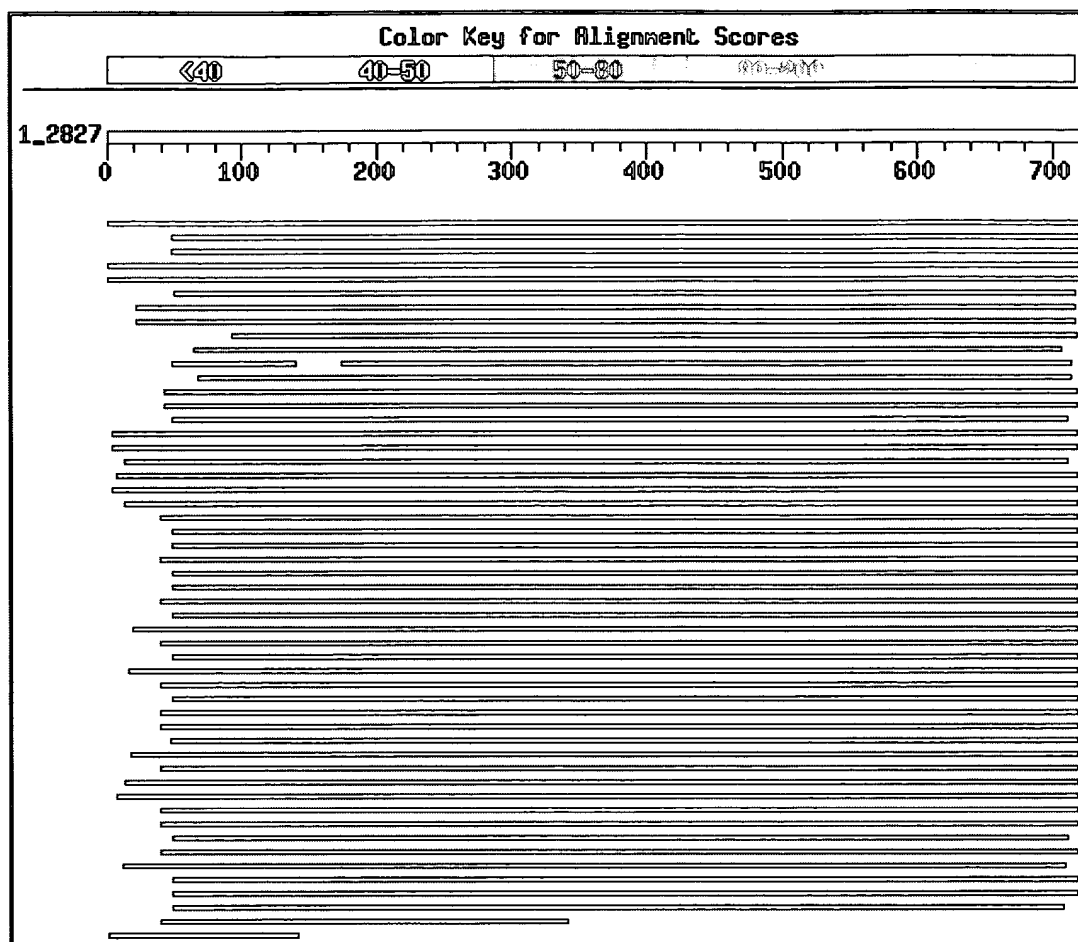
Database: All non-redundant GenBank CDS

translations+PDB+SwissProt+PIR+PRF excluding environmental samples
2,448,365 sequences; 829,394,864 total letters

If you have any problems or questions with the results of this search
please refer to the **BLAST FAQs**

Taxonomy reports**Distribution of 417 Blast Hits on the Query Sequence**

Mouse-over to show defline and scores. Click to show alignments



Related Structures

Sequences producing significant alignments:			Score (bits)	E Value	
gi 3294 emb CAA35886.1	phenylalanine ammonia-lyase [Rhodos...		915	0.0	
gi 169746 gb AAA33883.1	phenylalanine ammonia-lyase		901	0.0	
gi 225818 prf 1314202A	Phe ammonia lyase		888	0.0	
gi 56553841 pdb 1T6P H	Chain H, Crystal Structure Of Phenyl...		884	0.0	
gi 295942 emb CAA31486.1	phenylalanine ammonia-lyase [Rhod...		877	0.0	
gi 4127289 emb CAA09013.1	phenylalanine ammonium lyase [Am...		466	e-129	
gi 46096230 gb EAK81463.1	PALY_USTMA Phenylalanine ammonia...		436	e-120	
gi 15824531 gb AAL09388.1	phenylalanine ammonia-lyase [Ust...		428	e-118	
gi 40738860 gb EAA58050.1	hypothetical protein AN6075.2 [A...		428	e-118	
gi 32423291 ref XP_332083.1	hypothetical protein [Neurospo...		371	e-101	
gi 40739638 gb EAA58828.1	hypothetical protein AN3897.2 [A...		368	e-100	
gi 42553215 gb EAA76058.1	hypothetical protein FG09311.1 [...		367	e-100	
gi 32140421 gb AAP59438.1	phenylalanine ammonia lyase [Ara...		357	9e-97	
gi 1171991 sp P35510 PAL1_ARATH	Phenylalanine ammonia-lyase...		354	5e-96	
gi 7208616 gb AAF40224.1	phenylalanine ammonia-lyase 2 [Ru...		352	3e-95	
gi 23197654 gb AAN15354.1	phenylalanine ammonia-lyase [Ara...		350	9e-95	
gi 32140423 gb AAP59439.1	phenylalanine ammonia lyase [Ara...		350	1e-94	
gi 6647711 sp O64963 PAL1_PRUAV	Phenylalanine ammonia-lyase...		349	2e-94	
gi 1172001 sp P45730 PALY_POPTR	Phenylalanine ammonia-lyase...		348	3e-94	

gi 18377 emb CAA37129.1	phenylalanine ammonia-lyase [Glyci...	348	4e-94	
gi 497421 gb AAC18871.1	phenylalanine ammonia lyase [Arabi...	348	4e-94	
gi 32140425 gb AAP59440.1	phenylalanine ammonia lyase [Ara...	347	8e-94	G
gi 2631995 emb CAA05251.1	phenylalanine ammonia lyase [Dig...	347	8e-94	
gi 1172003 sp P45734 PALY_TRISU	Phenylalanine ammonia-lyase...	347	8e-94	
gi 19650 emb CAA41169.1	phenylalanine ammonia-lyase [Medic...	347	1e-93	
gi 1172002 sp P45732 PALY_STYHU	Phenylalanine ammonia-lyase...	347	1e-93	
gi 15100059 gb AAK84225.1	phenylalanine ammonia-lyase [Reh...	345	2e-93	
gi 535008 emb CAA57057.1	phenylalanine ammonia-lyase 3 [Pe...	344	5e-93	
gi 129585 sp P19142 PAL2_PHAVU	Phenylalanine ammonia-lyase ...	344	6e-93	
gi 58618148 gb AAW80640.1	phenylalanine ammonia lyase [Psi...	343	8e-93	
gi 3024361 sp Q42858 PAL2_IPOBA	Phenylalanine ammonia-lyase...	343	8e-93	
gi 3914262 sp O49836 PAL2_LITER	Phenylalanine ammonia-lyase...	343	8e-93	
gi 18001007 gb AAL55242.1	phenylalanine ammonia-lyase [Lac...	343	1e-92	
gi 28316386 dbj BAC56977.1	phenylalanine ammonia-lyase [Da...	343	1e-92	
gi 12240240 gb AAG49585.1	phenylalanine ammonia-lyase [Ipo...	343	1e-92	
gi 1524313 emb CAA68938.1	PAL1 protein [Petroselinum crisp...	342	2e-92	
gi 58618140 gb AAW80636.1	phenylalanine ammonia lyase [Lyc...	342	2e-92	
gi 1171998 sp P45726 PALY_CAMSI	Phenylalanine ammonia-lyase...	342	2e-92	
gi 50926498 ref XP_473196.1	OSJNBa0073E02.18 [Oryza sativa...	342	2e-92	G
gi 741010 prf 2006271A	Phe ammonia lyase	342	2e-92	
gi 13195320 gb AAK15640.1	phenylalanine ammonia-lyase [Aga...	342	3e-92	
gi 534893 emb CAA57056.1	phenylalanine ammonia-lyase 2 [Pe...	341	4e-92	
gi 24266655 gb AAN52279.1	phenylalanine ammonia-lyase [Pop...	341	4e-92	
gi 50910709 ref XP_466843.1	putative phenylalanine ammonia...	340	7e-92	G
gi 58533149 gb AAW78932.1	phenylalanine-ammonia lyase [Rho...	340	7e-92	
gi 266731 sp Q01861 PAL1_PEA	Phenylalanine ammonia-lyase 1 ...	340	9e-92	
gi 633597 emb CAA55075.1	phenylalanine ammonia-lyase [Nico...	340	1e-91	
gi 6433808 emb CAB60719.1	phenylalanine ammonia-lyase [Cic...	340	1e-91	
gi 3914261 sp O49835 PAL1_LITER	Phenylalanine ammonia-lyase...	340	1e-91	
gi 50910713 ref XP_466845.1	putative phenylalanine ammonia...	339	2e-91	G
gi 34541972 gb AAQ74878.1	phenylalanine ammonia lyase [Pop...	339	2e-91	
gi 39777534 gb AAR31107.1	phenylalanine ammonia-lyase [Que...	339	2e-91	
gi 4808126 emb CAB42793.1	phenylalanine-ammonia lyase [Cit...	338	3e-91	
gi 14486430 gb AAK62030.1	phenylalanine ammonia-lyase 1 [M...	338	3e-91	
gi 129594 sp P25872 PAL1_TOBAC	Phenylalanine ammonia-lyase ...	338	3e-91	
gi 417444 sp Q04593 PAL2_PEA	Phenylalanine ammonia-lyase 2 ...	338	3e-91	
gi 50926490 ref XP_473192.1	OSJNBa0073E02.14 [Oryza sativa...	338	3e-91	G
gi 738926 prf 2001451A	Phe ammonia lyase	337	6e-91	
gi 27436243 gb AAO13347.1	phenylalanine ammonia-lyase2; PA...	337	8e-91	
gi 3334285 sp O23865 PAL1_DAUCA	Phenylalanine ammonia-lyase...	337	8e-91	
gi 24266658 gb AAN52280.1	phenylalanine ammonia-lyase [Pop...	337	1e-90	
gi 50910721 ref XP_466849.1	putative phenylalanine ammonia...	337	1e-90	G
gi 3024360 sp Q42667 PALY_CITLI	Phenylalanine ammonia-lyase...	337	1e-90	
gi 14326457 gb AAK60274.1	phenylalanine ammonia-lyase 1 [M...	336	1e-90	
gi 56409806 emb CAH17686.1	phenylalanine ammonia lyase [Be...	335	2e-90	
gi 129587 sp P26600 PAL5_LYCES	Phenylalanine ammonia-lyase ...	335	2e-90	
gi 400725 sp P31425 PAL1_SOLTU	Phenylalanine ammonia-lyase 1	335	3e-90	
gi 7798554 dbj BAA95629.1	phenylalanine ammonia lyase [Cat...	335	3e-90	
gi 735957 emb CAA53733.1	phenylalanine ammonia-lyase [Cucu...	335	4e-90	
gi 322743 pir A44133	phenylalanine ammonia-lyase (EC 4.3.1...	335	4e-90	
gi 5332353 gb AAA34179.2	phenylalanine ammonia lyase [Lyco...	335	4e-90	
gi 58618156 gb AAW80644.1	phenylalanine ammonia lyase [Pte...	335	4e-90	
gi 1483610 emb CAA68036.1	phenylalanine ammonia-lyase [Tri...	334	5e-90	
gi 58618138 gb AAW80635.1	phenylalanine ammonia lyase [Hup...	334	5e-90	
gi 5566388 gb AAD45384.1	phenylalanine ammonia-lyase [Vign...	333	9e-90	
gi 38103129 gb EAA49872.1	hypothetical protein MG10036.4 [...	333	9e-90	G
gi 29367609 gb AAO72666.1	phenylalanine ammonia-lyase [Ory...	333	9e-90	

gi 400726 sp P31426 PAL2_SOLTU	Phenylalanine ammonia-lyase 2	333	1e-89	
gi 4808128 emb CAB42794.1	phenylalanine-ammonia lyase [Cit...	333	1e-89	
gi 548454 sp P35511 PAL1_LYCES	Phenylalanine ammonia-lyase ...	333	1e-89	
gi 2285893 dbj BAA21643.1	phenylalanine ammonia-lyase [Pop...	333	1e-89	
gi 38569936 gb AAR24505.1	phenylalanine ammonia-lyase [Bam...	332	2e-89	
gi 58618152 gb AAW80642.1	phenylalanine ammonia lyase [Oph...	332	2e-89	
gi 14326459 gb AAK60275.1	phenylalanine ammonia-lyase 2 [M...	332	2e-89	
gi 56966621 pdb 1W27 B	Chain B, Phenylalanine Ammonia-Lyase...	332	3e-89	S
gi 23451809 gb AAN32866.1	phenylalanine ammonia-lyase 1 [C...	332	3e-89	
gi 871494 emb CAA61198.1	phenylalanine ammonia-lyase [Oryz...	331	4e-89	
gi 51594297 gb AAU08174.1	phenylalanine ammonia-lyase [Cam...	331	4e-89	
gi 58618150 gb AAW80641.1	phenylalanine ammonia lyase [Bot...	331	4e-89	
gi 2570156 dbj BAA22963.1	phenylalanine ammonia-lyase [Nic...	331	4e-89	
gi 82496 pir S06475	phenylalanine ammonia-lyase (EC 4.3.1....	331	4e-89	
gi 17467274 gb AAL40137.1	phenylalanine ammonia-lyase [Zea...	331	6e-89	
gi 48869195 gb AAT47186.1	phenylalanine aminomutase [Taxus...	331	6e-89	
gi 58618144 gb AAW80638.1	phenylalanine ammonia lyase [Sel...	331	6e-89	
gi 58618146 gb AAW80639.1	phenylalanine ammonia lyase [Equ...	330	7e-89	
gi 38385686 gb AAR19393.1	phenylalanine ammonia-lyase [Ste...	330	1e-88	
gi 50910715 ref XP_466846.1	putative phenylalanine ammonia...	330	1e-88	G
gi 51341137 gb AAU01183.1	phenylalanine aminomutase [Taxus...	330	1e-88	
gi 50931453 ref XP_475254.1	putative phenylalanine ammonia...	329	2e-88	G
gi 58618142 gb AAW80637.1	phenylalanine ammonia lyase [Iso...	329	2e-88	
gi 51341139 gb AAU01184.1	phenylalanine aminomutase [Taxus...	329	2e-88	
gi 2052094 emb CAA89007.1	phenylalanine ammonia-lyase [Hor...	329	2e-88	
gi 295824 emb CAA34226.1	phenylalanine ammonia-lyase [Oryz...	329	2e-88	
gi 42529530 gb AAS18574.1	phenylalanine ammonia-lyase [Ara...	329	2e-88	
gi 1076371 pir S52992	phenylalanine ammonia-lyase (EC 4.3....	329	2e-88	
gi 14195674 sp P45725 PAL3_ARATH	Phenylalanine ammonia-lyase 3	329	2e-88	
gi 51341141 gb AAU01185.1	phenylalanine aminomutase [Taxus...	328	3e-88	
gi 3334284 sp O04058 PALY_HELAN	Phenylalanine ammonia-lyase...	328	4e-88	
gi 1491619 emb CAA68256.1	phenylalanine ammonia-lyase [Bro...	328	5e-88	
gi 7208614 gb AAF40223.1	phenylalanine ammonia-lyase 1 [Ru...	328	5e-88	
gi 30721857 gb AAP34199.1	phenylalanine ammonia-lyase [Pha...	328	5e-88	
gi 51341135 gb AAU01182.1	phenylalanine aminomutase [Taxus...	327	6e-88	
gi 23451811 gb AAN32867.1	phenylalanine ammonia-lyase 2 [C...	326	2e-87	
gi 11761146 dbj BAB19128.1	phenylalanine ammonia-lyase [Di...	326	2e-87	
gi 58618158 gb AAW80645.1	phenylalanine ammonia lyase [Pel...	325	2e-87	
gi 60459950 gb AAX20146.1	phenylalanine aminomutase [Taxus...	324	5e-87	
gi 1143312 gb AAA84889.1	phenylalanine ammonia-lyase >gi 1...	324	5e-87	
gi 49473532 gb AAT66434.1	phenylalanine ammonia lyase [Pin...	323	9e-87	
gi 9955578 emb CAC05505.1	phenylalanine ammonia-lyase PAL3...	323	1e-86	G
gi 3024362 sp Q43052 PAL2_POPKI	Phenylalanine ammonia-lyase...	322	2e-86	
gi 478740 pir S28185	phenylalanine ammonia-lyase (EC 4.3.1...	322	3e-86	
gi 1172000 sp P45731 PAL1_POPKI	Phenylalanine ammonia-lyase...	322	3e-86	
gi 18539331 gb AAL74336.1	phenylalanine ammonia-lyase [Pin...	321	6e-86	
gi 18539321 gb AAL74331.1	phenylalanine ammonia-lyase [Pin...	320	8e-86	
gi 18539309 gb AAL74325.1	phenylalanine ammonia-lyase [Pin...	320	8e-86	
gi 129589 sp P14166 PAL1_IPOBA	Phenylalanine ammonia-lyase ...	320	1e-85	
gi 129586 sp P19143 PAL3_PHAVU	Phenylalanine ammonia-lyase ...	320	1e-85	
gi 228615 prf 1807329B	Phe ammonia lyase	320	1e-85	
gi 18539313 gb AAL74327.1	phenylalanine ammonia-lyase [Pin...	318	4e-85	
gi 44889624 gb AAS48415.1	phenylalanine lyase [Allium cepa]	317	1e-84	
gi 32491955 gb AAP85251.1	phenylalanine ammonia-lyase [Pin...	313	9e-84	
gi 32491953 gb AAP85250.1	phenylalanine ammonia-lyase [Pin...	312	2e-83	
gi 1220270 emb CAA34715.1	unnamed protein product [Petrose...	310	1e-82	
gi 1171999 sp P45727 PALY_PERAE	Phenylalanine ammonia-lyase...	309	2e-82	
gi 2118318 pir S60043	phenylalanine ammonia-lyase (EC 4.3....	308	5e-82	
gi 58618154 gb AAW80643.1	phenylalanine ammonia lyase [Ble...	300	1e-79	

gi 3024358 sp Q40910 PAL4_POPKI	Phenylalanine ammonia-lyase...	298	4e-79	
gi 18072847 emb CAC81822.1	phenylalanine ammonia-lyase [Be...	280	9e-74	
gi 3513758 gb AAC33966.1	phenylalanine ammonia-lyase [Caps...	269	3e-70	
gi 29424039 gb AAO73468.1	phenylalanine ammonia-lyase [Gin...	266	1e-69	
gi 9965440 gb AAG02280.1	inducible phenylalanine ammonia-l...	266	2e-69	
gi 10732813 gb AAG22550.1	phenylalanine ammonia-lyase 2 [R...	259	2e-67	
gi 10732811 gb AAG22549.1	phenylalanine ammonia-lyase 1 [R...	249	2e-64	
gi 46102036 gb EAK87269.1	hypothetical protein UM06509.1 [...	244	7e-63	
gi 129583 sp P07218 PAL1_PHAVU	Phenylalanine ammonia-lyase ...	238	5e-61	
gi 81875 pir A24727	phenylalanine ammonia-lyase (EC 4.3.1....	236	2e-60	
gi 23123897 ref ZP_00105927.1	COG2986: Histidine ammonia-l...	229	3e-58	
gi 2052090 emb CAA89005.1	phenylalanine ammonia-lyase [Hor...	221	5e-56	
gi 1944573 emb CAA89006.1	phenylalanine ammonia-lyase [Hor...	217	1e-54	
gi 53763481 ref ZP_00158715.2	COG2986: Histidine ammonia-l...	215	3e-54	
gi 46107082 ref ZP_00188602.2	COG2986: Histidine ammonia-l...	209	2e-52	
gi 52009699 ref ZP_00337061.1	COG2986: Histidine ammonia-l...	208	5e-52	
gi 8249014 emb CAB93138.1	phenylalanine ammonia-lyase [Bet...	205	5e-51	
gi 8249041 emb CAB93139.1	phenylalanine ammonia-lyase [Bet...	204	8e-51	
gi 19073338 gb AAL84767.1	phenylalanine ammonia lyase 1 [C...	202	3e-50	
gi 48784800 ref ZP_00281105.1	COG2986: Histidine ammonia-l...	200	1e-49	
gi 56459245 ref YP_154526.1	Histidine ammonia-lyase [Idiom...	200	1e-49	G
gi 60299943 gb AAX18625.1	phenylalanine ammonia-lyase [Ner...	199	2e-49	
gi 81807 pir JQ1070	phenylalanine ammonia-lyase (EC 4.3.1....	199	3e-49	
gi 17548586 ref NP_521926.1	PROBABLE HISTIDINE AMMONIA-LYA...	198	6e-49	G
gi 1345583 emb CAA53581.1	phenylalanine ammonium lyase [Vi...	197	1e-48	
gi 28872212 ref NP_794831.1	histidine ammonia-lyase [Pseud...	197	1e-48	G
gi 60299945 gb AAX18626.1	phenylalanine ammonia-lyase [Pit...	196	2e-48	
gi 24575109 gb AAL06680.1	putative ammonia lyase/transfera...	196	2e-48	
gi 27361857 gb AAO10763.1	Histidine ammonia-lyase [Vibrio ...	195	5e-48	G
gi 37680136 ref NP_934745.1	histidine ammonia-lyase [Vibri...	195	5e-48	G
gi 49364851 gb AAT65681.1	phenylalanine ammonia-lyase [Gin...	194	8e-48	
gi 51246205 ref YP_066089.1	histidine ammonia-lyase [Desul...	194	1e-47	G
gi 37522635 ref NP_926012.1	histidine ammonia-lyase [Gloeo...	193	1e-47	G
gi 9655681 gb AAF94361.1	histidine ammonia-lyase [Vibrio c...	193	2e-47	G
gi 60326352 gb AAX18752.1	phenylalanine ammonia-lyase [Sty...	192	2e-47	
gi 60299941 gb AAX18624.1	phenylalanine ammonia-lyase [Jug...	191	9e-47	
gi 28898047 ref NP_797652.1	histidine ammonia-lyase [Vibri...	190	1e-46	G
gi 46323992 ref ZP_00224354.1	COG2986: Histidine ammonia-l...	189	2e-46	
gi 54301792 ref YP_131785.1	putative histidine ammonia-lya...	189	3e-46	G
gi 56678792 gb AAV95458.1	histidine ammonia-lyase [Silicib...	188	4e-46	G
gi 27359656 gb AAO08595.1	Histidine ammonia-lyase [Vibrio ...	187	8e-46	G
gi 27381353 ref NP_772882.1	histidine ammonia-lyase [Brady...	187	8e-46	G
gi 48787881 ref ZP_00283860.1	COG2986: Histidine ammonia-l...	187	1e-45	
gi 48782814 ref ZP_00279294.1	COG2986: Histidine ammonia-l...	187	1e-45	
gi 6563308 gb AAF17247.1	phenylalanine ammonia lyase [Prun...	187	1e-45	
gi 48732075 ref ZP_00265818.1	COG2986: Histidine ammonia-l...	186	2e-45	
gi 56418920 ref YP_146238.1	histidine ammonia-lyase (histi...	186	2e-45	G
gi 53719954 ref YP_108940.1	histidine ammonia-lyase [Burkh...	186	2e-45	G
gi 37679258 ref NP_933867.1	histidine ammonia-lyase [Vibri...	185	5e-45	G
gi 48770373 ref ZP_00274716.1	COG2986: Histidine ammonia-l...	184	6e-45	
gi 50083810 ref YP_045320.1	histidine ammonia-lyase protei...	184	6e-45	G
gi 53725657 ref YP_102423.1	histidine ammonia-lyase [Burkh...	184	6e-45	G
gi 17937636 ref NP_534425.1	histidine ammonia-lyase [Agrob...	184	6e-45	G

gi 54309352 ref YP_130372.1	putative histidine ammonia-lya...	184	8e-45	G
gi 53762553 ref ZP_00168547.2	COG2986: Histidine ammonia-l...	184	8e-45	
gi 17429668 emb CAD16353.1	PROBABLE HISTIDINE AMMONIA-LYAS...	184	1e-44	G
gi 24211821 sp Q8XW29 HUTH_RALSO	Histidine ammonia-lyase (H...	184	1e-44	
gi 58039620 ref YP_191584.1	Histidine ammonia-lyase [Gluc...	183	1e-44	G
gi 56478698 ref YP_160287.1	histidine ammonia-lyase, predi...	183	2e-44	G
gi 48768557 ref ZP_00272906.1	COG2986: Histidine ammonia-l...	182	3e-44	
gi 15807816 ref NP_285471.1	histidine ammonia-lyase [Deino...	182	3e-44	G
gi 28897663 ref NP_797268.1	putative histidine ammonia-lya...	182	3e-44	G
gi 22959589 ref ZP_00007239.1	COG2986: Histidine ammonia-l...	182	4e-44	
gi 5690433 gb AAD47085.1	phenylalanine ammonia lyase [Euca...	182	4e-44	
gi 10567350 dbj BAB16159.1	rriorf40 [Agrobacterium rhizogen...	181	5e-44	G
gi 56461550 ref YP_156831.1	Histidine ammonia-lyase [Idiom...	181	7e-44	G
gi 34101636 gb AAQ58004.1	histidine ammonia-lyase [Chromob...	181	9e-44	G
gi 37527077 ref NP_930421.1	Histidine ammonia-lyase (histi...	181	9e-44	G
gi 59711459 ref YP_204235.1	histidine ammonia-lyase [Vibri...	181	9e-44	G
gi 23106296 ref ZP_00092750.1	COG2986: Histidine ammonia-l...	181	9e-44	
gi 45916326 ref ZP_00197437.1	COG2986: Histidine ammonia-l...	180	1e-43	
gi 59713633 ref YP_206408.1	histidine ammonia-lyase [Vibri...	180	2e-43	G
gi 62321196 dbj BAD94354.1	phenylalanine ammonia lyase [Ar...	179	2e-43	
gi 46322661 ref ZP_00223029.1	COG2986: Histidine ammonia-l...	179	2e-43	
gi 16264579 ref NP_437371.1	putative histidine ammonia-lya...	179	3e-43	G
gi 46311453 ref ZP_00212059.1	COG2986: Histidine ammonia-l...	179	3e-43	
gi 28872387 ref NP_795006.1	histidine ammonia-lyase [Pseud...	179	4e-43	G
gi 53762102 ref ZP_00350913.1	COG2986: Histidine ammonia-l...	179	4e-43	
gi 51598141 ref YP_072332.1	histidine ammonia-lyase [Yersi...	178	6e-43	G
gi 54032435 ref ZP_00364567.1	COG2986: Histidine ammonia-l...	178	6e-43	
gi 22127907 ref NP_671330.1	putative histidine ammonia-lya...	177	8e-43	G
gi 48782713 ref ZP_00279219.1	COG2986: Histidine ammonia-l...	177	8e-43	
gi 8926197 gb AAF81735.1	putative phenylalanine ammonia ly...	177	1e-42	
gi 24375855 ref NP_719898.1	histidine ammonia-lyase, putat...	176	2e-42	G
gi 52141894 ref YP_084939.1	histidine ammonia-lyase (histi...	176	2e-42	G
gi 49478310 ref YP_037727.1	histidine ammonia-lyase (histi...	176	2e-42	G
gi 47567936 ref ZP_00238643.1	histidine ammonia-lyase [Bac...	176	2e-42	
gi 53795015 ref ZP_00021060.2	COG2986: Histidine ammonia-l...	176	2e-42	
gi 47528996 ref YP_020345.1	histidine ammonia-lyase [Bacil...	176	3e-42	G
gi 16125211 ref NP_419775.1	histidine ammonia-lyase [Caulo...	176	3e-42	G
gi 42782730 ref NP_979977.1	histidine ammonia-lyase [Bacil...	176	3e-42	G
gi 14210836 gb AAK57183.1	putative histidine ammonium lyas...	176	3e-42	
gi 48764895 ref ZP_00269446.1	COG2986: Histidine ammonia-l...	175	4e-42	
gi 16080986 ref NP_391814.1	histidase [Bacillus subtilis s...	175	4e-42	G
gi 20807326 ref NP_622497.1	Histidine ammonia-lyase [Therm...	175	4e-42	G
gi 30021749 ref NP_833380.1	Histidine ammonia-lyase [Bacil...	175	5e-42	G
gi 52841610 ref YP_095409.1	histidine ammonia lyase [Legio...	175	5e-42	G
gi 23471376 ref ZP_00126706.1	COG2986: Histidine ammonia-l...	175	5e-42	
gi 62317244 ref YP_223097.1	Huth, histidine ammonia-lyase ...	174	7e-42	G
gi 28395510 gb AAO39102.1	AdmH [Pantoea agglomerans]	174	9e-42	
gi 34763414 ref ZP_00144363.1	Histidine ammonia-lyase [Fus...	174	9e-42	
gi 54297290 ref YP_123659.1	hypothetical protein lpp1335 [...	174	1e-41	G
gi 1666265 emb CAB04783.1	phenylalanine ammonia-lyase [Aga...	173	1e-41	

gi 15600291 ref NP_253785.1 	histidine ammonia-lyase [Pseud...	172	3e-41	G
gi 54294266 ref YP_126681.1 	hypothetical protein lpl1331 [...	172	3e-41	G
gi 23464302 gb AAN34102.1 	histidine ammonia-lyase [Brucell...	172	3e-41	G
gi 53726619 ref ZP_00141570.2 	COG2986: Histidine ammonia-l...	172	3e-41	
gi 19714334 gb AAL94987.1 	Histidine ammonia-lyase [Fusobac...	172	4e-41	G
gi 48769861 ref ZP_00274205.1 	COG2986: Histidine ammonia-l...	170	1e-40	
gi 24371698 ref NP_715740.1 	histidine ammonia-lyase [Shewa...	170	1e-40	G
gi 19749213 gb AAL98596.1 	putative histidine ammonia-lyase...	170	1e-40	G
gi 20663605 pdb 1GKM A	Chain A, Histidine Ammonia-Lyase (Ha...	170	2e-40	S
gi 26991708 ref NP_747133.1 	histidine ammonia-lyase [Pseud...	169	3e-40	G
gi 9911054 sp P21310 HUTH_PSEPU	Histidine ammonia-lyase (Hi...	169	3e-40	
gi 18138050 emb CAD19072.1 	putative histidine ammonia lyas...	169	4e-40	
gi 13623078 gb AAK34741.1 	putative histidine ammonia-lyase...	168	5e-40	G
gi 20663602 pdb 1GKJ A	Chain A, Histidine Ammonia-Lyase (Ha...	168	5e-40	S
gi 29142511 ref NP_805853.1 	histidine ammonia-lyase [Salmo...	167	8e-40	G
gi 19715060 gb AAL95599.1 	Histidine ammonia-lyase [Fusobac...	167	8e-40	G
gi 49475437 ref YP_033478.1 	Histidine ammonia-lyase [Barto...	167	1e-39	G
gi 28211913 ref NP_782857.1 	histidine ammonia-lyase [Clost...	167	1e-39	G
gi 58582021 ref YP_201037.1 	histidine ammonia-lyase [Xanth...	167	1e-39	G
gi 14194864 sp Q9KBE6 HUTH_BACHD	Histidine ammonia-lyase (H...	167	1e-39	G
gi 20149835 pdb 1GK3 A	Chain A, Histidine Ammonia-Lyase (Ha...	167	1e-39	S
gi 20149798 pdb 1EB4 A	Chain A, Histidine Ammonia-Lyase (Ha...	167	1e-39	S
gi 51894329 ref YP_077020.1 	histidine ammonia-lyase [Symbi...	166	2e-39	G
gi 42526104 ref NP_971202.1 	histidine ammonia-lyase [Trepo...	166	2e-39	G
gi 16419296 gb AAL19728.1 	histidine ammonia lyase [Salmone...	166	2e-39	G
gi 20149834 pdb 1GK2 D	Chain D, Histidine Ammonia-Lyase (Ha...	166	2e-39	S
gi 56965691 ref YP_177425.1 	histidine ammonia-lyase [Bacil...	166	2e-39	G
gi 37526147 ref NP_929491.1 	hypothetical protein plu2234 [...	166	2e-39	G
gi 21107826 gb AAM36505.1 	histidine ammonia-lyase [Xanthom...	166	2e-39	G
gi 3288718 dbj BAA31258.1 	phenylalanine ammonia-lyase [Vit...	166	2e-39	
gi 28896688 ref NP_803038.1 	putative histidine ammonia-lya...	166	3e-39	G
gi 21231033 ref NP_636950.1 	histidine ammonia-lyase [Xanth...	165	4e-39	G
gi 7428403 pir A35251	histidine ammonia-lyase (EC 4.3.1.3)...	165	5e-39	
gi 33328224 gb AAQ09563.1 	phenylalanine ammonia lyase 1 [C...	165	5e-39	
gi 56414107 ref YP_151182.1 	histidine ammonia-lyase [Salmo...	165	5e-39	G
gi 62179359 ref YP_215776.1 	histidine ammonia lyase [Salmo...	165	5e-39	G
gi 28828820 gb AAO51415.1 	similar to Thermoanaerobacter te...	164	7e-39	
gi 49474269 ref YP_032311.1 	Histidine ammonia-lyase [Barto...	163	2e-38	G
gi 57546260 gb AAW51924.1 	phenylalanine ammonia-lyase [Rhi...	163	2e-38	
gi 13476871 ref NP_108440.1 	histidine ammonia-lyase hutH [...	162	4e-38	G
gi 2642329 gb AAB86963.1 	histidine ammonia-lyase [Sinorhiz...	161	6e-38	
gi 1483612 emb CAA68064.1 	phenylalanine ammonia-lyase [Tri...	160	1e-37	
gi 54032321 ref ZP_00364453.1 	COG2986: Histidine ammonia-l...	159	3e-37	
gi 50915120 ref YP_061092.1 	Histidine ammonia-lyase [Strep...	159	4e-37	G
gi 42524166 ref NP_969546.1 	hypothetical protein Bd2753 [B...	158	6e-37	G
gi 54023195 ref YP_117437.1 	putative histidine ammonia-lya...	158	6e-37	G
gi 16209615 gb AAL14120.1 	phenylalanine ammonia-lyase [Bra...	157	1e-36	
gi 50843607 ref YP_056834.1 	histidine ammonia-lyase [Propi...	156	2e-36	G
gi 22759717 dbj BAC10907.1 	phenylalanine ammonia-lyase 1 [...	154	7e-36	

gi 12407611 gb AAG53586.1	histidine ammonia-lyase-like pro...	154	7e-36	
gi 98963 pir JC1172	histidine ammonia-lyase (EC 4.3.1.3) [...	154	9e-36	
gi 14195667 sp P24221 HUTH_STRGR	Histidine ammonia-lyase (H...	154	9e-36	
gi 16554490 ref NP_444214.1	Histidine ammonia-lyase [Halob...	153	2e-35	G
gi 14194856 sp Q9HQD5 HUTH_HALN1	Probable histidine ammonia...	153	2e-35	
gi 48856699 ref ZP_00310856.1	COG2986: Histidine ammonia-l...	153	2e-35	
gi 14245775 dbj BAB56170.1	histidine ammonia-lyase [Staphy...	153	2e-35	G
gi 54037326 sp P64416 HUTH_STAAN	Histidine ammonia-lyase (H...	153	2e-35	
gi 13542184 ref NP_111872.1	Histidine ammonia-lyase [Therm...	152	3e-35	G
gi 16081388 ref NP_393722.1	probable histidine ammonia-lya...	152	4e-35	G
gi 57651116 ref YP_184919.1	histidine ammonia-lyase [Staph...	152	4e-35	G
gi 9367317 emb CAB97358.1	phenylalanine ammonia-lyase [Jug...	152	4e-35	
gi 49243363 emb CAG41780.1	putative histidine ammonia-lyas...	152	4e-35	G
gi 29606976 dbj BAC71036.1	putative histidine ammonia-lyas...	152	5e-35	G
gi 49482261 ref YP_039485.1	putative histidine ammonia-lya...	151	6e-35	G
gi 46193106 ref ZP_00005404.2	COG2986: Histidine ammonia-l...	150	1e-34	
gi 52694880 gb AAU85591.1	phenylalanine ammonia-lyase [Ole...	150	1e-34	
gi 21223306 ref NP_629085.1	histidine ammonia-lyase [Strep...	150	1e-34	G
gi 53715428 ref YP_101420.1	histidine ammonia-lyase [Bacte...	150	2e-34	G
gi 56112437 gb AAV71173.1	phenylalanine ammonia-lyase [Lot...	149	4e-34	
gi 28192468 gb AAM77981.1	aminotransferase [Streptomyces c...	149	4e-34	
gi 29340002 gb AAO77796.1	histidine ammonia-lyase [Bactero...	148	7e-34	G
gi 62424523 ref ZP_00379668.1	COG2986: Histidine ammonia-l...	146	3e-33	
gi 1262908 gb AAA96823.1	phenylalanine amonia-lyase	145	3e-33	
gi 49614765 dbj BAD26880.1	phenylalanine ammonia-lyase [Ph...	144	7e-33	
gi 33347403 gb AAQ15284.1	phenylalanine ammonia-lyase [Pyr...	144	1e-32	
gi 3643117 gb AAC36706.1	phenylalanine ammonia-lyase [Mani...	144	1e-32	
gi 48477179 ref YP_022885.1	histidine ammonia-lyase [Picro...	143	2e-32	G
gi 45383354 ref NP_989735.1	histidine ammonia lyase [Gallu...	142	4e-32	G
gi 28804480 dbj BAC58034.1	phenylalanine ammonia lyase [Ra...	141	6e-32	
gi 23335983 ref ZP_00121213.1	COG2986: Histidine ammonia-l...	141	6e-32	
gi 23465811 ref NP_696414.1	histidine ammonia-lyase [Bifid...	141	6e-32	G
gi 31414583 dbj BAC77270.1	phenylalanine ammonia-lyase [As...	140	1e-31	
gi 4504333 ref NP_002099.1	histidine ammonia-lyase [Homo s...	139	4e-31	G
gi 14588661 dbj BAB61863.1	histidase [Homo sapiens]	138	5e-31	G
gi 10580744 gb AAG19580.1	histidine ammonia-lyase; HutH [H...	138	7e-31	
gi 34396472 gb AAQ65538.1	histidine ammonia-lyase [Porphyr...	137	2e-30	G
gi 49903474 gb AAH76901.1	Histidine ammonia-lyase [Xenopus...	136	2e-30	G
gi 49256070 gb AAH74146.1	MGC81887 protein [Xenopus laevis]	136	2e-30	G
gi 48852611 ref ZP_00306796.1	COG2986: Histidine ammonia-l...	136	3e-30	
gi 60465347 gb EAL63438.1	hypothetical protein DDB0187742 ...	135	4e-30	
gi 16409 emb CAA44609.1	phenylalanine ammonia-lyase [Arabi...	134	1e-29	
gi 8393522 ref NP_058855.1	histidine ammonia lyase [Rattus...	134	1e-29	G
gi 55231264 gb AAV46683.1	histidine ammonia-lyase [Haloarc...	134	1e-29	G
gi 35505393 gb AAH57637.1	Hal protein [Mus musculus] >gi 6...	133	2e-29	G
gi 26324922 dbj BAC26215.1	unnamed protein product [Mus mu...	133	2e-29	G
gi 6746619 gb AAF27654.1	phenylalanine ammonia lyase [Coff...	133	2e-29	
gi 14326455 gb AAK60273.1	phenylalanine ammonia-lyase 3 [M...	131	6e-29	
gi 39594932 emb CAE70800.1	Hypothetical protein CBG17560 [...	129	4e-28	
gi 47224446 emb CAG08696.1	unnamed protein product [Tetrao...	128	7e-28	
gi 3877284 emb CAA91982.1	Hypothetical protein F47B10.2 [C...	126	3e-27	G
gi 6746621 gb AAF27655.1	phenylalanine ammonia lyase [Coff...	126	3e-27	

gi 57096783 ref XP_532657.1	PREDICTED: similar to histidas...	125	4e-27	G
gi 29691921 emb CAD88242.1	phenylalanine ammonium lyase [M...	125	4e-27	
gi 50603600 gb AAH77229.1	Hal-prov protein [Xenopus laevis]	125	6e-27	G
gi 13471681 ref NP_103248.1	histidine ammonia-lyase [Mesor...	124	1e-26	G
gi 15600286 ref NP_253780.1	probable histidine/phenylalani...	120	1e-25	G
gi 23471377 ref ZP_00126707.1	COG2986: Histidine ammonia-l...	119	4e-25	
gi 28872386 ref NP_795005.1	histidine ammonia-lyase [Pseud...	118	7e-25	G
gi 45916321 ref ZP_00197436.1	COG2986: Histidine ammonia-l...	117	1e-24	
gi 45916111 ref ZP_00197348.1	COG2986: Histidine ammonia-l...	116	2e-24	
gi 2352953 gb AAC50006.1	phenylalanine ammonia-lyase; PAL ...	115	4e-24	
gi 12656140 gb AAK00762.1	phenylalanine ammonia-lyase [Bra...	115	5e-24	
gi 12656136 gb AAK00760.1	phenylalanine ammonia-lyase [Bra...	115	5e-24	
gi 54032324 ref ZP_00364456.1	COG2986: Histidine ammonia-l...	115	6e-24	
gi 12656138 gb AAK00761.1	phenylalanine ammonia-lyase [Bra...	114	8e-24	
gi 2352959 gb AAC50009.1	phenylalanine ammonia-lyase; PAL ...	114	8e-24	
gi 17988713 ref NP_541346.1	IMIDAZOLONEPROPIONASE / HISTID...	114	1e-23	G
gi 2352957 gb AAC50008.1	phenylalanine ammonia-lyase; PAL ...	114	1e-23	
gi 2352955 gb AAC50007.1	phenylalanine ammonia-lyase; PAL ...	113	2e-23	
gi 2352951 gb AAC50005.1	phenylalanine ammonia-lyase; PAL ...	110	1e-22	
gi 16262618 ref NP_435411.1	putative histidine ammonia-lya...	109	3e-22	G
gi 38453641 emb CAD12637.1	phenylalanine ammonia-lyase [Al...	109	3e-22	
gi 13475933 ref NP_107503.1	histidine ammonia-lyase [Mesor...	108	5e-22	G
gi 21401571 ref NP_657556.1	PAL, Phenylalanine and histidi...	107	1e-21	G
gi 61864993 ref XP_598249.1	PREDICTED: similar to histidas...	107	2e-21	G
gi 25044813 gb AAM28276.1	phenylalanine ammonia-lyase [Ana...	106	2e-21	
gi 17937508 ref NP_534297.1	histidase [Agrobacterium tumef...	105	7e-21	G
gi 2765336 emb CAA73908.1	phenylalanine ammonia-lyase [Pic...	101	7e-20	
gi 55638677 ref XP_509282.1	PREDICTED: histidine ammonia-l...	101	9e-20	G
gi 13470444 ref NP_102012.1	histidine ammonia-lyase [Mesor...	100	2e-19	G
gi 29607157 dbj BAC71216.1	putative histidine ammonia-lyas...	99	5e-19	G
gi 28875457 gb AAO59945.1	HutH [uncultured bacterium]	98	8e-19	
gi 46324439 ref ZP_00224800.1	COG2986: Histidine ammonia-l...	98	1e-18	
gi 50955715 ref YP_063003.1	histidine ammonia-lyase [Leifs...	97	2e-18	G
gi 55821316 ref YP_139758.1	histidine ammonia-lyase [Strep...	97	2e-18	G
gi 55823228 ref YP_141669.1	histidine ammonia-lyase [Strep...	96	4e-18	G
gi 15075727 emb CAC47282.1	PUTATIVE HISTIDINE AMMONIA-LYAS...	96	5e-18	G
gi 51471866 gb AAU04403.1	phenylalanine-ammonia lyase [Cit...	95	7e-18	
gi 53719300 ref YP_108286.1	putative exported histidine am...	93	3e-17	G
gi 8650114 gb AAF78100.1	histidase [Sinorhizobium meliloti]	93	3e-17	
gi 54028766 ref ZP_00360912.1	COG2986: Histidine ammonia-l...	92	4e-17	
gi 46317515 ref ZP_00218093.1	COG2986: Histidine ammonia-l...	89	6e-16	
gi 48781751 ref ZP_00278333.1	COG2986: Histidine ammonia-l...	88	8e-16	
gi 1279515 emb CAA65978.1	phenylalanine ammonia-lyase [Hor...	87	1e-15	
gi 45916394 ref ZP_00195295.2	COG2986: Histidine ammonia-l...	83	3e-14	
gi 24374810 ref NP_718853.1	Pal/histidase family protein [...	81	1e-13	G
gi 21401570 ref NP_657555.1	PAL, Phenylalanine and histidi...	79	5e-13	G
gi 46911553 emb CAG27616.1	putative phenylalanine ammonia-...	79	5e-13	
gi 19904 emb CAA42497.1	phenylalanine ammonia-lyase [Nicot...	77	1e-12	
gi 510951 emb CAA53676.1	phenylalanine ammonia-lyase [Betu...	75	6e-12	
gi 853934 emb CAA86221.1	phenylalanine [Gerbera hybrid cul...	75	9e-12	
gi 45916390 ref ZP_00195291.2	COG2986: Histidine ammonia-l...	74	2e-11	
gi 23006774 ref ZP_00048941.1	COG2986: Histidine ammonia-l...	69	5e-10	
gi 17988712 ref NP_541345.1	HISTIDINE AMMONIA-LYASE [Bruce...	69	7e-10	G

gi 24250893 gb AAM96897.1	phenylalanine ammonia-lyase [Vac...	68	9e-10	
gi 24374579 ref NP_718622.1	Pal/histidase family protein [...	67	3e-09	G
gi 53690243 ref ZP_00121972.2	COG2986: Histidine ammonia-l...	66	3e-09	
gi 50978426 emb CAH10748.1	phenylalanine ammonia-lyase [Ca...	65	1e-08	
gi 14334230 gb AAK59810.1	phenylalanine ammonia lyase B [Lo...	62	6e-08	
gi 19652 emb CAA48231.1	phenylalanine ammonia-lyase [Malus...	61	1e-07	
gi 14334225 gb AAK59808.1	phenylalanine ammonia lyase A [L...	61	1e-07	
gi 100234 pir S20005	phenylalanine ammonia-lyase (EC 4.3.1...	57	3e-06	
gi 38322954 emb CAE54485.1	unnamed protein product [Pinus ...	55	6e-06	
gi 2462079 emb CAA59217.1	phenylalanine ammonia-lyase [Ara...	49	4e-04	
gi 14334224 gb AAK59807.1	phenylalanine ammonia lyase A [L...	47	0.002	
gi 2251083 dbj BAA21326.1	phenylalanine ammonia-lyase [Zin...	45	0.006	
gi 14334229 gb AAK59809.1	phenylalanine ammonia lyase B [Lo...	45	0.010	
gi 20452 emb CAA33500.1	unnamed protein product [Petroseli...	44	0.014	
gi 21499 emb CAA44818.1	phenylalanine ammonia-lyase [Solan...	40	0.20	
gi 60466744 gb EAL64793.1	hypothetical protein DDB0186415 ...	39	0.75	
gi 21497 emb CAA44817.1	phenylalanine ammonia-lyase [Solan...	38	1.3	
gi 56468325 gb EAL46185.1	hypothetical protein 158.t00015 ...	37	2.2	
gi 33594922 ref NP_882565.1	hypothetical protein BPP0204 [...	35	6.3	G
gi 15599877 ref NP_253371.1	hypothetical protein PA4682 [P...	35	6.3	G
gi 16125172 ref NP_419736.1	hypothetical protein CC0920 [C...	35	6.3	G
gi 49087370 gb AAT51452.1	PA4682 [synthetic construct]	35	6.3	
gi 46165104 ref ZP_00138243.2	COG2931: RTX toxins and rela...	35	6.3	

Alignments

Get selected sequences

Select all

Deselect all

☐ >gi|3294|emb|CAA35886.1| phenylalanine ammonia-lyase [Rhodosporidium toruloides]
gi|288351|emb|CAA31209.1| L-phenylalanine ammonia-lyase [Rhodosporidium toruloide
gi|129593|sp|P11544|PALY_RHOTO Phenylalanine ammonia-lyase
Length = 716

Score = 915 bits (2365), Expect = 0.0

Identities = 482/725 (66%), Positives = 563/725 (77%), Gaps = 14/725 (1%)

Query: 1 MAPSLDSLATTLANGFTNGSHAAPTKSAAGPTSALRRTPGLDGHAHQSQLEIVQELLSD 60
MAPSLDS++ + ANG A K A S G +Q++IV+++L+

Sbjct: 1 MAPSLDSISHSFANG-----VASAKQAVNGASTNLAVAGSHLPTTQVTQVDIVEKMLAA 54

Query: 61 PTDDVVELSGYSLTXXXXXXXXXXXXXXXXXQNDDEIRARVDKSVDLKAQLQNSVYGVTT 120
PTD +EL GYSL ++ DEIR+++DKSV+FL++QL SVYGVTT

Sbjct: 55 PTDDSTLELDGYSLNLGDVVSAAKGRPVVRKDSDEIRSKIDKSVEFLRSQLSMSVYGVTT 114

Query: 121 GFSGSADTRTEDAVSLQKALIEHQLCGVTPTSVSSFSVGRGLENLPLEVVRGAMVIRVN 180
GFSGSADTRTEDA+SLQKAL+EHQLCGV P+S SF +GRGLEN+LPLEVVRGAM IRVN

Sbjct: 115 GFSGSADTRTEDAISLQKALLEHQLCGVLPSSFDSFRLGRGLENSLPLEVVRGAMTIRVN 174

Query: 181 SLTRGHSVRLVLEALTNFLNHRITPIVPLRGSSISASGDLSPLSYIAGAITGHPDVKVH 240
SLTRGHSVRLVLEALTNFLNH ITPVPLRG+ISASGDLSPLSYIA AI+GHPD KVH

Sbjct: 175 SLTRGHSVRLVLEALTNFLNHGITPIVPLRG+ISASGDLSPLSYIAAIAISGHPDSKVH 234

Query: 241 VLHEGTEKIMFAEAI SLFGLEAVVLGPKEGLGLVNGTAVSASMATXXXXXXXXXXXXXXXXX 300
V+HEG EKI++AREA++LF LE VVLGPKEGLGLVNGTAVSASMAT

Sbjct: 235 VVHEGKEKILYAREAMALFNLEPVVLGPKEGLGLVNGTAVSASMATLALHDAHMLSLLSQ 294

Query: 301 XXXXXXVEAMVGQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGSSFAXXXXXXXXXXXXXX 360
 VEAMVG GSF PF+HDV RPHP Q+EVA NIR LL GS FA

Sbjct: 295 SLTAMTVEAMVGHAGSFHPFLHDVTRPHPTQIEVAGNIRKLLLEGSRFAVHHEEEVKVKDD 354

Query: 361 XGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLE-NNTTTDNPLLDVENKQTAHGGNFQ 419
 GILRQDRYPLRTSPQ+LGPLV D++HA++ L++E +TTDNPL+DVENK + HGGNFQ

Sbjct: 355 EGILRQDRYPLRTSPQWLGPLVSDLIHAHAVLTIEAGQSTTDNPLIDVENKTSHHGGNFQ 414

Query: 420 ASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCLAEDPSLNYHGKGLDIHI 479
 A+AV+ +MEKTRL LA IGKLNFTQ TE+LNA MNRGLPSCLAEDPSL+YH KGLDI

Sbjct: 415 AAAVANTMEKTRLGLAQIGKLNFTQLTEMLNAGMNRGLPSCLAEDPSLSYHCKGLDIAA 474

Query: 480 AAYASELGHLANPVTTFVQPAEMGNQAVNSLALISARRTAEANDVLSLLLASHLYCTLQA 539
 AAY SELGHLANPVT VQPAEM NQAVNSLALISARRT E+NDVLSLLLA+HLYC LQA

Sbjct: 475 AAYTSELGHLANPVTTHVQPAEMANQAVNSLALISARRTTESNDVLSLLLAATHLYCVLQA 534

Query: 540 VDLRAMELDFKKQFDPLLPTLLQQHLG---TGLDV-NALALEVKKALNKRLEQTTTYDLE 595
 +DLRA+E +FKKQF P + +L+ QH G TG ++ + L +V K L KRLEQT +YDL

Sbjct: 535 IDLRAIEFEFKKQFGPAIVSLIDQHFGSAMTGSNLRDELVEKVNKTAKRLEQTNSYDLV 594

Query: 596 PRWHDAFSYATGTVVELLSSSPSANVTLTAVNAWKVASAEKAISLTREVRNRFWQTPSSQ 655
 PRWHDAFS+A GTVVE+LSS+ +++L AVNAWKVA+AE AISLTR+VR FW S+

Sbjct: 595 PRWHDAFSFAAGTVVEVLSST---SLSLAAVNAWKVAAAESAISLTRQVRETFWSAASTS 651

Query: 656 APAHAYLSPRTRVLYSFVREELGVQARRGDVFGVQVQETIGSNVSRIYEAIKDGRINHL 715
 +PA +YLSPT++LY+FVREELGV+ARRGDVFG Q+ TIGSNVS+IYEAIK GRIN+VL

Sbjct: 652 SPALSYLSPTQILYAFVREELGVKARRGDVFLGKQEVETIGSNVSKIYEAIKSGRINNVL 711

Query: 716 VKMLA 720
 +KMLA

Sbjct: 712 LKMLA 716

☐ >gi|169746|gb|AAA33883.1| phenylalanine ammonia-lyase
 Length = 693

Score = 901 bits (2328), Expect = 0.0

Identities = 467/677 (68%), Positives = 545/677 (80%), Gaps = 8/677 (1%)

Query: 49 SQLEIVQELLSIPTDDVELSGYSLTXXXXXXXXXXXXXXXXXQNDDEIRARVDKSVDFLK 108
 +Q++IV+++L+ PTD +EL GYSL ++ DEIR+++DKSV+FL+

Sbjct: 20 TQVDIVEKMLAAPTDSTLELDGYSLNLGDVVSAAKGRPVVRVKDSDEIRSKIDKSVEFLR 79

Query: 109 AQLQNSVYGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPPTSVSFSVGRGLENLPL 168
 +QL SVYGVTTGFGGSADTRTEDA+SLQKAL+EHQLCGV P+S SF +GRGLEN+LPL

Sbjct: 80 SQLSMSVYGVTTGFGGSADTRTEDAISLQKALLEHQLCGVLPSSFDSFRLGRGLENSLPL 139

Query: 169 EVVRGAMVIRVNSLTRGHSVRLVLEALTNFLNHRITPIVPLRGSISASGDLSPLSYIA 228
 EVVRGAM IRVNSLTRGHSVRLVLEALTNFLNHRITPIVPLRG+ISASGDLSPLSYIA

Sbjct: 140 EVVRGAMTIRVNSLTRGHSVRLVLEALTNFLNHGITPIVPLRGTISASGDLSPLSYIA 199

Query: 229 GAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEAVVLGPKEGLGLVNGTAVSASMATXX 288
 AI+GHPD KVVH+HEG EKI++AREA++LF LE VVLGPKEGLGLVNGTAVSASMAT

Sbjct: 200 AAISGHPDSKVHVHVEGKEKILYAREAMALFNLEPVVLGPKEGLGLVNGTAVSASMATLA 259

Query: 289 XXXXXXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGSSFA 348
 VEAMVG GSF PF+HDV RPHP Q+EVA NIR LL GS FA

Sbjct: 260 LHDHMLSLLSQSLTAMTVEAMVGHAGSFHPFLHDVTRPHPTQIEVAGNIRKLLLEGSRFA 319

Query: 349 XXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLE-NNTTTDNPLLDV 407
 GILRQDRYPLRTSPQ+LGPLV D++HA++ L++E +TTDNPL+DV
 Sbjct: 320 VHHEEEVKVKDDEGILRQDRYPLRTSPQWLGPLVSDLIHAHAVLTIEAGQSTTDNPLIDV 379

Query: 408 ENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCLAEDPS 467
 ENK + HGGNFQA+AV+ +MEKTRL LA IGKLNFTQ TE+LNA MNRGLPSCLAEDPS
 Sbjct: 380 ENKTSHHGGNFQAAAVANTMEKTRLGLAQIGKLNFTQLTEMLNAGMNRGLPSCLAEDPS 439

Query: 468 LNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVNSLALISARRTAEANDVLSL 527
 L+YH KGLDI AAY SELGHLANPVTT VQPAEM NQAVNSLALISARRT E+NDVLSL
 Sbjct: 440 LSYHCKGLDIAAAAYTSELGHLANPVTHVQPAEMANQAVNSLALISARRTTESNDVLSL 499

Query: 528 LLASHLYCTLQAVDLRAMELDFKKQFDPDLLPTLLQQHLG---TGLDV-NALALEVKKALN 583
 LLA+HLYC LQA+DLRA+E +FKKQF P + +L+ QH G TG ++ + L +V K L
 Sbjct: 500 LLATHLYCVLQAIDLRAIEFEFKKQFGPAIVSLIDQHFGSAMTGSNLRDELVEKVNKTLA 559

Query: 584 KRLEQTTTYDLEPRWHDFAFSYATGTVVELLSSSPSANVTLTAVNAWKVASAEKAISLTRE 643
 KRLEQT +YDL PRWHDFAFS+A GTVVE+LSS+ +++L AVNAWKVA+AE AISLTR+
 Sbjct: 560 KRLEQTNSYDLVPRWHDFAFSFAAGTVVEVLSST---SLSLAAVNAWKVAAAESAISLTRQ 616

Query: 644 VRNRFWQTPSSQAPAHAYLSPRTRVLYSFVREELGVQARRGDVFGVGVQETIGSNVSRiy 703
 VR FW S+ +PA +YLSPT++LY+FVREELGV+ARRGDVF+G Q+ TIGSNVS+iy
 Sbjct: 617 VRETFWSAASTSSPALSYLSPRTQILYAFVREELGVKARRGDVFLGKQEVITIGSNVSKIY 676

Query: 704 EAIKDGRINHVLVKMLA 720
 EAIK GRIN+VL+KMLA
 Sbjct: 677 EAIKSGRINNVLKMLA 693

☐ >gi|225818|prf||1314202A Phe ammonia lyase
 Length = 705

Score = 888 bits (2294), Expect = 0.0

Identities = 467/689 (67%), Positives = 545/689 (79%), Gaps = 20/689 (2%)

Query: 49 SQLEIVQELLSDPTDDVVELSGYSLTXXXXXXXXXXXXXXXXXQNDDEIRARVDKSVDFLK 108
 +Q++IV+++L+ PTD +EL GYSL ++ DEIR+++DKSV+FL+
 Sbjct: 20 TQVDIVEKMLAAPTDSTLELDGYSLNLGDVVSAAARKGRPVRVKDSDEIRSKIDKSVEFLR 79

Query: 109 AQLQNSVYGVTTFGFGGSADTRTEDAVSLQKALIEHQ-----LCGVTPTSVSSFSVGR 160
 +QL SVYGVTTFGFGGSADTRTEDA+SLQKAL+EHQ LCGV P+S SF +GR
 Sbjct: 80 SQLSMSVYGVTTFGFGGSADTRTEDAISLQKALLEHQDAISLQKALCGVLPSSFDSFRLGR 139

Query: 161 GLENTLPLEVVRGAMVIRVNSLTRGHSAVRLVVLEALTNFLNHRITPIVPLRGSISASGD 220
 GLEN+LPLEVVRGAM IRVNSLTRGHSAVRLVVLEALTNFLNH ITPIVPLRG+ISASGD
 Sbjct: 140 GLENSLPLEVVRGAMTIRVNSLTRGHSAVRLVVLEALTNFLNHGITPIVPLRG+ISASGD 199

Query: 221 LSPLSYIAGAITGHPDVKVHVLHEGTEKIMFAREAI SLFGLEAVVLGPKEGLGLVNGTAV 280
 LSPLSYIA AI+GHPD KVHV+HEG EKI++AREA++LF LE VVLGPKEGLGLVNGTAV
 Sbjct: 200 LSPLSYIAAAISGHPDSKVHVHEGKEKILYAREAMALFNLEPVVLGPKEGLGLVNGTAV 259

Query: 281 SASMATXXXXXXXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQVEVARNIRT 340
 SASMAT VEAMVG GSF PF+HDV RPHP Q+EVA NIR
 Sbjct: 260 SASMATLALHDAHMLSLLSQSLTAMTVEAMVGHAGSFHPFLHDVTRPHPTQIEVAGNIRK 319

Query: 341 LLSGSSFAXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLE-NNTT 399
 LL GS FA GILRQDRYPLRTSPQ+LGPLV D++HA++ L++E +T
 Sbjct: 320 LLEGSFVAVHHEEEVKVKDDEGILRQDRYPLRTSPQWLGPLVSDLIHAHAVLTIEAGQST 379

Query: 400 TDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPS 459
 TDNPL+DVENK + HGGNFQA+AV+ +MEKTRL LA IGKLNFTQ TE+LNA MNRGLPS
 Sbjct: 380 TDNPLIDVENKTSHHGGNFQAAAVANTMEKTRLGLAQIGKLNFTQLTEMLNAGMNRGLPS 439

Query: 460 CLAAEDPSLNYHGKGLDIHIAAYASELGHL----ANPVTTFVQPAEMGNQAVNSLALISA 515
 CLAAEDPSL+YH KGLDI AAY SELGHL ANPVTT VQPAEM NQAVNSLALISA
 Sbjct: 440 CLAAEDPSLSYHCKGLDIAAAAYTSELGHLLNFTANPVTTHVQPAEMANQAVNSLALISA 499

Query: 516 RRTAEANDVLSLLLASHLYCTLQAVDLRAMELDFKKQFDPLLPTLLQQHLG---TGLDV- 571
 RRT E+NDVLSLLLA+HLYC LQA+DLRA+E +FKKQF P + +L+ QH G TG ++
 Sbjct: 500 RRTTESNDVLSLLLATHLYCQLQAI DLRAIEFEFKKQFGPAIVSLIDQHFGSAMTGSNLR 559

Query: 572 NALALEVKKALNKRLEQTTTYDLEPRWHDASFYATGTVVELLSSSPSANVTLTAVNAWKV 631
 + L +V K L KRLEQT +YDL PRWHDASF+A GTVVE+LSS+ +++L AVNAWKV
 Sbjct: 560 DELVEKVNKTLAKRLEQTNSYDLVPRWHDASFSAAGTVVEVLSST---SLSLAAVNAWKV 616

Query: 632 ASAEKAISLTREVRNRFWQTPSSQAPAHAYLSPRTRVLYSFVREELGVQARRGDVFGVQ 691
 A+AE AISLTR+VR FW S+ +PA +YLSPT++LY+FVREELGV+ARRGDVF+G Q
 Sbjct: 617 AAAESAISLTRQVRETFWSSAASTSSPALSYLSPRTQILYAFVREELGVKARRGDVFLGKQ 676

Query: 692 QETIGSNVSRIYEAIAKGRINHVLVKMLA 720
 + TIGSNVS+IYEAIAK GRIN+VL+KMLA
 Sbjct: 677 EVTIGSNVSKIYEAIAKSGRINNVLKMLA 705

☐ >gi|56553841|pdb|1T6P|H **S** Chain H, Crystal Structure Of Phenylalanine Ammonia Ly
 Rhodosporidium Toruloides

gi|56553840|pdb|1T6P|G **S** Chain G, Crystal Structure Of Phenylalanine Ammonia Lyas
 Rhodosporidium Toruloides

gi|56553839|pdb|1T6P|F **S** Chain F, Crystal Structure Of Phenylalanine Ammonia Lyas
 Rhodosporidium Toruloides

gi|56553838|pdb|1T6P|E **S** Chain E, Crystal Structure Of Phenylalanine Ammonia Lyas
 Rhodosporidium Toruloides

gi|56553837|pdb|1T6P|D **S** Chain D, Crystal Structure Of Phenylalanine Ammonia Lyas
 Rhodosporidium Toruloides

gi|56553836|pdb|1T6P|C **S** Chain C, Crystal Structure Of Phenylalanine Ammonia Lyas
 Rhodosporidium Toruloides

gi|56553835|pdb|1T6P|B **S** Chain B, Crystal Structure Of Phenylalanine Ammonia Lyas
 Rhodosporidium Toruloides

gi|56553834|pdb|1T6P|A **S** Chain A, Crystal Structure Of Phenylalanine Ammonia Lyas
 Rhodosporidium Toruloides

gi|56553832|pdb|1T6J|B **S** Chain B, Crystal Structure Of Phenylalanine Ammonia Lyas
 Rhodosporidium Toruloides

gi|56553831|pdb|1T6J|A **S** Chain A, Crystal Structure Of Phenylalanine Ammonia Lyas
 Rhodosporidium Toruloides
 Length = 714

Score = 884 bits (2284), Expect = 0.0

Identities = 473/724 (65%), Positives = 551/724 (76%), Gaps = 16/724 (2%)

Query: 2 APSLDSLATTLANGFTNGSHAAPT KSAAGPTSALRRTPGLDGHAHQSQLEIVQELSDP 61
 APSLDS++ + ANG A K A S G +Q++IV++ L+ P
 Sbjct: 2 APSLDSISHSFANG-----VASAKQAVNGASTNLAVAGSHLPTTQVTQVDIVEKXLAAP 55

Query: 62 TDDVVELSGYSLTXXXXXXXXXXXXXXXXXQNDDEIRARVDKSVDFLKAQLQNSVYGVTTG 121

TD +EL GYSL ++ DEIR+++DKSV+FL++QL SVYGVTTG
 Sbjct: 56 TDSTLELDGYSLNLGDVVSAAARKGRPVRVKDSDEIRSKIDKSVEFLRSQLSXSVYGVTTG 115
 Query: 122 FGGSADTRTEDAVSLQKALIEHQLCGVTPTSVSSFSVGRGLENLPLEVVRGAMVIRVNS 181
 FGGSADTRTEDA+SLQKAL+EHQLCGV P+S SF +GRGLEN+LPLEVVRGA IRVNS
 Sbjct: 116 FGGSADTRTEDAISLQKALLEHQLCGVLPSSFDSFRLGRGLENSLPLEVVRGAXTIRVNS 175
 Query: 182 LTRGHSAVRLVVLEALTNFLNHRITPIVPLRGSISASGDLSPLSYIAGAITGHPDVKVHV 241
 LTRGHSAVRLVVLEALTNFLNH ITPIVPLRG+IS DLSPLSYIA AI+GHPD KVHV
 Sbjct: 176 LTRGHSAVRLVVLEALTNFLNHGITPIVPLRGITISX--DLSPLSYIAAAISGHPDSKVHV 233
 Query: 242 LHEGTEKIMFAREAISLFGLEAVLGPKEGLGLVNGTAVSASMATXXXXXXXXXXXXXXXXX 301
 +HEG EKI++AREA +LF LE VVLGPKEGLGLVNGTAVSAS AT
 Sbjct: 234 VHEGKEKILYAREAXALFNLEPVVLPKEGLGLVNGTAVSASXATLALHDAHXLILLSQS 293
 Query: 302 XXXXXVEAMVGQQGSFAPFIHDVCRPHPGQVEVARNIRTLTSGSSFAXXXXXXXXXXXXXXXXX 361
 VEA VG GSF PF+HDV RPHP Q+EVA NIR LL GS FA
 Sbjct: 294 LTAXTVEAXVGHAGSFHPFLHDVTRPHPTQIEVAGNIRKLLGSRFAVHHEEEVKVKDDE 353
 Query: 362 GILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLE-NNTTTDNPLLDVENKQTAHGGNFQA 420
 GILRQDRYPLRTSPQ+LGPLV D++HA++ L++E +TTDNPL+DVENK + HGGNFQA
 Sbjct: 354 GILRQDRYPLRTSPQWLGPLVSDLIHAHAVLTIEAGQSTTDNPLIDVENKTSHHGGNFQA 413
 Query: 421 SAVSISMEKTRLALALIGKLNFTQCTELNNAAMNRGLPSCLAEDPSLNYHGKGLDIIHA 480
 +AV+ + EKTRL LA IGKLNFTQ TE LNA NRGLPSCLAEDPSL+YH KGLDI A
 Sbjct: 414 AAVANTXEKTRLGLAQIGKLNFTQLTEXLNAGXNRGLPSCLAEDPSLSYHCKGLDIAAA 473
 Query: 481 AYASELGHLANPVTTFVQPAEMGNQAVNSLALISARRTAEANDVLSLLLASHLYCTLQAV 540
 AY SELGHLANPVT VQPAE NQAVNSLALISARRT E+NDVLSLLLA+HLYC LQA+
 Sbjct: 474 AYTSELGHLANPVTTHVQPAEXANQAVNSLALISARRTTESNDVLSLLLATHLYCVLQAI 533
 Query: 541 DLRAMELDFKKQFDPLLPDLLQQLG---TGLDV-NALALEVKKALNKRLEQTTTYDLEP 596
 DLRA+E +FKKQF P + +L+ QH G TG ++ + L +V K L KRLEQT +YDL P
 Sbjct: 534 DLRAIEFEFKKQFGPAIVSLIDQHFGSAXTGSNLRDELVEKVNKTAKRLEQTN SYDLVP 593
 Query: 597 RWHDAFSYATGTVVELLSSSPSANVTLTAVNAWKVASAEKAIISLTREVRNRFWQTPSSQA 656
 RWHDAFS+A GTVVE+LSS+ +++L AVNAWKVA+AE AISLTR+VR FW S+ +
 Sbjct: 594 RWHDAFSFAAGTVVEVLSST---SLSLAAVNAWKVAAAESAISLTRQVRETFWSAASTSS 650
 Query: 657 PAHAYLSPRTRVLYSFVREELGVQARRGDVFGVQQETIGSNVSRIYEAIKDGRINHVLV 716
 PA +YLSPT++LY+FVREELGV+ARRGDVF+G Q+ TIGSNVS+IYEAIK GRIN+VL+
 Sbjct: 651 PALSYLSPRTQILYAFVREELGVKARRGDVFLGKQEVETIGSNVSKIYEAIKSGRINNVLL 710
 Query: 717 KMLA 720
 K LA
 Sbjct: 711 KXLA 714

☐ >gi|295942|emb|CAA31486.1| phenylalanine ammonia-lyase [Rhodotorula mucilaginosa]
 gi|129592|sp|P10248|PALY_RHORB Phenylalanine ammonia-lyase
 Length = 713

Score = 877 bits (2265), Expect = 0.0

Identities = 469/724 (64%), Positives = 549/724 (75%), Gaps = 15/724 (2%)

Query: 1 MAPSLDSLATTLANGFTNGSHAAPTSAAGPTSALRRTPGLDG--HAAHQSQLEIVQELL 58
 MAPS+DS+AT++AN +NG HAA +AA ++T G +QL+IV+ +L
 Sbjct: 1 MAPSVDSIATSVANSLSNGLHAA---AAANGGDVHKKTAGAGSLLPTTETTQLDIVERIL 57

Query: 59 SDP-TDDVVELSGYSLTXXXXXXXXXXXXXXXXXQNDDEIRARVDKSVDFLKAQLQNSVYG 117
 +D D ++L GY+LT + IR ++D SV+FL+ QL NSVYG
 Sbjct: 58 ADAGATDQIKLDGYTLTLGDVVGAAARRGRSVKVADSPHIREKIDASVEFLRTQLDNSVYG 117

Query: 118 VTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPTSVSSFSVGRGLENTLPLEVVVRGAMVI 177
 VTTGFGGSADTRTEDA+SLQKAL+EHQLCGV PTS+ F++GRGLEN+LPLEVVVRGAM I
 Sbjct: 118 VTTGFGGSADTRTEDAISLQKALLEHQLCGVLPSTMDGFALGRGLENSLPLEVVVRGAMTI 177

Query: 178 RVNSLTRGHSAVRLVVLEALTNFLNHRITPIVPLRGSISASGDLSPLSYIAGAITGHPDV 237
 RVNSLTRGHSAVR+VVLEALTNFLNH ITPIVPLRG+ISASGDLSPLSYIA +ITGHPD
 Sbjct: 178 RVNSLTRGHSAVRIVVLEALTNFLNHGITPIVPLRGTISASGDLSPLSYIAASITGHPDS 237

Query: 238 KVHVLHEGTEKIMFAREAISLFGLEAVVLGPKEGLGLVNGTAVSASMATXXXXXXXXXXXX 297
 KVHV KIM A+EAI+L GL+ VVLGPKEGLGLVNGTAVSASMAT
 Sbjct: 238 KVHV---DGKIMSAQEAIALKGLQPVVLGPKEGLGLVNGTAVSASMATLALTDHAVLSL 293

Query: 298 XXXXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGSSFAXXXXXXXXXX 357
 VEAMVG GSF PF+HDV RPHP Q+EVARNIRTLL GS +A
 Sbjct: 294 LAQALTALTVEAMVGHAGSFHPFLHDVTRPHPTQIEVARNIRTLLLEGSKYAVHHETEYKV 353

Query: 358 XXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLE-NNTTTDNPLLDVENKQTAHGG 416
 GILRQDRYPLR SPQ+LGPLV DM+HA++ LSLE +TTDNPL+D+ENK T HGG
 Sbjct: 354 KDDEGILRQDRYPLRCSQWLGPLVSDMIHAHAVLSLEAGQSTTDNPLIDLENKMTTHGG 413

Query: 417 NFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCLAAEDPSLNYHGKGLD 476
 F AS+V +MEKTRLA+AL+GK++FTQ TE+LNA MNR LPSCCLAAEDPSL+YH KGLD
 Sbjct: 414 AFMASSVGNTEKTRLAVALMGKVSFTQLTEMLNAGMNRALPSCLAAEDPSLSYHCKGLD 473

Query: 477 IHIAAYASELGHLANPVTTFVQPAEMGNQAVNSLALISARRTAEANDVLSLLLASHLYCT 536
 I AAY SELGHLANPV+T VQPAEMGNQA+NSLALISARRTAEANDVLSLLLA+HLYC
 Sbjct: 474 IAAAAYTSELGHLANPVSTHVQPAEMGNQAINSLALISARRTAEANDVLSLLLATHLYCV 533

Query: 537 LQAVDLRAMELDFKKQFDPLLPTLLQQHLGTGLDVNALALEVKKALNKRLEQTTTYDLEP 596
 LQAVDLRAME + K F+P++ LL+QH G L + +V+K++ KRL+Q +YDLE
 Sbjct: 534 LQAVDLRAMEFEHTKAFEPMTLELLKQHFG-ALATAEVEDKVRKSIYKRLQQNNNSYDLEQ 592

Query: 597 RWHDAFSYATGTVVVELLSSSPSANVTLTAVNAWKVASAEKAI SLTREVRNRFWQTPSSQA 656
 RWHD FS ATG VVE L+ V+L ++NAWKVA AEKAI+LTR VR+ FW PSS +
 Sbjct: 593 RWHDTFSVATGAVVEALAGQ---EVSLASLNAWKVACAIEKAIALTRSVRDSFWAAPSSSS 649

Query: 657 PAHAYLSPRTRVLYSFFVREELGVQARRGDVFGVQVQETIGSNVSRIYEAIKDGRINHLV 716
 PA YLSPRTRVLYSFFVREE+GV+ARRGDV++G Q+ TIG+NVSRIYEAIK G I VLV
 Sbjct: 650 PALKYLSPRTRVLYSFFVREEVGKARRGDVYLKGQEVETIGTNVSRIYEAIKSGCIAPVLV 709

Query: 717 KMLA 720
 KM+A
 Sbjct: 710 KMMA 713

☐ >gi|4127289|emb|CAA09013.1| phenylalanine ammonium lyase [Amanita muscaria]
 gi|30580473|sp|O93967|PALY_AMAMU Phenylalanine ammonia-lyase
 Length = 740

Score = 466 bits (1198), Expect = e-129

Identities = 283/691 (40%), Positives = 400/691 (57%), Gaps = 28/691 (4%)

Query: 51 LEIVQELLSDPTDDVVELSGYSLTXXXXXXXXXXXXXXXXXQNDDEIRARVDKSVDFL--K 108
 LE +EL +++ G +L+ ++ RV KS + K
 Sbjct: 53 LEAYRELEGYKNGRAIKVDGQTLISIAVAAAARYNAAVELDESPLVKERVKSQLAIAANK 112

Query: 109 AQLQNSVYGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPTSVSSFSVG--RGLENT- 165
SVYG++TGFGGSADTRT+ + L AL++HQ G+ PTS V + NT

Sbjct: 113 VSTGASVYGLSTGFGGSADTRTDKPMLLGFALLQHQHVIGILPTSTEPLDVLPLQDANNTS 172

Query: 166 LPLEVVRGAMVIRVNSLTRGHSASVRLVVLEALTNFLNHRITPIVPLRGSISASGDLSPLS 225
+P +RGA++IR+NSL RGHS +R ++E + L + P+VPLRGSIS+SGDLSPLS

Sbjct: 173 MPEAWIRGAILIRMNSLIRGHSIRWELIEKMRRELLAANVIPVVPLRGSISSSGDLSPLS 232

Query: 226 YIAGAITGHPDVKVH--VLHEGTEKIMFAREAISLFGLEAVVLGPKEGLGLVNGTAVSAS 283
YIAG I G+P +KV+ G +I +++ ++L +E L KE LG++NGTA SAS

Sbjct: 233 YIAGTIIGNPSIKVYHGPSKSGIRQIGSSKDVLALHNIIEPFPLESKEPLGILNGTAFSAS 292

Query: 284 MATXXXXXXXXXXXXXXXXXXXXXVEAMVGQQGSFAPFIHDVCRPHPGQVEVARNIRTLLS 343
+A EA++G + S APFIH RPHPGQVE A NI LL

Sbjct: 293 VAALALNEAHLVLLAQVCTAMGTEALIGTRASHAPFIHATARPHPGQVECAENIWNLLD 352

Query: 344 GSSFAXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENN--T'TTD 401
GS A LRQDRYPLRTSPQFLGP +ED++ A+ T++ E N TD

Sbjct: 353 GSKLAQLEEHEVRLEDDKYTLRQDRYPLRTSPQFLGPQIEDIISAFQTVTQECNYLPATD 412

Query: 402 NPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCL 461
NPL+D E ++ HGGNFQA AV+ +MEKTRLAL +GKL F+Q TEL+N AMNRGLP +

Sbjct: 413 NPLIDGETGESHHGGNFQAMAVTNAMEKTRLALHHVGKLLFSQSTELVNPAMNRGLPPSV 472

Query: 462 AAEDPSLNYHGKGLDIHIAAYASELGHLANPVTTTFVQPAEMGNQAVNSLALISARRTAEA 521
AA DPSLNYH KGLDI AAY +E A P T +Q AEM NQAVNSLALISAR T +

Sbjct: 473 AATDPSLNYHAKGLDIATAAYVAE----ATPGPTHIQSAEMHNQAVNSLALISARATITS 528

Query: 522 NDVLSLLLASHLYCTLQAVDLRAMELDFKKQFDPLLPTLLQQHLGTGL---DVNALALEV 578
+VL+ L+AS+LY QA+DLRA++ +F D ++ L+ G+ L + L +

Sbjct: 529 LEVLTSLIASYLYILCQALDLRALQREFLPGLDIIIEELRSSFGSFLSSEQMEKLQONL 588

Query: 579 KKALNKRLEQTTTYDLEPRWHDFAFSYATGTVVELLSSS-----PSANVTLTAVNAWKVAS 633
A L++TTT D R + ++ +++ + S PS+ L++V++++ +

Sbjct: 589 TSAFEDHLDKTTTMDNTDRMTTMAATSSSVLLQFFTDSGASVPPSSCDLLSSVSSFQSSV 648

Query: 634 AEKAISLTREVRNRFWQTPSSQAPAHAYLSPRTRVLVSFVREELGVQARRGDVF----- 687
A ++ L ++R + PA Y+ +TR +Y F+R +GV+ + +

Sbjct: 649 ATRSSVLMDDLKEYIFGDRGPTPASQYIG-KTRPVYQFIRTTIGVRKHGSENYNKFYNG 707

Query: 688 VGVQQETIGSNVSRIYEAIKGRINHVLVKM 718
+GV+ TIG N+SRIYE+I+DG++ ++V +

Sbjct: 708 LGVEDVTIGQNISRIYESIRDGKMQSIIVSL 738

☐ >gi|46096230|gb|EAK81463.1| PALY_USTMA Phenylalanine ammonia-lyase [Ustilago may
gi|49066806|ref|XP_397693.1| PALY_USTMA Phenylalanine ammonia-lyase [Ustilago may
Length = 724

Score = 436 bits (1121), Expect = e-120

Identities = 290/728 (39%), Positives = 406/728 (55%), Gaps = 41/728 (5%)

Query: 23 APTKSAAGPTSALRRTPGLDGHAHQSQLEIVQELLSDPTDDVVELSGYSLTXXXXXXXXX 82

APT P A R PGL Q +++ S T+ VV + GY+L

Sbjct: 2 APTADVLPPVEASTR-PGL----LVQPSDTKLKASSFRTEQVV-IDGYNLKIQGLVASA 55

Query: 83 XXXXXXXXQNDDEIRARVDKSVDFLKAQLQN--SVYGVTTGFGGSADTRTEDAVSLQKAL 140

E R R+D SV L A+L S+YG+ TGFGGSAD+RT + +LQ AL

Sbjct: 56 RYGHVPVLDPSAETRKRIDDSVQSLIAKLDRGESIYGINTGFGGSADSRTANTRALQLAL 115

Query: 141 IEHQLCGVTPTSVSSFSVGRG-----LENT-----LPLEVVRGAMVIRVNSLTRGHS 187
 ++ Q CGV P S+F G L +T +P VRGA+V+R++SL RGHS

Sbjct: 116 LQMQQCGVLPVP-STFPTGEPSSAPFALPLTDESSLIMPEAWVRGAIVVRLSSLMRGHS 174

Query: 188 AVRLVLEALTN-FLNHRITPIVPLRGSISASGDLSPLSYIAGAITGHPDVKVHVLHEGT 246
 VR VL+ + FL + +TP+VP+R SISASGDLSPLSY+AGA+ G + V

Sbjct: 175 GVRWEVLDMQKLFLQNNVTPVVPVRSSISASGDLSPLSYVAGALAGQRGIYCFVTDGRG 234

Query: 247 EKI-MFAREAISLFGLEAVVLGPKEGLGLVNGTAVSASMATXXXXXXXXXXXXXXXXXXXXX 305
 +++ + A EA + + V PKE LGL+NGTA SAS+A

Sbjct: 235 QRVKVTADEACRMHKITPVQYEPKEALGLLNGTAFSASVAGLATYEAENLASLTQLTTAM 294

Query: 306 XVEAMVGQQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGSSFAXXXXXXXXXXXXXX--GI 363
 VEA+ G SFAPFIH++ RPHPGQ++ A+ IR LLSGS A G

Sbjct: 295 AVEALKGTDAFAPFIHEIARPHPGQIKSAKFIRALLSGSRLAEHLENEKHVLFSEDNGT 354

Query: 364 LRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTNDNPLLDVENK--QTAHGGNFQAS 421
 LRQDRY LRT+ Q++GP +ED+ +A ++ +E N+TTDNP++D + + HGGNFQA

Sbjct: 355 LRQDRYTLRTASQWVGPGLEDIENAKRSVDIEINSTTDNPMIDPYDGDGRIHHGGNFQAM 414

Query: 422 AVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCLAEE-DPSLNYHGKGLDIHIA 480
 A++ ++EK RLAL +GK+ F Q TEL+N AMNRGLP+ LA+ D SLN+H KG+DI +A

Sbjct: 415 AMTNAVEKIRLALCAMEGKMTFQQMTELVPAMNRGLPANLASTPDLNLFHAKGIDIALA 474

Query: 481 AYASELGHLANPVTTTFVQPAEMGNQAVNSLALISARRTAEANDVLSLLLASHLYCTLQAV 540
 + SEL L NPV+T VQ AEM NQA+NSLALIS R+T +A + LS++ A LY QA+

Sbjct: 475 SVTSELMFLGNPVSTHVQSAEMANQAINSLALISGRQTLQAIECLSMIQAWSLYLLCQAL 534

Query: 541 DLRAMELDFKKQFDPLLPTLLQQHLGTGLD---VNALALEVKKALNKRLEQTTTYDLEPR 597
 D+RA++ +Q L+ L H G +D +A +V K+++KRL++T++ DL R

Sbjct: 535 DIRALQYKVAEQPLTLILASLHSHFGEWMDTEKQQEIAAQVLKSMKRLDETSSKDLRDR 594

Query: 598 WHDAFSYATGTVVLELLSSSPSANVT--LTAVNAWKVASAEKAISLTREVRNRFWQTPSSQ 655
 + + A+ +V S PS L + W+ + R+V F P +

Sbjct: 595 LVETYQDASSVLVRYFSELPSGGGADPLRNIVKWRATGVADTEKIYRQVTIEFLDNPYAC 654

Query: 656 APAHAYLSPRTRVLVSFVREELGVQARRGD---VFVG--VQQETIGSNVSRIYEAIKDGR 710
 +H L +T+ Y FVR+ LGV + F G Q T G VS IY +I+DG

Sbjct: 655 HASH--LLGKTKRAYEFVRKTLGVPMHGKENLNEFKGEFEQWNTTGGYVSVIYASIRDGE 712

Query: 711 INHVLVKM 718
 + ++L ++

Sbjct: 713 LYNMLSEL 720

☐ >gi|15824531|gb|AAL09388.1| phenylalanine ammonia-lyase [Ustilago maydis]
 gi|30580484|sp|Q96V77|PALY_USTMA Phenylalanine ammonia-lyase
 Length = 724

Score = 428 bits (1101), Expect = e-118

Identities = 287/728 (39%), Positives = 404/728 (55%), Gaps = 41/728 (5%)

Query: 23 APTKSAAGPTSALRRTPGLDGHAAHQSQLEIVQELLSDPTDDVVELSGYSLTXXXXXXXXX 82
 APT P A R PGL Q +++ S T+ VV + GY+L

Sbjct: 2 APTADVLPPEASTR-PGL----LVQPSDTKLRKASSFRTEQVV-IDGYNLKIQGLVASA 55

Query: 83 XXXXXXXXQNDDEIRARVDKSVDFLKAQLQN--SVYGVTTGFGGSADTRTEDAVSLQKAL 140

Sbjct: 56 + E R R+D SV L A+L S+YG+ TGFGGSad+RT + +LQ AL
RYGHVTRPRPSAETRKRIDDSVQSLIAKLDGGESiYGINTGFGGSADSRtANTRALQLAL 115

Query: 141 IEHQLCGVTPtSVSSFSVGRG-----LEnt-----LPLeVVRGAMVIRVNSLTRGHS 187
++ Q CGV P S+F G L +T +P VRGA+V+R++SL RGHS

Sbjct: 116 LQMQQCGVLPVP-STFPTGEPSSAPFALPLTDTESSLIMPEAWVRGAIVRLSSLMRGHS 174

Query: 188 AVRLVVLEALTN-FLNHRITPIVPLRGSISASGDLSPLSYIAGAITGHPDVKVHVLHEGT 246
VR VL+ + FL + +TP+VP+R SISASGDLSPLSY+AGA+ G + V

Sbjct: 175 GVRWEVLDMQKFLQNNVTPVVPVRSSISASGDLSPLSYVAGALAGQRGIYCFVTDGRG 234

Query: 247 EKI-MFAREAISLFGLEAVVLGPKEGLGLVNGTAVSASMATXXXXXXXXXXXXXXXXXXXX 305
+++ + A EA + + V PKE LGL+NGTA SAS+A

Sbjct: 235 QRVKVTADEACRMHKITPVQYEPKEALGLNGTAFSASVAGLATYEAENLASLTQLTTAM 294

Query: 306 XVEAMVGQQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGSSFAXXXXXXXXXXXXXX--GI 363
VEA+ G SFAPFIH++ RPHPGQ++ A+ IR LSGS A G

Sbjct: 295 AVEALKGTDA SFAPFIHEIARPHPGQIKSAKFIRAHLSGSRLEHLENEKHVLFSEDNGT 354

Query: 364 LRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTDNPLLDVENK--QTAHGGNFQAS 421
LRQDRY L+T+ Q++GP +ED+ +A ++ E N+TTDNP++D + + HGGNFQA

Sbjct: 355 LRQDRYTLQTASQWVGPLEDIENAKRSVD FEINSTTDNPMIDPYDGDGRIHHGGNFQAM 414

Query: 422 AVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCLAEE-DPSLNHYHGKGLDIHIA 480
A++ ++EK RLAL +GK+ F Q TEL+N AMNRGLP+ LA+ D SLN+H KG++I +A

Sbjct: 415 AMTNAVEKIRLALCAGKMTFQQMTLNPAMNRGLPANLASTPDLNLFHAKGINIALA 474

Query: 481 AYASELGHLANPVTTFVQPAEMGNQAVNSLALISARRTAEANDVLSLLLASHLYCTLQAV 540
+ SEL L NPV+T VQ AEM NQA NSLALIS R+T +A + LS++ A LY QA+

Sbjct: 475 SVTSELMFLGNPVSTHVQSAEMANQAFNSLALISGRQTLQAIECLSMIQAWSLYLLCQAL 534

Query: 541 DLRAMELDFKKQFDPPLLPTLLQQHLGTGLD---VNALALEVKKALNKRLEQT'TTYDLEPR 597
D+RA++ +Q L+ L H G +D +A +V K+++KRL++T++ DL R

Sbjct: 535 DIRALQYKVAEQLPTLILASLHSHFGEWMDETKQQEIAAQVLKSMKRLDETSSKDLRDR 594

Query: 598 WHDAFSYATGTVVELLSSSPSANVT--LTAVNAWKVASAEKAI SLTREVRNRFWQTPSSQ 655
+ + A+ +V S PS L + W+ + R+V F P +

Sbjct: 595 LVETYQDASSVLVRYFSELPSSGGADPLRNIVKWRATGVADTEKIYRQVTIEFLDNPYAC 654

Query: 656 APAHAYLSPRTRVLYSFVREELGVQARRGD---VFVG--VQQETIGSNVSRIEAIKDGR 710
+H L +T+ Y FVR+ LGV + F G Q T G VS IY +I+DG

Sbjct: 655 HASH--LLGKTKRAYEFVRKTLGVPMHGKENLNEFKGEFEQWNTTGGYVSVIYASIRDGE 712

Query: 711 INHVLVKM 718
+ ++L ++

Sbjct: 713 LYNMLSEL 720

☐ >gi|40738860|gb|EAA58050.1| ☒ hypothetical protein AN6075.2 [Aspergillus nidular
gi|49097504|ref|XP_410212.1| ☒ hypothetical protein AN6075.2 [Aspergillus nidulan
Length = 701

Score = 428 bits (1100), Expect = e-118
Identities = 267/643 (41%), Positives = 381/643 (59%), Gaps = 26/643 (4%)

Query: 93 DDEIRARVDKSVDFLKAQLQN--SVYGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTP 150
D + +D S+ LK +L SVYGV TGFGGSad+RT+ +LQ AL++ GV

Sbjct: 64 DPAVLNIDASIRLLKDRNLNQYGSVYGVNTGFGGSADSRtDKMTALQSALLQLTQAGVLL 123

Query: 151 TSVSSFSVGRGLEN-TLPLEVVRGAMVIRVNSLTRGHSAVRLVVLEALTNFLNHRITPIV 209
 S S + + LE+ +P VRG M+ R NS RGHS+L +L+++ L HRITPIV
 Sbjct: 124 ESDKSGNQKLLSHAMPASWVRGTMLARCSNLRGHS+VLSILQSIVKLLQHRITPIV 183

Query: 210 PLRGSISASGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIMFAREAI SLFGLEAVVLGPK 269
 PLRGSISASGDL PLSYIAGAI G+PDV V V +IM + E + GLEA LGPK
 Sbjct: 184 PLRGSISASGDL MPLSYIAGAI EGNPDVYVQVDGLDMPRIMKSIEGLQYAGLEAQKLGPK 243

Query: 270 EGLGLVNGTAVSASMATXXXXXXXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHP 329
 EGLGL+NGT+ SA+++A+ +EA+ G S+ PFI V RPH
 Sbjct: 244 EGLGLINGTSTSAVASLVLVETNQLSVLVQALSAMGLEALTGTAE SYHPFISAV-RPHD 302

Query: 330 GQVEVARNIRTLLSGSSFAXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAY 389
 GQVE A N+ +LL GS L QDRY LR PQ++GP +ED++ A+
 Sbjct: 303 GQVECANLLSLRGSKL VQGLDGQKFQDRPG--LIQDRYALRCVPQWVG PQLEDLLLAH 360

Query: 390 STLLENNTTTDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELL 449
 ++ E N+T DNPL+DV++K GGNFQA +++ +MEKTR L + G+L F+Q TE++
 Sbjct: 361 RQVTTELNSTCDNPLVDVKS KSIYSGGNFQAVSITSAMEKTRQCLQMFGRLIFSQATEMI 420

Query: 450 NAAMNRGLPSCLAEDPSLNYHGKGLDIHIAAYASELGH LANPVTTFVQPAEMGNQAVNS 509
 + ++N GLP+ L A+DPSL++ KG+DI +A+Y +ELG+L+NPV++ VQ AEM NQA+NS
 Sbjct: 421 DPSINNGLPNTNLVADDP SLSTMKGVDISMASYMAELGYLSNPVSSHVQSAEMRNQAINS 480

Query: 510 LALISARRTAEANDVLSLLLASHLYCTLQAVDLRAMELDFKKQFDPLLPTLLQQHLGTGL 569
 +AL+SAR + +A +VLSL+ A +Y QA+DLR + F ++ P L ++ ++ L L
 Sbjct: 481 MALVSARYSMQAVEVLSLMCACDVYICCCALDLRVLHNTFLEKAI PQLHSVTERVLS PFL 540

Query: 570 DVNALALEVKKALNKRLEQT--TTYDLEP--RWHDAFSYATGTVVELLSSSPSANVTLTA 625
 AL ++ ++L++ L QT T L P R H A ++E L S +L
 Sbjct: 541 PQPALE-DLNRSLDQHLTQTWPMTNRLSPADRVHTVIEKAI PVLENLKS--HRGPS LGD 597

Query: 626 VNAWKVASAEKAI SLTREVRNRFWQT PSSQAPAHAYLSPRTRVLYS FVREELGVQARRG- 684
 + WK + + +E+ F+ P + YL + LY VR+ELG+ +G
 Sbjct: 598 LETWKSQARNLLNVVYQEIAESFFVKPHTA----DYLGE GAKALYVMVRQELGIPFHQGF 653

Query: 685 -----DVFVG VQQETIGSNVSRIYEA IKDGRINHVLVKML 719
 ++ G ++T GS +S IYEA I+D R+ L++ L
 Sbjct: 654 IEHPTVENEILNGRPKKT TGSWISIIYEAIRDSRLMGPLIQAL 696

☐ >gi|32423291|ref|XP_332083.1| ☒ hypothetical protein [Neurospora crassa]
 gi|28920117|gb|EAA29498.1| ☒ hypothetical protein [Neurospora crassa]
 Length = 762

Score = 371 bits (952), Expect = e-101
 Identities = 254/695 (36%), Positives = 364/695 (52%), Gaps = 74/695 (10%)

Query: 66 VELSGYSLTXXXXXXXXXXXXXXXXXQNDDEIRARVDKSVDFLKAQLQ--NSVYGVT TGF 123
 +E+SG +LT +D + +VD+S+ L+ ++Q + +YGV TGF
 Sbjct: 29 IEISGSNLT IADVVAVSLHGAKAHLSDDTQ---QVDRSIALLEERI QAGDVIYGVNTGF 85

Query: 124 GSADTRT----EDAVSLQKALIEHQLCGVTPTSV-----SSFSVGRGLEN-----TLPL 168
 GSADTRT E + LQ AL++H G+ + S+ G+ +N LP
 Sbjct: 86 GSADTRTDAGSEPLMRLQ GALVQHLNVGILTHADKDRDGSNSWAGKPYDNELLRSHALPS 145

Query: 169 EVVRGAMVIRVNSLTRGHSAVRLVVLEALTNFLNHRITPIVPLRGSISASGDLSPLSYIA 228

VVR M+IR NSL RGHS VR +++E + LN + PIVPLRGSISASGDLS LSYIA
 Sbjct: 146 PVVRATMLIRCNLSMRGHSVRPLIMENILKLLNRDMVPIVPLRGSISASGDLSLTSYIA 205

Query: 229 GAITGHPDV--KVHVLHEGTEKIMFAREAISLFGLEAVVLGPKEGLGLVNGTAVSASMAT 286
 GA+ G+PD+ K H TE I+ A +A+SL GLE V KEGLG+ NGTA S + A+
 Sbjct: 206 GALEGNPDIYLKARKPHNRTE-ILPADKALSLAGLEPVRFQVKEGLGITNGTAPSCATAS 264

Query: 287 XXXXXXXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGSS 346
 EA+ G ++ PFI V RPHPGQ E A NI L+GS
 Sbjct: 265 IAIQEANQLAVLVQLLTAMGTEALAGTAANYHPFISSV-RPHPGQAEAAASNILAFLAGSK 323

Query: 347 FAXXXXXXXXXXXXXXGILR---QDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTDDNP 403
 A +R QDRY LRT+PQ++GP +ED+ A + E N+TDDNP
 Sbjct: 324 IAAPCEAHPSEDEPAKVRGLAQDRYALRTAPQWIGPQLEDLELATKQVQTELNSTDDNP 383

Query: 404 LLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCLA 463
 L+D + HGGNFQA A++ +MEKT LAL +G+L + Q +ELLN N+GLP L+A
 Sbjct: 384 LIDPTSGLIHHGGNFQAMALTSAMEKTLALQNLGRLLYAQSSELLNNMTNKGLPPNLSA 443

Query: 464 EDPSLNYHGKGLDIHIAAYASELGHLANPVTTTFVQPAEMGNQAVNSLALISARRTAEAND 523
 ++PS +Y KG D+++AAY +EL +LA P++ VQ AEM NQ+VNS+AL++AR EA +
 Sbjct: 444 DEPSQSYTCKGFDVNMAAYMAELAYLAKPISPHVQVAEMNNQSVNSMALVAARYALEAVE 503

Query: 524 VLSLLLASHLYCTLQAVDLRAMELDFKKQFDPLLP TLLQQHLGTGLDVNALALEVKKALN 583
 V++L+ A+++Y QA+DLR ++L+F++ L L+ H+ +L+ K+ +
 Sbjct: 504 VVNLMATYIYVLCQALDLRVLQLEFREALSVRLRDLVLSHV-----ARQRSLSKSEEEH 558

Query: 584 KRLEQTTTYDLEPRWHDFAFSYATGTVVELLSSSPSANVTLTAVNAWKVASAEKAISLTR- 642
 K L + + + R G + E + +L VA+ + A+
 Sbjct: 559 KGLSEVDITESQRR-----AGKLAECILDQWDKLASLDVAERASVATKQSALDALEL 610

Query: 643 -----EVRNRFWQTPSSQA-----PAHAYLSPRTRVLYSF 672
 E R W QA +LS + V+Y F
 Sbjct: 611 LHCGETEYGRRTWGFSDLQAYHLKTARVVADCYGDHRNALLEGKQDTRRWLSSGGSTVVYDF 670

Query: 673 VREELGVQARRGDVFGVQVQETIGSNVSRIYEAIK 707
 VR+EL RG V + ++R+ EAI+
 Sbjct: 671 VRKELKTPLNRG---VVDHPPLLKEQLTRLKEAIR 702

☐ >gi|40739638|gb|EAA58828.1| ☒ hypothetical protein AN3897.2 [Aspergillus nidular
 gi|49093146|ref|XP_408034.1| ☒ hypothetical protein AN3897.2 [Aspergillus nidulan
 Length = 543

Score = 368 bits (944), Expect = e-100

Identities = 230/552 (41%), Positives = 309/552 (55%), Gaps = 25/552 (4%)

Query: 175 MVIRVNSLTRGHSVRLVLEALTNFLNHRITPIVPLRGSISASGDLSPLSYIAGAITGH 234
 MV R NSL RGHS AVR+ ++ L +N TP+VPLRGSISASGDL+PL+YIAGA+ G+
 Sbjct: 1 MVARCNLSIRGHS AVRIDIVRNLATMINEDYTPV VPLRGSISASGDLTPLAYIAGALEGN 60

Query: 235 PDVKVHVLHEGTEKIMFAREAISLFGLEAVVLGPKEGLGLVNGTAVSASMATXXXXXXXXX 294
 PD+ V +KI+ A A+ GLE + PKE LGL+NGTA S A+
 Sbjct: 61 PDIYVQCGGTCKDDKIVTADAALKELGLEPLTFRPKEALGLLNGTAFSTGAASLVLFANQ 120

Query: 295 XXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGSSFAXXXXXX 354
 EA++G +F PFI + RPHPGQ EVA NI LS S
 Sbjct: 121 LILLTQVLTAMTTEALLGTMRNFDPIAEARPHPGQKEVAANIFRFLSDSQLTTDHDHS 179

Query: 355 XXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTDNPLLDVENKQTAH 414
 L QDRYPLRT+ Q++GP VE+M A + +++E N+TTDNPL DV N H
 Sbjct: 180 PSDND----LAQDRYPLRTASQWIGPHVENMALAQVAIELNSTTDNPLFDVANDTIHH 235

Query: 415 GGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCLAEDPSLNYHGKG 474
 GGNFQA +++ +MEKT A+ +GKL F QC+EL+N +++GLP L A+DPSL++ KG
 Sbjct: 236 GGNFQAMSITSAMEKTTSAMQTLGKLVFGQCSELINPMLSKGLPPNLCADDPSLSFALKG 295

Query: 475 LDIHIAAYASELGHLANPVTTTFVQPAEMGNQAVNSLALISARRTAEANDVLSLLLASHLY 534
 +DI++A+Y SELG+L NPV+ FVQ A++ NQ VNSLALI AR A+A +V SL+ ASH+Y
 Sbjct: 296 VDIINMASYMSELGYLNNPVSFVQSAVDVNNQVNSLALIGARYAADAVEVFSLMAASHIY 355

Query: 535 CTLQAVDLRAMELDF----KKQFDPLLPTLLQQHLGTGLDVNALALEVKKALNKRLEQTT 590
 QAVDLR + F +K L Q L T D+N L E+ + N T
 Sbjct: 356 ALCQAVDLREIHRTFETIARKHVVEYTSDFGQSL-TDNDINTLWGELMRHWN----CTA 410

Query: 591 TYDLEPRWHDAFSYATGTVVELLSSSPSANVTLTAVNAWKVASAEKAISLTREVRNRWFQ 650
 T DLE R A S GT+ L S S ++ V W+ + R ++
 Sbjct: 411 TLDLEQRATTAVSQTMGTFLFILSSKPSPSIDGNVVREWQSTVTDLLKYHCAANRKAYFT 470

Query: 651 TPSSQAPAHAYLSPRTRVLYSFVREELGVQARRGDVFGV-----QQETIGSNVSR IY 703
 P P L + +Y+FVR+ L V +G V + TIGS++ IY
 Sbjct: 471 DP-----PTGKLLCSSSAKIYNFVRDTLKVPMHKGLVDHPTYPSCGCEGDKRTIGSHIGTIY 526

Query: 704 EAIKDGRINHVL 715
 A+++G+ VL
 Sbjct: 527 AALREGQFMSVL 538

☐ >gi|42553215|gb|EAA76058.1| ☒ hypothetical protein FG09311.1 [Gibberella zeae PH
 gi|46134925|ref|XP_389487.1| ☒ hypothetical protein FG09311.1 [Gibberella zeae PH
 Length = 720

Score = 367 bits (942), Expect = e-100

Identities = 247/677 (36%), Positives = 353/677 (52%), Gaps = 43/677 (6%)

Query: 68 LSGYSLTXXXXXXXXXXXXXXXXXQNDDEIRARVDKSVDLKAQLQNS--VYGVTTGFGGS 125
 L G SL D+++ R++ SVD L L + VYGV TGFGGS
 Sbjct: 31 LDGNSLDIASLVAVARYGIEPEISKDEDLARRINLSVDALAEYLSHKYVVYGVNTGFGGS 90

Query: 126 ADTRTEDAVSLQKALIEHQLCGVTPTSVSSFSVGRGLE--NTLPLEVVRGAMVIRVNSLT 183
 AD RT+D + Q +++H + +S + E + +P + VRGA++ R N
 Sbjct: 91 ADVRTDDWLENQIGVLQHTQSAIITSSDKNLGGNSEREPSHVMPPKWVRGAILARANQNM 150

Query: 184 RGHSAVRLVVLEALTNFLNHRITPIVPLRGSISASGDLSPLSYIAGAITGHPDVKVHVLH 243
 RG S+VRL VLE L L+H ITP+VP+RG+ISASGDL P+SYIAGA+TG+PD+ V V
 Sbjct: 151 RGQSSVRLEVLERLIKLLHHDITPLVPIRGTISASGDLMPMSYIAGAVTGNPDIFVQVGK 210

Query: 244 EGTEKIMFAREAI SLFGLEAVVLGPKEGLGLVNGTAVSASMATXXXXXXXXXXXXXXXXX 303
 + K+M + +A+ GL LGPKE LGL+NGTA S S+A+
 Sbjct: 211 GTSAKVMPDQKALQQNGLSPSGLGPKEALGLINGTAPSVSLASLVLHESQQLTLLAQVLT 270

Query: 304 XXXVEAMVGQQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGSSFAXXXXXXXXXXXXXXXXXGI 363
 E+M G APFIH V RPHPGQ+E A NIR+ L GS F
 Sbjct: 271 AFTAESMGNNVEWTAPFIHAV-RPHPGQIEAAANIRSFLQGSEFVVGLENRKRTGDG--- 326

Query: 364 LRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTDNPLLDVENK-----QTAHGGN 417

L QDRY RTSPQ++GP +ED++ A +++E N+T+DNPL+D K + GGN
 Sbjct: 327 LWQDRYSTRTPSQWIGPYLEDLLAQRQITVELNSTSDNPLVDATEKDRKVVEVYSGGN 386
 Query: 418 FQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCLAEDPSLNYHGKGLDI 477
 FQA AV+ +M+KTRLAL +IG++ F+Q +E++N N GL + L D N+ KG+D+
 Sbjct: 387 FQAVAVTSAMDKTRLALQMIGRMLFSQVSEMINPCTNNGLEANLNVSDKE-NFTMKGIDV 445
 Query: 478 HIAAYASELGHLANPVTTFFVQPAEMGNQAVNSLALISARRTAEANDVLSLLLASHLYCTL 537
 +++AY SEL LA+PV++ V AEM NQ +NSLAL+SARRT EA D+++ + A H+Y +
 Sbjct: 446 NMSAYMSELAALAHVPSSHVMSAEMHNQGINSLALLSARRTMEAADLVAHMCACHIYVSC 505
 Query: 538 QAVDLRAMELDFKKQFDPLLPTLLQQHLGTGLDVNALALEVKKALNKRLEQTTTYDLEPR 597
 QAV+LRA F + + D + K+ K L + +E
 Sbjct: 506 QAVELRATHRLFLETLHDKI-----KAKDGPFHVFRNLKSALKDLGEKVLAVVEKA 556
 Query: 598 WHDAFSYATGTVVVELLSSSPSANVTLTAVNAWKVASAEKAIISLTREVRNRFWQTPSS--- 654
 W+D + + + A VT + E+ + SS
 Sbjct: 557 WYDHNAGCWKDRIVPTVDAAMAPVTQYLTSEEMDCPMSSLAVFRGELHKYIVEVASSIFY 616
 Query: 655 -----QAPAHAYLSPRTRVLYSFVREELGVQARRG---DVFVGVSQ-----QETIGSN 698
 L T LY+++R +LGV + G D Q ++TIGS
 Sbjct: 617 PNMAIRPVDVATKLGDTAPLYAWIRSKLGVPTQCGIDDDPLYNAQKGLPTEGKKTIGSW 676
 Query: 699 VSRIYEAIKDGRINHVL 715
 VS +YE++KD ++ V+
 Sbjct: 677 VSIVYESLKDDMMDVVM 693

>gi|32140421|gb|AAP59438.1| [G] phenylalanine ammonia lyase [Arabidopsis thaliana]
 gi|19310727|gb|AAL85094.1| [G] putative phenylalanine ammonia lyase PAL1 [Arabidops
 gi|15028193|gb|AAK76593.1| [G] putative phenylalanine ammonia lyase PAL1 [Arabidops
 gi|20197947|gb|AAM15324.1| [G] phenylalanine ammonia lyase (PAL1) [Arabidopsis thal
 gi|28058755|gb|AAO29949.1| [G] Unknown protein [Arabidopsis thaliana]
 gi|15228074|ref|NP_181241.1| [G] phenylalanine ammonia-lyase 1 (PAL1) [Arabidopsis
 gi|25292167|pir|G84787 [G] phenylalanine ammonia lyase (PAL1) [imported] - Arabido
 thaliana
 Length = 725

Score = 357 bits (915), Expect = 9e-97

Identities = 248/696 (35%), Positives = 363/696 (52%), Gaps = 39/696 (5%)

Query: 43 GHAAHQ---SQLEIVQELLSDPTDDVVELSGYSLTXXXXXXXXXXXXXXXXXQNDDEIRAR 99
 G AA Q S L+ V+ ++++ VV L G +LT + + RA
 Sbjct: 39 GAAAEQMKGSHLDEVKRMVAEFRKPVVNLGGETLTIGQVAAISTIGNSVKVELSETARAG 98
 Query: 100 VDKSVDFLKAQLQNSV--YGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPTSVSSFS 157
 V+ S D++ + YGVTTGFG ++ RT++ V+LQK LI G+ F
 Sbjct: 99 VNASSDWVMESMNKGTDSYGVTTGFGATSHRRTKNGVALQKELIRFLNAGI-----FG 151
 Query: 158 VGRGLENLTPLEVVRGAMVIRVNSLTRGHSVAVRLVVLEALTNFLNHRITPIVPLRGSISA 217
 + +TLP R AM++R+N+L +G S +R +LEA+T+FLN+ ITP +PLRG+I+A
 Sbjct: 152 STKETSHLPHSATRAAMLVRINTLLQGFSGIRFEILEAITSFLNNNITPSLPLRGTTITA 211
 Query: 218 SGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEAVV--LGPKEGLGLV 275
 SGDL PLSYIAG +TG P+ K + + A EA L G+ + L PKEGL LV
 Sbjct: 212 SGDLVPLSYIAGLLTGRPNKAT---GPNGEALTAEEAFKLAGISSGFFDLQPKGLALV 268

Query: 276 NGTAVSASMATXXXXXXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQVEVA 335
 NGTAV + MA+ E M G+ F + + HPGQ+E A
 Sbjct: 269 NGTAVGSGMASMVLFTNVLVLAELSAVFAEVMMSGKP-EFTDHLTHRLKHHPGQIEAA 327

Query: 336 RNIRTLGSSSFAXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLE 395
 + +L GSS+ +QDRY LRTSPQ+LGP +E + +A ++ E
 Sbjct: 328 AIMEHILDGSSYMKLAQKLHEMDPLQKP-KQDRYALRTSPQWLGPQIEVIRYATKSIERE 386

Query: 396 NNTTTDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNR 455
 N+ DNPL+DV + HGGNFQ + + +SM+ TRLA+A IGKL F Q +EL+N N
 Sbjct: 387 INSVDNPLIDVSRNKAIHGGNFQGTPIGVSMNTRLAIAAIGKLMFAQFSELVNDFFYN 446

Query: 456 GLPSCL-AAEDPSLNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVNSLALIS 514
 GLPS L A+ +PSL+Y KG +I +A+Y SEL +LANPVT+ VQ AE NQ VNSL LIS
 Sbjct: 447 GLPSNLTAARNPSLDYGFKAELIAMASYCSELQYLANPVTSHVQSAEQHNQDVNSLGLIS 506

Query: 515 ARRTAEANDVLSLLLASHLYCTLQAVDLRAMELDFKKQFDPLLPTLLQQHLGTGLDVNAL 574
 +R+T+EA D+L L+ + L QAVDLR +E + ++ + + ++ L TG++
 Sbjct: 507 SRKTSEAVDILKLMSTTFLVAICQAVDLRHLEENLRQTVKNTVSQVAKKVLTTGVNGE-- 564

Query: 575 ALEVKKALNKRL-----EQTTTYDLEP--RWHDAFSYATGTVE--LLSSSPSANVTLT 624
 L + K L EQ TY +P + +V+ L++ N +
 Sbjct: 565 -LHPSRFCEKDLLKVVDRQVYTYADDPCSATYPLIQKLQVIVDHALINGESEKNAVTS 623

Query: 625 AVNAWKVASAEKAISLTREVR-NRFWQTPSSQAPAHAYLSPRTRVLYSFVREELGVQARR 683
 + E L +EV R + A + R+ LY FVREELG
 Sbjct: 624 IFHKIGAFEEELKAVLPKEVEAARAAYDNGTSAIPNRIKECRSYPLYRFVREELGT---- 679

Query: 684 GDVFGVQQETIGSNVSRIYEAIKGRINHVLVKML 719
 ++ G + + G +++ AI +G+I +++ L
 Sbjct: 680 -ELLTGEKVTSPEGEEFDKVF+TAICEGKIIDPMMECL 714

☐ >gi|1171991|sp|P35510|PAL1_ARATH Phenylalanine ammonia-lyase 1
 gi|497419|gb|AAC18870.1| phenylalanine ammonia lyase [Arabidopsis thaliana]
 Length = 725

Score = 354 bits (909), Expect = 5e-96

Identities = 247/696 (35%), Positives = 362/696 (52%), Gaps = 39/696 (5%)

Query: 43 GHAAHQ---SQLEIVQELLSDPDDEVVLSGYSLTXXXXXXXXXXXXXXXXXQNDDEIRAR 99
 G AA Q S L+ V+ ++++ VV L G +LT + + RA
 Sbjct: 39 GAAAEQMKGSHLDEVKRMVAEFRKPVVNLGGETLTIGQVAAISTIGNSVKVELSETARAG 98

Query: 100 VDKSVDFLKAQLQNSV--YGVTTFGFGSADTRTEDAVSLQKALIEHQLCGVTPTSVSSFS 157
 V+ S D++ + YGVTTFGFG ++ RT++ V+LQK LI G+ F
 Sbjct: 99 VNASSDWVMESMNKGTDSYGVTTFGFGATSHRRTKNGVALQKELIRFLNAGI-----FG 151

Query: 158 VGRGLENLPLEVVRGAMVIRVNSLTRGHSVRLVLEALTNFLNHRITPIVPLRGSISA 217
 + +TLP R AM++R+N+L +G S +R +LEA+T+FLN+ ITP +PLRG+I+A
 Sbjct: 152 STKETSHLPHSATRAAMLVRINTLLQGFSGIRFEILEAITSFLNNITPSLPLRGITITA 211

Query: 218 SGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEAVV--LGPKEGLGLV 275
 SGDL PLSYIAG +TG P+ K + + A EA L G+ + L PKEGL LV
 Sbjct: 212 SGDLVPLSYIAGLLTGRPNKAT---GPNGEALTAEEAFKLAGISSGFFDLQPKLEGLALV 268

Query: 276 NGTAVSASMATXXXXXXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQVEVA 335
 NGTAV + MA+ E M G+ F + + HPGQ+E A
 Sbjct: 269 NGTAVGSGMASMVLFTNVLVLAELSAVFAEVMMSGKP-EFTDHLTHRLKHHPGQIEAA 327

Query: 336 RNIRTLGSSSFAXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLE 395
 + +L GSS+ +QDRY LRTSPQ+LGP +E + +A ++ E
 Sbjct: 328 AVMEHILDGSSYMKLAQKLHEMDPLQKP-KQDRYALRTSPQWLGPQIEVIRYATKSIERE 386

Query: 396 NNTTTDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNR 455
 N+ DNPL+DV + HGGNFQ + + +SM+ TRLA+ IGKL F Q +EL+N N
 Sbjct: 387 INSVNDNPLIDVSRNKAIGHGGNFQGTPIGVSMNTRLAIRAIGKLMFAQFSELVNDFFYNN 446

Query: 456 GLPSCL-AAEDPSLNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVNSLALIS 514
 GLPS L A+ +PSL+Y KG +I +A+Y SEL +LANPVT+ VQ AE NQ VNSL LIS
 Sbjct: 447 GLPSNLTASRNPSLDYGFKGAEIAMASYCSELQYLANPVTSHVQSAEQHNQDVNSLGLIS 506

Query: 515 ARRTAEANDVLSLLASHLYCTLQAVDLRAMELDFKKQFDPLLPTLLQQHLGTGLDVNAL 574
 +R+T+EA D+L L+ + L QAVDLR +E + ++ + + ++ L TG++
 Sbjct: 507 SRKTSEAVDILKLMSTTFLVAICQAVDLRHLLENLRQTVKNTVSQVAKKVLTTGVNGE-- 564

Query: 575 ALEVKKALNKRL-----EQTTTYDLEP--RWHDAFSYATGTVVE--LLSSSPSANVTLT 624
 L + K L EQ TY +P + +V+ L++ N +
 Sbjct: 565 -LHPSRFCEKDLLKVVDREQVYTYADDPSCSATYPLIQKLRQVIVDHALVNGESEKNAVTS 623

Query: 625 AVNAWKVASAEKAIISLTREVRN-RFWQTPSSQAPAHAYLSPRTRVLYSFVREELGVQARR 683
 + E L +EV R + A + R+ LY FVREELG
 Sbjct: 624 IFHKIGAFEEELKAVLPKEVEAARAAYDNGTSAIPNRIKECRSYPLYRFVREELGT---- 679

Query: 684 GDVFGVQQETIGSNVSRIYEAIKDGRINHVLVKML 719
 ++ G + + G +++ AI +G+I +++ L
 Sbjct: 680 -ELLTGEKVTSPGEEFDKVFТАICEGKIIDPMMECL 714

☐ >gi|7208616|gb|AAF40224.1| phenylalanine ammonia-lyase 2 [Rubus idaeus]
 Length = 730

Score = 352 bits (902), Expect = 3e-95
 Identities = 243/683 (35%), Positives = 357/683 (52%), Gaps = 44/683 (6%)

Query: 49 SQLEIVQELLSIPTDDVVELSGYSLTXXXXXXXXXXXXXXXXXQNDDEIRARVDKSVDFLK 108
 S L+ V+ ++++ VV+L G +LT + + RA V S D++
 Sbjct: 53 SHLDEVRRMVAEYRKPVVKGGETLTISQVAAIANHDSGVKVELAESARAGVKASSDWVM 112

Query: 109 AQLQNSV--YGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPTSVSSFSVGRGLENLTL 166
 + YGVTTGFG ++ RT+ +LQK LI GV S +TL
 Sbjct: 113 DSMNKGTD SYGVTTGFGATSHRRTKQGAALQKELIRFLNAGVLRNGTES-----AHTL 165

Query: 167 PLEVVRGAMVIRVNSLTRGHSVRLVLEALTNFLNHRITPIVPLRGSISASGDLSPLSY 226
 P R AM++R+N+L +G+S +R +LEA++ FLNH ITP +PLRG+I+ASGDL PLSY
 Sbjct: 166 PHSATRAAMLVRINTLLQGYSGIRFEILEAISKFLNHNITPCLPLRGTTITASGDLVPLSY 225

Query: 227 IAGAITGHPDVKVHVLHEGTEKIMFAREAIISLFGLEA--VVLGPKEGLGLVNGTAVSASM 284
 IAG +TG P+ K V +G + + A EA + G+ + L PKEGL LVNGTAV + +
 Sbjct: 226 IAGLLTGRPNKA-VGPKG--ETLNAAEAFQVGISSGFFELQPKGLALVNGTAVGSGL 282

Query: 285 ATXXXXXXXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQVEVARNIRTLGSSG 344
 A+ E M G+ F + + HPGQ+E A + +L G
 Sbjct: 283 ASTVLFETNILALLSEILSAIFAEVMQKGP-EFTDHLTHKLKHHPGQIEAAAIMHILDG 341

Query: 345 SSFAXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTNDNPL 404
 SS+ +QDRY LRTSPQ+LGP +E + + ++ E N+ DNPL
 Sbjct: 342 SSVVKAEEKLHEQDPLQKP-KQDRYALRTSPQWLGPQIEVIRFSTKSIEREINSVNDNPL 400

Query: 405 LDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCLA-A 463
 +DV + HGGNFQ + + +SM+ TRLA+A IGKL F Q +EL+N N GLPS L+
 Sbjct: 401 IDVSRNKALHGGNFQGTPIGVSMNTRLAIASIGKLMFAQFSELVNDNFYNNGLPSNLSGG 460

Query: 464 EDPSLNYHGKGLDIHIAAYASELGHLANPVTTTFVQPAEMGNQAVNSLALISARRTAEAND 523
 DPSL+Y KG +I +A+Y SEL LANPVT VQ AE NQ VNSL LIS+R+TAEA D
 Sbjct: 461 RDPSLDYGFKAIEAMASYCSELQFLANPVTNHVQSAEQHNQDVNSLGLISSRKTAEAVD 520

Query: 524 VLSLLLASHLYCTLQAVDLRAMELDFKKQFDPLLPTLLQQHLGTGL-----DVNA 573
 +L L+ ++ L QA+DLR +E + K + L ++ L TG+ + +
 Sbjct: 521 ILKLMSSTFLVALCQAIDLRHLEENLKSTVKNTVSQLAKRVLTGTGVNGLHPSRFCEKDL 580

Query: 574 LALEVKKALNKRLEQ--TTTYDLEPRWHDAFSYATGTVVELLSSSPSANVTLTAVNAWKV 631
 L + ++ L ++ + TY L R V L++ + T++ K+
 Sbjct: 581 LMOVVEREYLFAYIDDPSCATYPLMQRLRQVL-----VEHALTNGENEKNASTSI-FQKI 633

Query: 632 ASAEKAIS--LTREVRN-RFQWTPSSQAPAHAYLSRTRVLYSFVREELGVQARRGDVFFV 688
 + E+ + L +EV + R + A + + R+ LY FVREELG G+
 Sbjct: 634 TAFEEELKTILPKEVESARAAYESGNAAIPNRIVECRSYPLYKFVREELG-----GEFLT 688

Query: 689 GVQQTIGSNVSRIYEAIKDGRI 711
 G + + G +++ A+ G I
 Sbjct: 689 GEKVRSPGEECDKVFTAMCQONI 711

☐ >gi|23197654|gb|AAN15354.1| phenylalanine ammonia-lyase [Arabidopsis thaliana]
 gi|20260116|gb|AAM12956.1| phenylalanine ammonia-lyase [Arabidopsis thaliana]
 Length = 717

Score = 350 bits (898), Expect = 9e-95

Identities = 254/733 (34%), Positives = 377/733 (51%), Gaps = 45/733 (6%)

Query: 5 LDSLATTLANGFTNGSHAAPTKSAAGPTSALRRTPGLDGHAHQSQLEIVQELLSIPTDD 64
 +D + L G A TK+ A P + GL S L+ V+++++
 Sbjct: 1 MDQIEAMLCGGGEKTKVAVTTKTLADPLNW-----GLAADQMKGSHLDEVKKMVAEYRRP 55

Query: 65 VVELSGYSLTXXXXXXXXXXXXXXXXXQNDDEIRARVDKSVDFLKAQLQNSV--YGVTTGF 122
 VV L G +LT + + RA V S D++ + YGVTTGF
 Sbjct: 56 VVNLGGETLTIGQVAAISTVGGSVKVELAETSRAVKASSDWMESMNKGTDSYGVTTF 115

Query: 123 GGSADTRTEDAVSLQKALIEHQLCGVTPTSVSSFSVGRGLENTLPLEVVRGAMVIRVNSL 182
 G ++ RT++ +LQ LI G+ F + +TLP R AM++RVN+L
 Sbjct: 116 GATSHRRTKNGTALQTELIRFLNAGI-----FGNTKETCHTL PQSATRAAMLVRVNTL 168

Query: 183 TRGHSAVRLVVLEALTNFLNHRITPIVPLRGSISASGDLSPLSYIAGAITGHPDKVHVHL 242
 +G+S +R +LEA+T+ LNH I+P +PLRG+I+ASGDL PLSYIAG +TG P+ K
 Sbjct: 169 LQGYSGIRFEILEAITSLLNHNISPSLPLRGTTITASGDLVPLSYIAGLLTGRPNKA--- 225

Query: 243 HEGTE-KIMFAREAISLFGLEAVV--LGPKEGLLVNGTAVSASMATXXXXXXXXXXXXX 299
 G + + + A+EA G+ L PKEGL LVNGTAV + MA+
 Sbjct: 226 -TGPDGESLTAKAFKAGISTGFFDLQPKGLLVNGTAVSGMASMVLFEANVQAVLA 284

Query: 300 XXXXXXVEAMVGQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGSSFAXXXXXXXXXXXXX 359
 E M G+ F + + HPGQ+E A + +L GSS+
 Sbjct: 285 EVLSAIFAEMSGKP-EFTDHLTHRLKHHPGQIEAAIMEHILDGSSYMKLAQKVHEMDP 343

Query: 360 XXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTNDNPLLDVENKQTAHGGNFQ 419
 +QDRY LRTSPQ+LGP +E + A ++ E N+ DNPL+DV + HGGNFQ

Sbjct: 344 LQKP-KQDRYALRTSPQWLGPQIEVIRQATKSIEREINSVNDNPLIDVSRNKAIHGGNFQ 402

Query: 420 ASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCL-AAEDPSLNYHGKGLDIH 478
 + + +SM+ TRLA+A IGKL F Q +EL+N N GLPS L A+ +PSL+Y KG +I

Sbjct: 403 GTPIGVSMDNTRLAIAAIGKLMFAQFSELVNDFYNNGLPSNLTASSNPSLDYGFKAIEA 462

Query: 479 IAAYASELGHLANPVTTFVQPAEMGNQAVNSLALISARRTAEANDVLSLLLASHLYCTLQ 538
 +A+Y SEL +LANPVT+ VQ AE NQ VNSL LIS+R+T+EA D+L L+ + L Q

Sbjct: 463 MASYCSELQYLANPVTSHVQSAEQHNQDVNSLGLISSRKTSEAVDILKLMSTTFLVGICQ 522

Query: 539 AVDLRAMELDFKKQFDPLLPTLLQQHLGTGLDVNALALEVKKALNKRL-----EQTTTY 592
 AVDLR +E + ++ + + ++ L TG++ L + K L EQ TY

Sbjct: 523 AVDLRHLEENLRQTVKNTVSQVAKVLTGTINGE---LHPSRFCEKDLLKVVDREQVFTY 579

Query: 593 DLEP--RWHDAFSYATGTVE-LLSSSPSANVTLTAVNAWKVASAEKAIS--LTREVRNR 647
 +P + +V+ LS+ + +T++ K+ + E+ + L +EV

Sbjct: 580 VDDPCSATYPLMQRLRQVIVDHALSNGETEKNAVTSI-FQKIGAFEEELKAVLPKEVEAA 638

Query: 648 FWQTPSSQAPAHAYLSP-RTRVLYSFVREELGVQARRGDVFGVQQETIGSNVSRIYEA 706
 + AP + R+ LY FVREELG + G+ V + G +++ A+

Sbjct: 639 RAAYGNGTAPIPNRIKECRSYPLYRFVREELGTKLLTGEKV-----SPGEEFDKVFTAM 693

Query: 707 KDGRINHVLVKML 719
 +G++ L+ L

Sbjct: 694 CEGKLIDPLMDCL 706

☐ >gi|32140423|gb|AAP59439.1| ☒ phenylalanine ammonia lyase [Arabidopsis thaliana]
 gi|22137160|gb|AAM91425.1| ☒ AT3g53260/T4D2_190 [Arabidopsis thaliana]
 gi|13605819|gb|AAK32895.1| ☒ AT3g53260/T4D2_190 [Arabidopsis thaliana]
 gi|6630746|emb|CAB64229.1| ☒ phenylalanine ammonia-lyase [Arabidopsis thaliana]
 gi|21264489|sp|P45724|PAL2_ARATH ☒ Phenylalanine ammonia-lyase 2
 gi|15231778|ref|NP_190894.1| ☒ phenylalanine ammonia-lyase 2 (PAL2) [Arabidopsis
 Length = 717

Score = 350 bits (897), Expect = 1e-94

Identities = 254/733 (34%), Positives = 376/733 (51%), Gaps = 45/733 (6%)

Query: 5 LDSLATTLANGFTNGSHAAPTKSAAGPTSALRRTPGLDGHAHQSQLEIVQELSDPTDD 64
 +D + L G A TK+ A P + GL S L+ V++++ +

Sbjct: 1 MDQIEAMLCGGGEKTKVAVTTKTLADPLNW-----GLAADQMKGSHLDEVKKMVEEYRRP 55

Query: 65 VVELSGYSLTXXXXXXXXXXXXXXXXXQNDDEIRARVDKSVDFLKAQLQNSV--YGVTTGF 122
 VV L G +LT + + RA V S D++ + YGVTTGF

Sbjct: 56 VVNLGGETLTIGQVAAISTVGGSVKVELAETSRAGVKASSDWVMESMNKGTDSYGVTTGF 115

Query: 123 GGSADTRTEDAVSLQKALIEHQLCGVTPTSVSSFSVGRGLENLTPLEVVRGAMVIRVNSL 182
 G ++ RT++ +LQ LI G+ F + +TLP R AM++RVN+L

Sbjct: 116 GATSHRRTKNGTALQTELIRFLNAGI-----FGNTKETCHTLPQSATRAAMLVRVNTL 168

Query: 183 TRGHSAVRLVVLEALTNFLNHRITPIVPLRGSIASGDLSPLSYIAGAITGHPDVKVHVL 242
 +G+S +R +LEA+T+ LNH I+P +PLRG+I+ASGDL PLSYIAG +TG P+ K

Sbjct: 169 LQGYSGIRFEILEAITSLLNHNISPSLPLRGITITASGDLVPLSYIAGLLTGRPNKA--- 225

Query: 243 HEGTE-KIMFAREAISLFGLEAVV--LGPKEGLGLVNGTAVSASMATXXXXXXXXXXXXX 299
 G + + + A+EA G+ L PKEGL LVNGTAV + MA+

Sbjct: 226 -TGPDGESLTAKEAFEKAGISTGFFDLQPEGLALVNGTAVGSGMASMVLFEANVQAVLA 284

Query: 300 XXXXXXXVEAMVGQQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGSSFAXXXXXXXXXXX 359
 E M G+ F + + HPGQ+E A + +L GSS+
 Sbjct: 285 EVLSAIFAEVMSGKP-EFTDHLTHRLKHHPGQIEAAAIMEHILDGSSYMKLAQKVHEMDP 343

Query: 360 XXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTNDNPLLDVENKQTAHGGNFQ 419
 +QDRY LRTSPQ+LGP +E + A ++ E N+ DNPL+DV + HGGNFQ
 Sbjct: 344 LQKP-KQDRYALRTSPQWLGPQIEVIRQATKSIEREINSVNDNPLIDVSRNKAIHGGNFQ 402

Query: 420 ASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCL-AAEDPSLNYHGKGLDIH 478
 + + +SM+ TRLA+A IGKL F Q +EL+N N GLPS L A+ +PSL+Y KG +I
 Sbjct: 403 GTPIGVSMNTRLAIAAIGKLMFAQFSELVNDFFYNGLPSNLTASSNPGLDYGFKAIEA 462

Query: 479 IAAAYASELGHLANPVTTFVQPAEMGNQAVNSLALISARRTAEANDVLSLLLASHLYCTLQ 538
 +A+Y SEL +LANPVT+ VQ AE NQ VNSL LIS+R+T+EA D+L L+ + L Q
 Sbjct: 463 MASYCSELQYLANPVTSHVQSAEQHNQDVNSLGLISSRKTSSEAVDILKLMSTTFLVGICQ 522

Query: 539 AVDLRAMELDFFKKQFDPLLPTLLQQHLGTGLDVNALALEVKKALNKRL-----EQTTTY 592
 AVDLR +E + ++ + + ++ L TG++ L + K L EQ TY
 Sbjct: 523 AVDLRHLEENLRQTVKNTVSQVAKKVLTTGINGE---LHPSRFCEKDLLKVVDREQVFTY 579

Query: 593 DLEP--RWHDAFSYATGTVVE-LLSSSPSANVTLTAVNAWKVASAEKAIS--LTREVRNR 647
 +P + +V+ LS+ + +T++ K+ + E+ + L +EV
 Sbjct: 580 VDDPCSATYPLMQRLRQVIVDHALSNGETEKNAVTSI-FQKIGAFEEELKAVLPKEVEAA 638

Query: 648 FWQTPSSQAPAHAYLSP-RTRVLYSFVREELGVQARRGDVFGVQQETIGSNVSRIYEA 706
 + AP + R+ LY FVREELG + G+ V + G +++ A+
 Sbjct: 639 RAAYGNGTAPIPNRIKECRSYPLRFVREELGTKLLTGEKVV-----SPGEEFDKVFTAM 693

Query: 707 KDGRINHVLVKML 719
 +G++ L+ L
 Sbjct: 694 CEGKLIDPLMDCL 706

☐ >gi|6647711|sp|O64963|PAL1_PRUAV Phenylalanine ammonia-lyase 1
 gi|2935294|gb|AAC78457.1| phenylalanine ammonia-lyase; PAL1 [Prunus avium]
 Length = 717

Score = 349 bits (896), Expect = 2e-94

Identities = 244/717 (34%), Positives = 364/717 (50%), Gaps = 46/717 (6%)

Query: 14 NGFTNGSHAAPTKSAAGPTSALRRTP---GLDGHAHQSQLQLEIVQELLSIPTDDVVELSG 70
 NG NGS P +++ P G+ S L+ V+ +++ VV+L G
 Sbjct: 9 NGHKNGSVELPEL-----CIKKDPLNWGVAAETLKGSHLDEVKRMVAEYRKPVVKLGG 61

Query: 71 YSLTXXXXXXXXXXXXXXXXXQNDDEIRARVDKSVDFLKAQLQNSV--YGVTTGFGGSADT 128
 SLT + + RA V S D++ + YGVTTGFG ++
 Sbjct: 62 ESLTISQVAAIATHDSGVKVELSESARAGVKASSDWVMDSMSKGTDSYGVTTGFGATSHR 121

Query: 129 RTEDAVSLQKALIEHQLCGVTPTSVSSFSVGRGLENTLPLEVVRGAMVIRVNSLTRGHSA 188
 RT+ +LQK LI GV ++ S +TLP + R AM++R+N+L +G+S
 Sbjct: 122 RTKQGAALQKELIRFLNAGVFGSTKES-----GHTLPHQATRAAMLVRINTLLQGYSG 174

Query: 189 VRLVVLEALTNFLNHRITPIVPLRGSISASGDLSPLSYIAGAITGHPDVKVHVLHEGTEK 248
 +R +LE +T FLN+ +TP +PLRG+I+ASGDL PLSYIAG +TG P+ K V +G +
 Sbjct: 175 IRFEILEVITKFLNNNVTPCLPLRGITITASGDLVPLSYIAGMLTGRPNKA-VGPDG--Q 231

Query: 249 IMFAREAISLFGLEA--VVLGPKEGLGLVNGTAVSASMATXXXXXXXXXXXXXXXXXXXXX 306
 + A EA G+ + L PKEGL LVNGTAV + +A+

Sbjct: 232 TLSAAEAFEFVGINSGLFFELQPK EGLALVNGTAVGSGLASTVLFDTNILLALLSEILSAIF 291

Query: 307 VEAMVGQQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGSSFAXXXXXXXXXXXXXGILRQ 366
E M G+ F + + HPGQ+E A + +L GSS+ +Q

Sbjct: 292 AEVMQGKP-EFTDHLTHKLKHHPGQIEAAAIMEHILDGSSYVKAACKLHEQDPLQKP-KQ 349

Query: 367 DRYPLRTSPQFLGPLVEDMMHAYSTLSLENNNTTNDNPLLDVENKQTAHGGNFQASAVSIS 426
DRY LRTSPQ+LGP +E + ++ ++ E ++ DNPL+DV + HGGNFQ + + +S

Sbjct: 350 DRYALRTSPQWLGPQIEVIRYSTKSIEREIDSVNDNPLIDVSRNKALHGGNFQGTPIGVS 409

Query: 427 MEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCLA-AEDPSLNYHGKGLDIHIAAYASE 485
M+ TRLA+A IGKL F Q +EL+N N GLPS L+ +PSL+Y KG +I +A+Y SE

Sbjct: 410 MDNTRLAIASIGKLMFAQFSELVNDFYNNGLPSNLSGGRNPSLDYGFKA EIAMASYCSE 469

Query: 486 LGHLANPVTTFVQPAEMGNQAVNSLALISARRTAEANDVLSLLLASHLYCTLQAVDLRAM 545
L LANPVT VQ AE NQ VNSL LIS+R+TAEA D+L L+ ++ L QA+DLR +

Sbjct: 470 LQFLANPVTNHVQSAEQHNQDVNSLGLISSRKTA EAVDILKLMSSSTFLVALCQAIDLRHL 529

Query: 546 ELDFKKQFDPLLPTLLQQHLGTGLDVNALALEVKKALNKRLEQT'TTYDLEPRWHD AFSYA 605
E + + + + ++ L TG++ L + K L + + + D A

Sbjct: 530 EENLRNTVKNTVSQVAKRTLTTGVNGE---LHPSRFCEKDLLKVVDREYVFAYIDDP CSA 586

Query: 606 TGTVVE-----LLSSSPSANVTLTAVNAWKVASAEKAISLTREVRNRFWQTPSSQ 655
T +++ L + N + + E + L +EV + S

Sbjct: 587 TYPLMQKLRQVLVEHALTNGENEKNASTSIFQKIVAFEEELKVLLPKEVDSARAALDSGS 646

Query: 656 APAHAYLSP-RTRVLYSFVREELGVQARRGDVFGVGVQETIGSNVSRIYEA IKDGRI 711
A ++ R+ LY FVREELG + G + + G +++ AI +G+I

Sbjct: 647 AGVPNRITECRSYPLYKFVREELG-----AEYLTGEKVRSPGEECDKVFTAICEGKI 698

□ >gi|1172001|sp|P45730|PALY_POPTR Phenylalanine ammonia-lyase
gi|169454|gb|AAA33805.1| phenylalanine ammonia lyase [Populus balsamifera subsp.
x Populus deltoides]
gi|541843|pir|JQ2265 phenylalanine ammonia-lyase (EC 4.3.1.5) - western balsam p
cottonwood
Length = 715

Score = 348 bits (894), Expect = 3e-94

Identities = 248/729 (34%), Positives = 367/729 (50%), Gaps = 42/729 (5%)

Query: 8 LATTLANGFTNGSHAAPTKSAAGPTSALRRTPGLDGHAHQSQLEIVQELLSDPD VVE 67
+ T NG+ NGS + + P S G+ A S L+ V+ +++D VV+

Sbjct: 1 METVTKNQYQNGSLES LCVNQRDPLSW-----GVAAEAMKGS HLDEVKRMVADYRKPVVK 55

Query: 68 LSGYSLTXXXXXXXXXXXXXXXXX-QNDDEIRARVDKSVDFLKAQLQNSV--YGVTTGFGG 124
L G +LT + + R V S D++ + YGVTTGFG

Sbjct: 56 LGGETLTIAQVASIAGHDTGDVKVELSESARPGVKASSDWVMDSMDKGTDSYGVTTGFGA 115

Query: 125 SADTRTEDAVSLQKALIEHQLCGVTPPTS SVSSFSVGRGLENTLPLEVVRGAMVIRVNSLTR 184
++ RT+ +LQK LI G+ F G +TLP R AM++R+N+L +

Sbjct: 116 TSHRRTKQGGALQKELIRFLNAGI-----FGNGTETCHTLPHSATRAAMLVRINTLLQ 168

Query: 185 GHSAVRLVLEALTNFLNHRITPIVPLRGSISASGDLSPLSYIAGAITGHPDKVHVHLHE 244
G+S +R +LEA+T LN+ ITP +PLRG+I+ASGDL PLSYIAG +TG P+ K

Sbjct: 169 GYSGIRFEILEAITRLNNNITPCLPLRGITITASGDLVPLSYIAGLLTGRPN SKAT---G 225

Query: 245 GTEKIMFAREAISLFGLEA--VVLGPKEGLGLVNGTAVSASMATXXXXXXXXXXXXXXXXX 302
T +++ A EA G+E+ L PKEGL LVNGTAV + +A+

Sbjct: 226 PTGEVLDAAEAFKAAGIESGFFELQPKEGLALVNGTAVGSGGLASMLVLFETNVLA VLSELL 285

Query: 303 XXXXVEAMVGQQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGSSSFAXXXXXXXXXXXXXXG 362
E M G+ F + + HPGQ+E A + +L GS++

Sbjct: 286 SAIFAENVNGKP-EFTDHLTHKLKHHPGQIEAAAI MEHILDGSAYMKA AKKLHETDPLQK 344

Query: 363 ILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTT DNPLLDVENKQTAHGGNFQASA 422
+QDRY LRTSPQ+LGP +E + + ++ E N+ DNPL+DV + HGGNFQ +

Sbjct: 345 P-KQDRYALRTSPQWLGPQIEVIRFSTKSIEREINSVNDNPLIDVSRNKAIHGGNFQGTG 403

Query: 423 VSISMEKTRLALALIGKLNFTQCTELLNAAMNRLPSCL-AAEDPSLNYHGKGLDIHIAA 481
+ +SM+ RLA+A IGKL F Q +EL+N N GLPS L A+ +PSL+Y KG +I +A+

Sbjct: 404 IGVSMDNVRLAIASIGKLLFAQFSELVNDFYNNGLPSNLTA SRNPSLDYGFKGAEIAMAS 463

Query: 482 YASELGHLANPVTTTFVQPAEMGNQAVNSLALISARRTAEANDVLSLLLASHLYCTLQAVD 541
Y SEL +LANPVTT VQ AE NQ VNSL LIS+R+TAEA D+L L+ + L QA+D

Sbjct: 464 YCSELQYLANPVTTTHVQSAEQHNQDVNSLGLISSRKTA EAVDILKLMSTTFLVALCQAID 523

Query: 542 LRAMELDFKKQFDPLLPTLLQQHLGTGLDVNALALEVKKALNKRLEQTTTYDLEPRWHDA 601
LR +E + K + + ++ L TG + L + K L + + + D

Sbjct: 524 LRHLEENLKS AVKNTVSQVSKRVLTTGANGE---LHPSRFCEKELLKVVDREYVFAYVDD 580

Query: 602 FSYATGTVVELL-----SSSPSANVTLTAVNAWKVASAEKAI SLTREVRN-RFWQ 650
AT +++ L + N + + + E L +EV + R

Sbjct: 581 PCSATYPLMQKLRQVFDHALENGENEKNFSTSVFQKIEAFEEELKALLPKEVESARAAY 640

Query: 651 TPSSQAPAHAYLSPRTRVLYSFVREELGVQARRGDVFGVQQETIGSNVSR IYEAIKDGR 710
+ A + R+ LY FVREELG + G + ++ G +++ A+ G+

Sbjct: 641 DSGNSAIDNKIKECRSYPLYKFVREELGTV-----LLTGEKVQSPGEEFDKVF T AMCQ GK 695

Query: 711 INHVLVKML 719
I +++ L

Sbjct: 696 IIDPMLECL 704

☐ >gi|18377|emb|CAA37129.1| phenylalanine ammonia-lyase [Glycine max]
gi|129584|sp|P27991|PAL1_SOYBN Phenylalanine ammonia-lyase 1
Length = 713

Score = 348 bits (892), Expect = 4e-94

Identities = 254/722 (35%), Positives = 370/722 (51%), Gaps = 40/722 (5%)

Query: 14 NGFTNGSHAAPTKSAAGPTSALRRTPGLDGHAHQSQLEIVQELLSDPTDDVVELSGYSL 73
NG NGS T A G L G A S L+ V+ ++++ VV L G +L

Sbjct: 5 NGHQNGSFCLST--AKGNNDPLNW--GAAAEAMKGS HLDEVKRMVAEYRKPVVRLGGETL 60

Query: 74 TXXXXXXXXXXXXXXXXXQNDDEIRARVDKSVDFLKAQLQNSV--YGVTTGFGGSADTRTE 131
T + + R V S +++ + N YGVTTGFG ++ RT+

Sbjct: 61 TIAQVA AVAGHDHGVAVELSESAREGVKASSEWVMNSMNNGTDSYGVTTGFGATSHRRTK 120

Query: 132 DAVSLQKALIEHQLCGVTPTSVSSFSVGRGLEN TLPLEVVRGAMVIRVNSLTRGHSAVRL 191
+LQK LI G+ F G +TLP R AM++R+N+L +G+S +R

Sbjct: 121 QGGALQKELIRFLNAGI-----FGNGTESSHTLPHTATRAAMLVRINTLLQGYSGIRF 173

Query: 192 VVLEALTNFLNHRITPIVPLRGSISASGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIMF 251
+LEA+T LN+ +TP + LRG+I+ASGDL PLSYIAG +TG P+ K V G +++

Sbjct: 174 EILEAITKLLNNNVTPCLDLRGTTITASGDLVPLSYIAGLLTGRPN SKA-VGPSG--EVLN 230

Query: 252 AREAISLFGL--EAVVLGPKEGLGLVNGTAVSASMATXXXXXXXXXXXXXXXXXXXXXVEA 309

A+EA L + E L PKEGL LVNGTAV + +A+ E
 Sbjct: 231 AKEAFELASINSEFFELQPKGLALVNGTAVGSGGLASMLFEANILAVLSEVLSAIFAEV 290

Query: 310 MVGQQGSFAPFIHDVCRPHPGQVEVARNIRTLGSSSFAXXXXXXXXXXXXXGILRQDRY 369
 M G+ F + + HPGQ+E A + +L GSS+ +QDRY
 Sbjct: 291 MQGKP-EFTDHLTHKLKHHPGQIEAAIMEHILDGSSSYMKAACKLHEIDPLQKP-KQDRY 348

Query: 370 PLRTSPQFLGPLVEDMMHAYSTLSLENNNTTDDNPLLDVENKQTAHGGNFQASAVSISMEK 429
 LRTSPQ+LGPL+E + + ++ E N+ DNPL+DV + HGGNFQ + + +SM+
 Sbjct: 349 ALRTSPQWLGLPIEVIRFSTKSIEREINSVNDNPLIDVSRNKALHGGNFQGTPIGVSMND 408

Query: 430 TRLLALALIGKLNFTQCTELLNAAMNRGLPSCL-AAEDPSLNYHGKGLDIHIAAYASELGH 488
 TRLLALA IGKL F Q +EL+N N GLPS L A+ +PSL+Y KG +I +A+Y SEL +
 Sbjct: 409 TRLLALASIGKLMFAQFSELVNDNFYNNGLPSNLTASRNPSLDYGFKAELAMASYCSELQY 468

Query: 489 LANPVTTTFVQPAEMGNQAVNSLALISARRTAEANDVLSLLLASHLYCTLQAVDLRAMELD 548
 LANPVTT VQ AE NQ VNSL LIS+R+T EA ++L L+ ++ L QA+DLR +E +
 Sbjct: 469 LANPVTTTHVQSAEQHNQDVNSLGLISSRKTNEAIEILKMSSTFLIALCQAIDLRHLEEN 528

Query: 549 FKKQFDPLLPTLLQQHLGTGLDVNALALEVKKALNKRLEQTTTYDLEPRWHDFAFSYATGT 608
 K + + ++ L TG++ L + K L + + + D AT
 Sbjct: 529 LKNSVKNTVSQVSKRILTTGVNGE---LHPSRFCEKDLLKVVDREYIFSYIDDPCSATYP 585

Query: 609 VVELLSSSSPSANVTTLTA-----VNA---WKVASAEKAIS--LTREVRNRFWQTPSSQAPA 658
 +++ L + + A VN+ K+A E+ + L +EV S +A
 Sbjct: 586 LMQKLRQVLVDHALVNAECEKDVNSSIFQKIAIFEEELKNLLPKEVEGARAAYESGKAAI 645

Query: 659 HAYLSP-RTRVLYSFVREELGVQARRGDVFGVQQETIGSNVSRIYEAIKDGRIHVLVK 717
 + R+ LY FVREELG + G + + G +++ A+ G+I L++
 Sbjct: 646 PNKIQECRSYPLYKFVREELGT-----GLLTGEKVRSPGEEFDKLFTAMCQGIIDPLME 700

Query: 718 ML 719
 L
 Sbjct: 701 CL 702

☐ >gi|497421|gb|AAC18871.1| phenylalanine ammonia lyase [Arabidopsis thaliana]
 Length = 717

Score = 348 bits (892), Expect = 4e-94

Identities = 255/733 (34%), Positives = 375/733 (51%), Gaps = 45/733 (6%)

Query: 5 LDSLATTLANGFTNGSHAAPTKSAAGPTSAALRRTPGLDGHAHQSQLEIVQELLSIPTDD 64
 +D + L G A TK+ A P + GL S L+ V++++ +.
 Sbjct: 1 MDQIEAMLCGGGEKTKVAVTTKTLADPLNW-----GLAADQMKGSHLDEVKKMVEEYRRP 55

Query: 65 VVELSGYSLTXXXXXXXXXXXXXXXXXQNDDEIRARVDKSVDFLKAQLQNSV--YGVTTGF 122
 VV L G +LT + + RA V S D++ + YGVTTGF.
 Sbjct: 56 VVNLGGETLTIGQVAAISTVGGSVKVELAETSRAVGKASSDWVMEISMNKGTDYGVTTGF 115

Query: 123 GGSADTRTEDAVSLQKALIEHQLCGVTPTSVSSFSVGRGLENTLPLEVVRGAMVIRVNSL 182
 G ++ RT++ +LQ LI G+ F + +TLP R AM++RVN+L
 Sbjct: 116 GATSHRRTKNGTALQTELIRFLNAGI-----FGNTKETCHTLTPQSATRAAMLVRVNTL 168

Query: 183 TRGHSAVRLVLEALTNFLNHRITPIVPLRGSISASGDLSPLSYIAGAITGHPDKVHVHL 242
 +G+S +R +LEA+T+ LNH I+P +PLRG+I+ASG L PLSYIAG +TG P+ K
 Sbjct: 169 LQGYSGIRFEILEAITSLLNHNISPSPPLRGITITASGHLVPLSYIAGLLTGRPNKA-TG 227

Query: 243 HEG---TEKIMFAREAISLFGLEAVVLGPKEGLGLVNGTAVSASMATXXXXXXXXXXXXX 299

+G TEK F + IS + L PKEGL LVNGTAV + MA+
Sbjct: 228 PDGESLTEKEAFEKAGISTGFFD---LQPK EGLALVNGTAVGSGMASMVLFEANVQAVLA 284
Query: 300 XXXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGSSFAXXXXXXXXXXXXX 359
E M G+ F + + HPGQ+E A + +L GSS+
Sbjct: 285 EVLSAIFAEVMSGKP-EFTDHLTHRLKHHPGQIEAAAIMEHILDGSSYMKLAQKVHEMDP 343
Query: 360 XXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTNDNPLLDVENKQTAHGGNFQ 419
+QDRY LRTSPQ+LGP +E + A ++ E N+ DNPL+DV + HGGNFQ
Sbjct: 344 LQKP-KQDRYALRTSPQWLGPQIEVIRQATKSIEREINSVNDNPLIDVSRNKAIHGGNFQ 402
Query: 420 ASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCL-AAEDPSLNYHGKGLDIH 478
+ + +SM+ TRLA+A IGKL F Q +EL+N N GLPS L A+ +PSL+Y KG +I
Sbjct: 403 GTPIGVSMNDTRLAIAAIGKLMFAQFSELVNDFYNNGLPSNLTASSNPSLDYGFKGAEIA 462
Query: 479 IAAAYASELGHLANPVTTTFVQPAEMGNQAVNSLALISARRTAEANDVLSLLLASHLYCTLQ 538
+A+Y SEL +LANPVT+ VQ AE NQ VNSL LIS+R+T+EA D+L L+ + L Q
Sbjct: 463 MASYCESELQYLANPVTSHVQSAEQHNQDVNSLGLISSRKTSEAVDILKLMSTTFLVGICQ 522
Query: 539 AVDLRAMELDFKKQFDPLLPTLLQQHLGTGLDVNALALEVKKALNKRL-----EQTTY 592
AVDLR +E + ++ + + ++ L TG++ L + K L EQ TY
Sbjct: 523 AVDLRHLEENLRQTVKNTVSQVAKKVLTTGINGE---LHPSRFCEKDLLKVVDREQVFTY 579
Query: 593 DLEP--RWHDAFSYATGTVE--LLSSSPSANVTLTAVNAWKVASAEKAIS--LTREVRNR 647
+P + +V+ LS+ + +T++ K+ + E+ + L +EV
Sbjct: 580 VDDPCSATYPLMQRLRQVIVDHALSNGETEKNVTSI-FQKIGAFEEELKAVLPKEVEAA 638
Query: 648 FWQTPSSQAPAHAYLSP-RTRVLYSFVREELGVQARRGDVFGVQQETIGSNVSRIYEA 706
+ AP + R+ LY FVREELG + G+ V + G +++ A+
Sbjct: 639 RAYGNGTAPIPNRIKECRSYPLYRFVREELGKLLTGEKV-----SPGEEFDKVFMTAM 693
Query: 707 KDGRINHVLVKML 719
+G++ L+ L
Sbjct: 694 CEGKLIDPLMDCL 706

☐ >gi|32140425|gb|AAP59440.1| ☒ phenylalanine ammonia lyase [Arabidopsis thaliana]
gi|6056192|gb|AAF02809.1| ☒ putative phenylalanine ammonia-lyase [Arabidopsis tha
gi|23198088|gb|AAN15571.1| ☒ putative phenylalanine ammonia-lyase [Arabidopsis th
gi|20466382|gb|AAM20508.1| ☒ putative phenylalanine ammonia-lyase [Arabidopsis th
gi|14195018|sp|Q9SS45|PAL4_ARATH ☒ Probable phenylalanine ammonia-lyase
gi|15228269|ref|NP_187645.1| ☒ phenylalanine ammonia-lyase, putative [Arabidopsis
Length = 707

Score = 347 bits (890), Expect = 8e-94
Identities = 242/687 (35%), Positives = 351/687 (51%), Gaps = 36/687 (5%)

Query: 49 SQLEIVQELLSDPTDDVVELSGYSLTXXXXXXXXXXXXXXXXXQNDDEIRARVDKSVDFLK 108
S L+ V+ ++ + + V+L G +LT + +E RA V S +++
Sbjct: 30 SHLDEVKRMVKEYRKEAVKLGGETLTIGQVAAVARGGGGSTVELAEEARAGVKASSEWVM 89
Query: 109 AQLQNSV--YGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPTSVSSFSVGRG-LENT 165
+ YGVTTGFG ++ RT+ +LQ LI G+ F G G +T
Sbjct: 90 ESMNRGTD SYGVTTGFGATSHRRTKQGGALQNELIRFLNAGI-----FGPGAGDTSHT 142
Query: 166 LPLEVVRGAMVIRVNSLTRGHSVRLVLEALTNFLNHRITPIVPLRGSISASGDLSPLS 225
LP R AM++RVN+L +G+S +R +LEA+T LNH ITP +PLRG+I+ASGDL PLS

Sbjct: 143 LPKPTTRAAMLVRVNTLLQGYSGIRFEILEAITKLLNHEITPCLPLRGTTITASGDLVPLS 202

Query: 226 YIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEAVV-LGPKEGLGLVNGTAVSASM 284
YIAG +TG P+ K V G + + A EA L G+ + L PKEGL LVNGTAV + +

Sbjct: 203 YIAGLLTGRPNKA-VGPSG--ETLTASEAFKLAGVSSFFELQPKEGLALVNGTAVGSGL 259

Query: 285 ATXXXXXXXXXXXXXXXXXXXXXVEAMVQOQSFAPFIHDVCRPHPGQVEVARNIRTLLSG 344
A+ E M G+ F + + HPGQ+E A + +L G

Sbjct: 260 ASTVLF DANILAVLSEVMSAMFAEVMQGP-EFTDHLTHKLKHHPGQIEAAAIMEHILDG 318

Query: 345 SSFAXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTDNPL 404
SS+ +QDRY LRTSPQ+LGP +E + A + E N+ DNPL

Sbjct: 319 SSVYKEAQLLHEMDPLQKP-KQDRYALRTSPQWLGPQIEVIRAATKMIEREINSVNDNPL 377

Query: 405 LDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRLPSCLA-A 463
+DV + HGGNFQ + + ++M+ +RLA+A IGKL F Q +EL+N N GLPS L+

Sbjct: 378 IDVSRNKALHGGNFQGTPIGVAMDNSRLAIASIGKLMFAQFSELVNDFYNNGLPSNLSGG 437

Query: 464 EDPSLNYHGKGLDIHIAAYASELGHLANPVTTTFVQPAEMGNQAVNSLALISARRTAEAND 523
+PSL+Y KG +I +A+Y SEL LANPVT VQ AE NQ VNSL LIS+R+TAEA D

Sbjct: 438 RNPSLDYGFKAIEIAMASYCSELQFLANPVTNHVQSAEQHNQDVNSLGLISSRKTAEAVD 497

Query: 524 VLSLLLASHLYCTLQAVDLRAMELDFKKQFDPLLPTLLQQHLGTGLDVNALALEVKKALN 583
+L L+ ++L QAVDLR +E + KK + + ++ L G + L +

Sbjct: 498 ILKLMSTTYLVALCQAVDLRHLEENLKKAVKSAVSQVAKRVLTVGANGE---LHPSRFTE 554

Query: 584 KRLEQTTTYDLEPRWHDASFYATGTVVE-----LLSSSPSANVTLTAVNAWKVAS 633
+ + Q + + D T +++ L AN + +

Sbjct: 555 RDVLQVVDREYVFSYADDPCSLTYPLMQKLRLHILVDHALADPEREANSATSVFHKIGAFE 614

Query: 634 AEKAISLTREV-RNRFWQTPSSQAPAHAYLSPRTRVLYSFVREELGVQARRGDVFGVQVQ 692
AE + L +EV R R + A A+ R+ LY FVR+EL ++ G

Sbjct: 615 AELKLLLPKEVERVRVEYEEGTSIAIANRIKECRSYPLYRFVRDELNT-----ELLTGENV 669

Query: 693 ETIGSNVSRIYEAIKDGRINHLVKML 719
+ G +++ AI DG++ L++ L

Sbjct: 670 RSPGEEFDKVFLAISDGKLIDPLLECL 696

☐ >gi|2631995|emb|CAA05251.1| phenylalanine ammonia lyase [Digitalis lanata]
gi|3334286|sp|O23924|PALY_DIGLA Phenylalanine ammonia-lyase
Length = 713

Score = 347 bits (890), Expect = 8e-94

Identities = 240/685 (35%), Positives = 348/685 (50%), Gaps = 31/685 (4%)

Query: 49 SQLEIVQELLSDPTDDVVELSGYSLTXXXXXXXXXXXXXXXXXQNDDEIRARVDKSVDFLK 108
S L+ V+ ++ + VV+L G +LT Q + RA V S D++

Sbjct: 35 SHLDEVKRMVEEFRKTIVKLGGETLTISQVAAIAARDNEVAVQLAESSRAGVKASSDWVM 94

Query: 109 AQLQNSV--YGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPTSVSSFSVGRGLENLTL 166
+ YGVTTGFG ++ RT+ +LQK LI G+ F G +TL

Sbjct: 95 ESMNKGTD SYGVTTGFGATSHRRTKQGGALQKELIRFLNAGI-----FGNGTESTHTL 147

Query: 167 PLEVVRGAMVIRVNSLTRGHSAVRLVLEALTNFLNHRITPIVPLRGSISASGDLSPLSY 226
P R AM++R+N+L +G+S +R +LE +T FLNH ITP +PLRG+I+ASGDL PLSY

Sbjct: 148 PHSATRAAMLVRINTLLQGYSGIRFEILETITKFLNHNITPCLPLRGTTITASGDLVPLSY 207

Query: 227 IAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEAVV---LGPKEGLGLVNGTAVSAS 283

IAG +TG P+ K V G + A +A L G + + L PKEGL LVNGTAV +
 Sbjct: 208 IAGLLTGRPNska-VGPNGES--LNAEQAFKLAGANSGLFFELQPKEGLALVNGTAVGSG 264
 Query: 284 MATXXXXXXXXXXXXXXXXXXXXVEAMVGQQGSFAPFIHDVCRPHPGQVEVARNIRTLLS 343
 +A+ E M G+ F + + HPGQ+E A + +L
 Sbjct: 265 LASIALYEANILSLLAEVMSAVFAEVMNGKP-EFTDHLTHKLKHHPGQIEAAAIMEHILD 323
 Query: 344 GSSFAXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTDNP 403
 GSS+ +QDRY LRTSPQ+LGP +E + A + E N+ DNP
 Sbjct: 324 GSSYVKAQKMHEMDPLQKP-KQDRYALRTSPQWLGPQIEVIRTATKMIEREINSVNDNP 382
 Query: 404 LLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCLA- 462
 L+DV + HGGNFQ + + +SM+ +RLA+A IGKL F Q +EL+N N GLPS L+
 Sbjct: 383 LIDVSRNKALHGGNFQGTPIGVSMDSRLAIASIGKLMFAQFSELVNDFYNNGLPSNLSG 442
 Query: 463 AEDPSLNYHGKGLDIHIAAYASELGHLANPVTTTFVQPAEMGNQAVNSLALISARRTAEAN 522
 +PSL+Y KG +I +A+Y SEL LANPVT VQ AE NQ VNSL LIS+R+T EA
 Sbjct: 443 GRNPSLDYGFKGSEIAMASYCSELQFLANPVTNHVQSAEQHNQDVNSLGLISSRKTVEAL 502
 Query: 523 DVLSTLLASHLYCTLQAVDLRAMELDFKKQFDPLLPPLLQHLGTGLD-----VNALALE 577
 D+L L+ +++L QA+DLR +E + + + + ++ L TG++ L+
 Sbjct: 503 DILKLMSSSTYLVALCQAIDLRHLEENLRLSVKNTISQVAKRTLTTGVNGELHPSRFCELD 562
 Query: 578 VKKALNKRLEQTTTYDLEPRWHDAFSYATGTVE--LLSSSPSANVTLTAVNAWKVASAE 635
 + + +++ D + +VE L + N + + + AE
 Sbjct: 563 LLRVVDREYVFAYVDDPCSATYPLMQKLQVLVEHALKNGENEKNASTSIFQKIEAFEAE 622
 Query: 636 KAISLTREVRN-RFQWTPSSQAPAHAYLSPRTRVLYSFVREELGVQARRGDVFGVQOQET 694
 L +EV + R A A+ R+ LY F+REELG + G + +
 Sbjct: 623 LKAVLPKEVESARVALEDGKPAIANRITECRSYPLYKFIREELGT-----NFLTGEKVMS 677
 Query: 695 IGSNVSRIYEAIKDGRINHVLVKML 719
 G R++ A+ G I L+K L
 Sbjct: 678 PGECDRVFTAMSKGLIVDPLLKCL 702

>gi|1172003|sp|P45734|PALY_TRISU Phenylalanine ammonia-lyase
 gi|484062|gb|AAA17993.1| phenylalanine ammonia-lyase
 Length = 725

Score = 347 bits (890), Expect = 8e-94

Identities = 245/700 (35%), Positives = 361/700 (51%), Gaps = 45/700 (6%)

Query: 40 GLDGHAHQSQLEIVQELLSDPDDEVELSGYSLTXXXXXXXXXXXXXXXXXQNDDEIRAR 99
 G+ A S L+ V+ ++ + VV L G +LT + + RA
 Sbjct: 40 GVAAEAMKGSHLDEVKRMVEEYRKPVVRLGGETLTISQVAAIAAHDGATV-ELSESARAG 98
 Query: 100 VDKSVDFLKAQLQNSV--YGVTTFGFGSADTRTEDAVSLQKALIEHQLCGVTPTSVSSFS 157
 V S D++ + YGVTTFGFG ++ RT+ +LQK LI G+ F
 Sbjct: 99 VKASSDWVMESMNKGTDSYGVTTFGFGATSHRRTKQGGALQKELIRFLNAGI-----FG 151
 Query: 158 VGRGLENLPLEVVRGAMVIRVNSLTRGHSVRLVLEALTNFLNHRITPIVPLRGSISA 217
 G +TLP R AM++R+N+L +G+S +R +LEA+T LN+ ITP +PLRG+I+A
 Sbjct: 152 NGTESNHTLPHTATRAAMLVRINTLLQGYSGIRFEILEAITKLLNNNITPCLPLRGTTITA 211
 Query: 218 SGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEAVV--LGPKEGLGLV 275
 SGDL PLSYIAG +TG + K H + +++ A+EA L G+ A L PKEGL LV
 Sbjct: 212 SGDLVPLSYIAGLLTGRSNSKAH---GPSGEMLNAKEAFQLAGINAEFFELQPKEGLALV 268

Query: 276 NGTAVSASMATXXXXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQVEVA 335
 NGTAV + +A+ E M G+ F + + HPGQ+E A
 Sbjct: 269 NGTAVGSGLASIVLFEANILAVLSEVLSAIFAEVMQKGP-EFTDHLTHKLKHHPGQIEAA 327

Query: 336 RNIRTLGSSSFAXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLE 395
 + +L GS++ +QDRY LRTSPQ+LGPL+E + + ++ E
 Sbjct: 328 AIMEHILHGSAYVKDAKKLHEMDPLQKP-KQDRYALRTSPQWLGPLIEVIRFSTKSIERE 386

Query: 396 NNTTNDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNR 455
 N+ DNPL+DV + HGGNFQ + + +SM+ TRLALA IGKL F Q +EL+N N
 Sbjct: 387 INSVDNPNLIDVSRNKALHGGNFQGTPIGVSMNTRLALASIGKLLFAQFSELVNDNFYNN 446

Query: 456 GLPSCL-AAEDPSLNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVNSLALIS 514
 GLPS L A+ +PSL+Y KG +I +A+Y SEL +LANPVTT VQ AE NQ VNSL LIS
 Sbjct: 447 GLPSNLSASRNPSLDYGFKGSEIAMASYCSELQYLANPVTHVQSAEQHNQDVNSLGLIS 506

Query: 515 ARRTAEANDVLSLLASHLYCTLQAVDLRAMELDFKKQFDPLLPTLLQQHLGTGLDVNAL 574
 +R+T EA ++L L+ ++ L QA+DLR +E + K + + ++ L G+
 Sbjct: 507 SRKTKEAIEILQLMSSTFLIALCQAIDLRHLEENLKNVKNVTSQVAKKTLTIGVSGE-- 564

Query: 575 ALEVKKALNKRLEQTTTYDLEPRWHDAFSYATGTVVELL-----SSSPSANVT 622
 L + K L + + + D AT + + L S ++N +
 Sbjct: 565 -LHPSRFCEKDLLKVVDREHVSFYIDDPSCSATYPLAQKLQVLVDHALVNGESEKNSNTS 623

Query: 623 LTAVNAWKVASAEKAIS--LTREVRN-RFWQTPSSQAPAHAYLSRTRVLYSFVREELGV 679
 + K+A+ E+ + L +EV + R + A+ R+ LY FVREELG
 Sbjct: 624 IFQ----KIATFEEELKTLKPKEVESARTAYENGNSTIANKINGCRSYPLYKFVREELGT 679

Query: 680 QARRGDVFGVQQETIGSNVSRIYEAIKDGRINHVLVKML 719
 G+ + + G +++ A+ G+I L+K L
 Sbjct: 680 SLLTGERVI-----SPGEECDKLFAMCQGGKIIDPLLKCL 714

☐ >gi|19650|emb|CAA41169.1| phenylalanine ammonia-lyase [Medicago sativa]
 gi|129590|sp|P27990|PALY_MEDSA Phenylalanine ammonia-lyase
 Length = 725

Score = 347 bits (889), Expect = 1e-93

Identities = 241/696 (34%), Positives = 357/696 (51%), Gaps = 36/696 (5%)

Query: 40 GLDGHAHQSQLEIVQELLSDPTDDVVELSGYSLTXXXXXXXXXXXXXXXXXXQNDDEIRAR 99
 G+ A S L+ V+ ++++ VV L G +LT + R
 Sbjct: 39 GVAAEAMKGSHLDEVKRMVAEYRKPVVRLGGETLTISQVAAIAAHDHGVQVDLSESARDG 98

Query: 100 VDKSVDFLKAQLQNSV--YGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPPTS SVSSFS 157
 V S +++ + YGVTTGFG ++ +RT+ +LQK LI G+ F
 Sbjct: 99 VKASSEWVMESMNKGTDSYGVTTGFGATSHSR TKQGGALQKELIRFLNAGI-----FG 151

Query: 158 VGRGLENLPLEVVVRGAMVIRVNSLTRGHSVRLVLEALTNFLNHRITPIVPLRGSISA 217
 G +TLP R AM++R+N+L +G+S + +LEA+T LN +TP +PLRG+I+A
 Sbjct: 152 NGTESNHTLPKATATRAAMLVRINTLLQGYSGIDFEILEAITKPLNKTVPCLPLRGTTITA 211

Query: 218 SGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEAVV--LGPKEGLGLV 275
 SGD L PLSYIAG +TG P+ K H + +++ A+EA +L G+ A L PKEGL LV
 Sbjct: 212 SGD LVPLSYIAGLLTGRPNKAH---GPSGEVLNAKEAFNLAGINAEFFELQPKEGLALV 268

Query: 276 NGTAVSASMATXXXXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQVEVA 335
 NGTAV + +A+ E M G+ F + + HPGQ+E A
 Sbjct: 269 NGTAVGSGLASIVLFEANILAVLSEVLSAIFAEVMQKGP-EFTDHLTHKLKHHPGQIEAA 327

Query: 336 RNIRTLTSGSSFAXXXXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLE 395
 + +L GSS+ +QDRY LRTSPQ+LGPLVE + + ++ E
 Sbjct: 328 AIMEHILDGSSSYVKAACKLHEIDPLQKP-KQDRYALRTSPQWLGPLVEVIRFSTKSIERE 386

Query: 396 NNTTNDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNR 455
 N+ DNPL+DV + HGGNFQ + + +SM+ TRLALA IGKL F Q +EL+N N
 Sbjct: 387 INSVDNPNLIDVSRNKALHGGNFQGTPIGVSMNTRLALASIGKLMFAQFSELVNDFYNN 446

Query: 456 GLPSCL-AAEDPSLNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVNSLALIS 514
 GLPS L A+ +PSL+Y KG +I +A+Y SEL +LANPVT VQ AE NQ VNSL LIS
 Sbjct: 447 GLPSNLSASRNPSLDYGFKGAEIAMASYCSELQYLANPVTTHVQSAEQHNQDVNSLGLIS 506

Query: 515 ARRTAEANDVLSLLLASHLYCTLQAVDLRAMELDFKKQFDPLLPTLLQQHLGTGLDVNAL 574
 AR+T EA ++L L+ ++ L QA+DLR +E + K + + ++ L G++
 Sbjct: 507 ARKTNEAIEILQLMSSTFLIALCQAIDLRHLEENLKNVKNVTSQVAKKTLTMGVNGE-- 564

Query: 575 ALEVKKALKNRLEQTTTYDLEPRWHDASFYATGTVVELLSS--SPSANVTLTAVNAWKVA 632
 L + K L + + + D AT + + L A V + + +
 Sbjct: 565 -LHPSRFCEKDLLKVVDREHVFAYIDDPSCATYPLSQKLRQVLVDHALVNGESEKNFNNTS 623

Query: 633 SAEKAISLTREVRNRFWQTPSSQAPAHAYLSP-----RTRVLYSFVREELGVQARR 683
 +K + E++ + S A+ +P R+ LY FVREELG
 Sbjct: 624 IFQKIATFEELKTLPLKEVESARTAYESGNPTIPNKINGCRSYPLYKFVREELGTGLLT 683

Query: 684 GDVFGVGVQETIGSNVSRIYEAIKDGRINHLVKML 719
 G+ + + G +++ A+ G+I L++ L
 Sbjct: 684 GENVI-----SPGEECDKLFSAMCQGIIDPLLECL 714

☐ >gi|1172002|sp|P45732|PALY_STYHU Phenylalanine ammonia-lyase
 gi|556424|gb|AAA99500.1| phenylalanine ammonia lyase
 Length = 715

Score = 347 bits (889), Expect = 1e-93

Identities = 240/685 (35%), Positives = 349/685 (50%), Gaps = 32/685 (4%)

Query: 49 SQLEIVQELLSDPTDDVVELSGYSLTXXXXXXXXXXXXXXXXXQNDDEIRARVDKSVDFLK 108
 S L+ V+ ++S+ +V L G +LT Q + RA V S D++
 Sbjct: 38 SHLDEVKRMVSEYRKPLVNLGGQTLTISQVAAIAANDQGVSVQLSEASRAGVKASSDWVM 97

Query: 109 AQLQNSV--YGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPTSVSSFSVGRGLENLTL 166
 + N YGVTTGFG ++ RT+ +LQK LI G+ F G TL
 Sbjct: 98 DSMNNGTDSYGVTGFGATSHRRTKQGGALQKELIRFLNAGI-----FGNGTETNCTL 150

Query: 167 PLEVVRGAMVIRVNSLTRGHSVRLVLEALTNFLNHRITPIVPLRGSISASGDLSPLSY 226
 P R AM++R+N+L +G+S +R +LEA+T LN+ ITP +PLRG+I+ASGDL PLSY
 Sbjct: 151 PHTATRAAMLVRINTLLQGYSGIRFEILEAITKLLNNNITPCLPLRGTITASGDLVPLSY 210

Query: 227 IAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEAVVLGPKEGLGLVNGTAVSASMAT 286
 IAG +TG P+ K + T A +A + G + L PKEGL LVNGT V + +A+
 Sbjct: 211 IAGLLTGRPNKAVGPNGETLNAKEAFQAAGI-GSDFELQPEGLALVNGTPVGSGLAS 269

Query: 287 XXXXXXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQVEVARNIRTLTSGSS 346
 E M G+ F + + HPGQ+E A + +L GSS
 Sbjct: 270 VVLFEANILAVLSEVLSAIFAEMVQKGP-EFTDHLTHKLKHHPGQIEAAAIMEHILDGSS 328

Query: 347 FAXXXXXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTNDNPLLD 406
 + +QDRY LRTSPQ+LGPLVE + + ++ E N+ DNPL+D

Sbjct: 329 YVKAACKLHEIDPLQKP-KQDRYALRTSPQWLGPLVEVIRFSTKSIEREINSVNDNPLID 387

Query: 407 VENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSC-L-AAED 465
V + HGGNFQ + + +SM+ TRLA+A IGKL F Q +EL+N N GLPS L A+ +

Sbjct: 388 VSRNKALHGGNFQGTPIGVSMNTRLAVASIGKLMFAQFSELVNDFYNNGLPSNLSASRN 447

Query: 466 PSLNYHGKGLDIHIAAYASELGHLANPVTTTFVQPAEMGNQAVNSLALISARRTAEANDVL 525
PSL+Y KG +I +A+Y SEL +LANPVT+ VQ AE NQ VNSL LISAR+T EA ++L

Sbjct: 448 PSLDYGFKGTEIAMASYCSELQYLANPVTSHVQSAEQHNQDVNSLGLISARKTNEAVEIL 507

Query: 526 SLLLASHLYCTLQAVDLRAMELDFKKQFDPLLPTLLQQHLGTGLDVNALALEVKKALNKR 585
L+ ++L QA+DLR +E + K + + ++ L TG++ L + K

Sbjct: 508 KLMSPTYLIALCQAIDLRHLEENLKNVTVKSQVAKRTLTTGVNGE---LHPSRFCEKD 564

Query: 586 LEQTTTYDLEPRWHDFAFSYATGTVE-----LLSSSPSANVTLTAVNAWKVASAE 635
L + + + D AT +++ L ++ NV + E

Sbjct: 565 LLKIVDREYCFAYIDDPSCATYPLMQKLRQVLVEHALANAENEKNVNTSIFQKITTFEEE 624

Query: 636 KAISLTREVRN-RFQWTPSSQAPAHAYLSRTRVLYSFVREELGVQARRGDVFGVQOQET 694
L +EV R A + R+ LY FVREELG ++ G + +

Sbjct: 625 LKTLLPKEVEGARIAYENGQSAIPNKIKECRSYPLYKFVREELGT-----EMLTGEKVRS 679

Query: 695 IGSNVSRIYEAIKDGRINHVLVKML 719
G +++ A+ G+I L++ +

Sbjct: 680 PGEECDKLFAMCQCKIIDPLLECI 704

☐ >gi|15100059|gb|AAK84225.1| phenylalanine ammonia-lyase [Rehmannia glutinosa]
Length = 708

Score = 345 bits (886), Expect = 2e-93

Identities = 241/686 (35%), Positives = 346/686 (50%), Gaps = 35/686 (5%)

Query: 49 SQLEIVQELSDPTDDVVELSGYSLTXXXXXXXXXXXXXXXXXQNDDEIRARVDKSVDFLK 108
S L+ V+ ++ + V+L G SLT + + RA V S D++

Sbjct: 32 SHLDEVKRMVEEFRKPAVKLGESLTIAQVAAIAARDNAVAVELAETARAGVKASSDWVM 91

Query: 109 AQLQNSV--YGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPTSVSSFSVGRGLENLTL 166
+ YGVTTGFG ++ RT+ +LQK LI G+ F G + L

Sbjct: 92 ESMNKGTD SYGVTTGFGATSHRRTKQGGALQKELIRFLNAGI-----FGNGTESNHAL 144

Query: 167 PLEVVRGAMVIRVNSLTRGHSAVRLVLEALTNFLNHRITPIVPLRGSISASGDLSPLSY 226
P R AM++R+N+L +G+S +R +LEALT FLNH ITP +PLRG+I+ASGDL PLSY

Sbjct: 145 PHSATRAAMLVRINTLLQGYSGIRFEILEALTFLNHNITPCLPLRGTITASGDLVPLSY 204

Query: 227 IAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEAVV-LGPKEGLGLVNGTAVSASMA 285
IAG +TG P+ K V G + + A EA SL G+ L PKEGL LVNGTAV + +A

Sbjct: 205 IAGLLTGRPNKA-VGPNG--EALNAGEAFSLAGVSGFFELQPKEGLALVNGTAVGSGLA 261

Query: 286 TXXXXXXXXXXXXXXXXXXXXVEAMVGQQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGS 345
+ E M G+ F + + HPGQ+E A + +L GS

Sbjct: 262 SIALYDANILAVLSEVTSVIFAEVMNGKP-EFTDHLTHKLKHHPGQIEAAAIMHILDGS 320

Query: 346 SFAXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTNDNPLL 405
++ +QDRY LRTSPQ+LGP +E + A + E N+ D PL+

Sbjct: 321 AYVKAQKLHETDPLQKP-KQDRYALRTSPQWLGPQIEVIRTATKMIEREINSVNDTPLI 379

Query: 406 DVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSC-L-AE 464
DV + HGGNFQ + + +SM+ TRLA+A IGKL F Q +EL+N N GLPS L+

Sbjct: 380 DVSRNKALHGGNFQGTPIGVSMNTRLAIAAIGKLMFAQFSELVNDFYNNGLPSNLSGGR 439

Query: 465 DPSLNHYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVNSLALISARRTAEANDV 524
+PSL+Y KG +I +A+Y SEL LANPVT VQ AE NQ VNSL LIS+R+T EA D+

Sbjct: 440 NPSLDYGFKGSEIAMASYCSELQFLANPVTNHVQSAEQHNQDVNSLGLISSRKTVEALDI 499

Query: 525 LSLLLASHLYCTLQAVDLRAMELDFKKQFDPLLPTLLQQHLGTGLDVNALALEVKKALNK 584
L L+ +++L QAVDLR +E + + + + ++ L G++ L + K

Sbjct: 500 LKLMSSTYLIALCQAVDLRHLEENLRSLVKNTVSQVAKRTLTMGINGE---LHPSRFCEK 556

Query: 585 RLEQTTTYDLEPRWHDFAFSYATGTVVELL-----SSSPSANVTLTAVNAWKVASA 634
L + + + D T +++ L + NV+ + +

Sbjct: 557 DLLRVVDREYVFAYIDDPSCSGTYPLMQKLRQVLVDHALNNGESEKNVSTSIFQKIEAFEV 616

Query: 635 EKAISLTREVRN-RFWQTPSSQAPAHAYLSPRTRVLYSFVREELGVQARRGDVFGVQQE 693
E L +EV + R + A + R+ LY F+REELG G+ V

Sbjct: 617 ELKAILPKEVESARIALESNPAGNRITECRSYPLYKFIREELGTNYLTGEKV----- 671

Query: 694 TIGSNVSRIYEAIKDGRINHVLVKML 719
+ G +++ A+ G I L+K L

Sbjct: 672 SPGEECDKVFTALSKGLIVDPLLKCL 697

☐ >gi|535008|emb|CAA57057.1| phenylalanine ammonia-lyase 3 [Petroselinum crispum]
gi|1171996|sp|P45729|PAL3_PETCR Phenylalanine ammonia-lyase 3
Length = 718

Score = 344 bits (883), Expect = 5e-93

Identities = 248/700 (35%), Positives = 354/700 (50%), Gaps = 42/700 (6%)

Query: 40 GLDGHAHQSQLEIVQELLSDPDQVVELSGYSLTXXXXXXXXXXXXXXXXX-QNDDEIRA 98
G+ A S L+ V+ ++++ VV+L G +LT + +E RA

Sbjct: 30 GVAAEALTGSHLDEVKRMVAEYRKPVVKLEGETLTISQVAAISARDDSGVKVELSEEARA 89

Query: 99 RVDKSVDFLKAQLQNSV--YGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPTSVSSF 156
V S D++ + YGVTTGFG ++ RT+ +LQK LI G+

Sbjct: 90 GVKASSDWMDSMNKGTD SYGVTTGFGATSHRRTKQGGALQKELIRFLNAGI----- 141

Query: 157 SVGRGLE---NTLPLEVVRGAMVIRVNSLTRGHSAVRLVVLEALTNFLNHRITPIVPLRG 213
G G E NTLR R AM++R+N+L +G+S +R +LEA+T FLNH ITP +PLRG

Sbjct: 142 -FGSGAEAGNNTLPHSATRAAMLVRINTLLQGYSGIRFEILEAITKFLNHNITPCLPLRG 200

Query: 214 SISASGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEA--VVLGPKEG 271
+I+ASGDL PLSYIAG +TG P+ K T + EA L G+E L PKEG

Sbjct: 201 TITASGDLVPLSYIAGLLTGRPNKAV---GPTGVTLSPEEAFKLAGVEGGFFELQPKEG 257

Query: 272 LGLVNGTAVSASMATXXXXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQ 331
L LVNGTAV + MA+ E M G+ F + + HPGQ

Sbjct: 258 LALVNGTAVGSGMASMVLFEANILAVLAEVMSAIFAEVMQGKP-EFTDHLTHKLKHHPGQ 316

Query: 332 VEARNIRTLLSGSSFAXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYST 391
+E A + +L GS++ +QDRY LRTSPQ+LGP +E + +

Sbjct: 317 IEAAAIMHILDGSAYVKAQKLHEMDPLQKP-KQDRYALRTSPQWLGPQIEVIRSSTKM 375

Query: 392 LSLENNTTTDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNA 451
+ E N+ DNPL+DV + HGGNFQ S + +SM+ TRLA+A IGKL F Q +EL+N

Sbjct: 376 IEREINSVNDNPLIDVSRNKAIHGGNFQGSPIGVSMNTRLAIAAIGKLMFAQFSELVND 435

Query: 452 AMNRGLPSCLA-AEDPSLNHYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVNSL 510

N GLPS L+ +PSL+Y KG +I +A+Y SEL LANPVT VQ AE NQ VNSL
 Sbjct: 436 FYNNGLP SNLSGGRNPSLDYGFKGAEIAMASYCSELQFLANPVTNHVQSAEQHNQDVNSL 495

Query: 511 ALISARRTAEANDVLSLLLASHLYCTLQAVDLRAMELDFKKQFDPLLPTLLQQHLGTGLD 570
 LIS+R+T+EA ++L L+ + L QA+DLR +E + K + + ++ L G++
 Sbjct: 496 GLISSRKTSEAVEILKLMSTTFLVGLCQAIDLRHLEENLKSTVKNTVSQVAKRVLTMGVN 555

Query: 571 VNALALEVKKALNKRLEQTTTYDLEPRWHDAFSYAT-----GTVVELLSSSPSANVT 622
 L + K L + + + D AT T+VE ++
 Sbjct: 556 GE---LHPSRFCEKDLLRVVDREYIFAYIDDPSCSATYPLMQKLRETLVEHALNNGDKERN 612

Query: 623 LTAVNAWKVASAEKAIS--LTREVRN-RFWQTPSSQAPAHAYLSPRTRVLYSFVREELGV 679
 L+ K+A+ E + L +EV R + A + R+ LY FVREELG
 Sbjct: 613 LSTSIFQKIAAFEDELKALLPKEVETARAALESGNPAIPNRIKECRSYPLYKFVREELGT 672

Query: 680 QARRGDVFGVQQETIGSNVSRIYEAIKGRINHVLVKML 719
 + G + + G +++ A+ G I L++ L
 Sbjct: 673 -----EYLTGEKVRSPGEEFEKVFTAMSKGEIIDPLLECL 707

☐ >gi|129585|sp|P19142|PAL2_PHAVU Phenylalanine ammonia-lyase class II
 gi|228614|prf||1807329A Phe ammonia lyase
 Length = 712

Score = 344 bits (882), Expect = 6e-93
 Identities = 242/686 (35%), Positives = 357/686 (52%), Gaps = 34/686 (4%)

Query: 49 SQLEIVQELLSIPTDDVVELSGYSLTXXXXXXXXXXXXXXXXXQNDDEIRARVDKSVDFLK 108
 S L+ V+ ++++ V L G +LT + + RA V D++
 Sbjct: 35 SHLDEVKRMVAEYRKPAVRLGGQTLTIAQVAATAAHDQGLKVELAESARACVKAISDWVM 94

Query: 109 AQLQNSV--YGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPPTS SVSSFSVGRGLEN-- 164
 + YG+TTGFG ++ RT+ +LQK LI G+ G G E+
 Sbjct: 95 ESMDKGTDSYGITTTGFGATSHRRTKQGGALQKELIRFLNAGI-----FGNGTESNC 145

Query: 165 TLPLEVVRGAMVIRVNSLTRGHSVRLVLEALTNFLNHRITPIVPLRGSISASGDL SPL 224
 TLP R AM++RVN+L +G+S +R +LEA+T LN+ ITP +PLRG+I+ASGDL PL
 Sbjct: 146 TLPHTATRAAMLVRVNTLLQGYSGIRFEILEAITKLLNNNITPCLPLRGITITASGDLVPL 205

Query: 225 SYIAGAITGHPDVKVHVLHEGTEKIMFAREAI SL--FGLEAVVLGPKEGLGLVNGTAVSA 282
 SYIAG +TG P+ K V G +I+ A+EA L G E L PKEGL LVNGTAV +
 Sbjct: 206 SYIAGLLTGRPNKA-VGPSG--EILNAKEAFELANIGSEFFELQPKEGLALVNGTAVGS 262

Query: 283 SMATXXXXXXXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQVEVARNIRTLL 342
 +A+ E M G+ F + + HPGQ+E A + +L
 Sbjct: 263 GLASIVLFEANILAVLSEVISAIFAEVMQGP-EFTDHLTHKLKHHHPGQIEAAAIMEHIL 321

Query: 343 SGSSFAXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTDN 402
 GSS+ +QDRY LRTSPQ+LGP +E + + ++ E N+ DN
 Sbjct: 322 DGSSYIKAAKKLHEIDPLQKP-KQDRYALRTSPQWLGPQIEVIRFSTKSIEREINSVNDN 380

Query: 403 PLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCL- 461
 PL+ V + HGGNFQ + + +SM+ TRLA+A IGKL F Q ++L+N N GLPS L
 Sbjct: 381 PLISVSRNKALHGGNFQGTPIGVSMDNTRLAIASIGKLMFAQFSDLVNDYNNGLPSNLT 440

Query: 462 AAEDPSLNYHGKGLDIHIAAYASELGHLANPVTTTFVQPAEMGNQAVNSLALISARRTAEA 521
 A+ +PSL+Y KG +I +A+Y SEL +LANPVT+ VQ AE NQ VNSL LIS+R+T EA
 Sbjct: 441 ASRNPSLDYGFKGAEIAMASYCSELQYLANPVTSHVQSAEQHNQDVNSLGLISSRKTNEA 500

Query: 522 NDVLSLLLASHLYCTLQAVDLRAMELDFKKQFDPLLPDLLQQLHGTGLDVNALALE-VKK 580
 ++L L+ ++ L QA+DLR +E + K ++ + ++ L TG++ +K
 Sbjct: 501 LEILKLMSSTFLVALCQAIDLRHLEENLNKNTVKNVVSQVAKRTLTTGVNGELHPSRFCEK 560

Query: 581 ALNKRLEQTTTY----DLEPRWHDFAFSYATGTVVELLSSSPSANVTLTAVNAWKVASAEK 636
 AL K +E+ T+ D + +V+ ++ L K+AS E+
 Sbjct: 561 ALLKVVEREYTFAYIDDPCSGTYPLMQKLQVLDYALANGENEKNLNTSIFQKIASFEE 620

Query: 637 AIS--LTREVRNRWFQTPSSQ-APAHAYLSPTRVLYSFVREELGVQARRGDVFGVQQE 693
 + L +EV + Q A + R+ LY FVREELG G+ +
 Sbjct: 621 ELKTLPLKEVEGARLAYENDQCAIPNKIKDCRSYPLYKFVREELGTSLLTGEKVI----- 675

Query: 694 TIGSNVSRIYEAIKDGRINHLVKML 719
 + G +++ A+ G+I L++ L
 Sbjct: 676 SPGEECDKVFSAQCQGIIDPLLECL 701

☐ >gi|58618148|gb|AAW80640.1| phenylalanine ammonia lyase [Psilotum nudum]
 Length = 772

Score = 343 bits (881), Expect = 8e-93

Identities = 246/718 (34%), Positives = 363/718 (50%), Gaps = 41/718 (5%)

Query: 19 GSHAAPTKSAAGPTSALRRTPGLDGHAHQSQLEIVQELLSDPD-DVVELSGYSLTXXX 77
 G P KS P + + S L+ V+ ++ + +D +VV L G +LT
 Sbjct: 25 GGRLLPKHSEGDPLKWVE-----SAQESECSHLDEVRRMVKEFSDGNVSLQGLNLTVAQ 79

Query: 78 XXXXXXXXXXXXXQNDDEIRARVDKSVDFLKAQLQNSV--YGVTTGFGGSADTRTEDAVS 135
 + R RVD+S +++ + YGVTTGFG ++ RT +
 Sbjct: 80 VAAVARRPDVKVELDSAVARRRVDSESEWVNHNIMKGTDTYGVTTGFGATSHRRTNQIE 139

Query: 136 LQKALIEHQLCGVTPPTSVSSFSVGRGLENLPLEVVIRGAMVIRVNSLTRGHSAVRLVVLE 195
 LQK LI G+ + G+ N+LP VR A+++R N+L +G S +R +LE
 Sbjct: 140 LQKELIRFLNAGI-----LTDGKEECNSLPTPAVRAAILVRTNTLMQGFSGIRWAILE 192

Query: 196 ALTNFLNHRITPIVPLRGSISASGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIMFAREA 255
 A+ LN +ITP +PLRG+I+ASGDL PLSYIAG +T P+ + V EG E + EA
 Sbjct: 193 AMEKLNSQITPRLPLRGITITASGDLVPLSYIAGLLTARPNSRA-VTAEGKE--VTGEEA 249

Query: 256 ISLFGL-EAVVLGPKEGLGLVNGTAVSASMATXXXXXXXXXXXXXXXXXXXXXVEAMVGQQ 314
 + L G+ E L PKEGL LVNGTAV A +A E M G+
 Sbjct: 250 LKLAGIQEPFDLQPKGLALVNGTAVGAGLAHVVCYDANIFALLAEVLSALFCEVMQKGP 309

Query: 315 GSFAPFIHDVCRPHPGQVEVARNIRTLLSGSSFAXXXXXXXXXXXXXXXXXGILRQDRYPLRTS 374
 F + + HPGQ+E A + LL GSS+ +QDRY LRTS
 Sbjct: 310 -EFTDHLTHRLKHHPGQIEAAAIMEWLLDGSSYMKAAAKLHETDPLKKP-KQDRYALRTS 367

Query: 375 PQFLGPLVEDMMHAYSTLSLENNTTTDNPLLDVENKQTAHGGNFQASAVSISMEKTRLAL 434
 PQ+LGP +E + A + E N+ DNPL+DV + HGGNFQ + + +SM+ RLA+
 Sbjct: 368 PQWLGPQIEVIRLATHAIQREINSVNDNPLIDVARDKALHGGNFQGTPIGVSMNDNMLAI 427

Query: 435 ALIGKLNFTQCTELLNAAMNRLPSCLA-AEDPSLNYHGKGLDIHIAAYASELGHLANPV 493
 A IGKL F Q +EL+N N GLPS L+ + +PSL+Y KG +I +A+Y SE+ +LANPV
 Sbjct: 428 AAIGKLMFAQFSELVNDLYNGLPSNLGSPNPSLDYGFKAELALASYTSEMQLANPV 487

Query: 494 TTFVQPAEMGNQAVNSLALISARRTAEANDVLSLLLASHLYCTLQAVDLRAMELDFKKQF 553
 TT Q AE NQ VNSL LISAR+T EA D+L L+++++ QAVDLR +E + K
 Sbjct: 488 TTHSQSAEQHNQDVNSLGLISARKTKEAIDILKLMISTYIVALCQAVDLRHLEENMKAAI 547

Query: 554 DPLLPTLLQQHLGTGLDVNALALE---VKKALNKRLEQTTTYDLEPRWHDAFSYATGTVV 610
 ++ + ++ L D N L L +K L +E + S +
 Sbjct: 548 KHMVCQVARRTL--YFDHNGLLLP SRFCEKELLHVVEHEPIFLYIDNASSDASILMQKLR 605

Query: 611 ELLSSSPSANVTLTAVNAWKVASAEKAISLTREVRNRF-WQTPSSQ-----APAHAY 661
 ++L NV ++ + + E++N F + P ++ A +
 Sbjct: 606 QVLVDQAMKNVEKEKEKLGAASTLNRILLFEEELKNLFDSEIPRARERFDRGQFAVLNRI 665

Query: 662 LSPRTRVLVSFVREELGVQARRGDVFGVQVQETIGSNVSRIYEAIKDGRINHVLVKML 719
 + RT LY FVR++LG Q + G Q + G + ++ +AI +G++ L+K +
 Sbjct: 666 QNCRTYPLYRFVRDDLGTQ-----LLSGTQTHSPGQDFQKVLDAISEGKLVAPLLKCI 718

☐ >gi|3024361|sp|Q42858|PAL2_IPOBA Phenylalanine ammonia-lyase
 gi|1122743|dbj|BAA11459.1| Phenylalanine Ammonia-Lyase [Ipomoea batatas]
 Length = 708

Score = 343 bits (881), Expect = 8e-93

Identities = 245/687 (35%), Positives = 354/687 (51%), Gaps = 37/687 (5%)

Query: 49 SQLEIVQELLSDPDDEVELSGYSLTXXXXXXXXXXXXXXXXXQNDDEIRARVDKSVDFLK 108
 S L+ V+ ++++ + V++ G +LT + + AR + S D++
 Sbjct: 32 SHLDEVKRMVAEFRNPAVKIGGQTLTSLRSPPIAARDNASKWSSP-RLPARRESSSDWVM 90

Query: 109 AQLQNSV--YGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPTSVSSFSVGRGLENLTL 166
 + N YGVTTGFG ++ RT++ +LQ+ LI G+ F G G +TL
 Sbjct: 91 NSMNGTDSYGVTGFGATSHRRTKNGHALQQLIRFLNAGI-----FGTGTGASHTL 143

Query: 167 PLEVVRGAMVIRVNSLTRGHSAVRLVLEALTNFLNHRITPIVPLRGSISASGDLSPLSY 226
 P R AM++R+N+L +G+S +R +LEA+T LNH ITP +PLRG+I+ASGDL PLSY
 Sbjct: 144 PHSATRAAMLVRINTLLQGYSGIRFEILEAITKLLNHNITPCLPLRGITITASGDLVPLSY 203

Query: 227 IAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEA--VVLGPKEGLGLVNGTAVSASM 284
 IAG +TG P+ K V G + + A EA L G++ L PKEGL LVNGTAV + M
 Sbjct: 204 IAGLLTGRPNKA-VGPNG--EALTAEEAFKLAGVQGGFFELQPKEGLALVNGTAVGSGM 260

Query: 285 ATXXXXXXXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQVEVARNIRTLLSG 344
 A+ E M G+ F + + HPGQ+E A + +L
 Sbjct: 261 ASMVLFEANVLAVLSEVLSAIFAEMVNGKP-EFTDHLTHKLKHHPGQIEAAIMEHILDR 319

Query: 345 SSFAXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTNDNPL 404
 S + +QDRY LRTSPQ+LGP +E + A + E N+ DNPL
 Sbjct: 320 SYMKAQAQKLHEMDPLQKP-KQDRYALRTSPQWLGPQIEVIRQAATKMIEREINSVNDNPL 378

Query: 405 LDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSC-L-AA 463
 +DV + HGGNFQ + + +SM+ +RLALA IGKL F Q +EL+N N GLPS L A
 Sbjct: 379 IDVSRNKALHGGNFQGTPIGVSMDNSRLALASIGKLIFAQFSELVNDYNNGLPSNLTAG 438

Query: 464 EDPSLNYHGKGLDIHIAAYASELGHLANPVTTTFVQPAEMGNQAVNSLALISARRTAEAND 523
 +PSL+Y KG++I +A+Y SEL LANPVT VQ AE NQ VNSL LISAR+TAEA D
 Sbjct: 439 RNPSLDYGFKGVEIAMASYCSELQFLANPVTNHVQSAEQHNQDVNSLGLISARKTAEAVD 498

Query: 524 VLSLLLASHLYCTLQAVDLRAMELDFKKQFDPLLPTLLQQHLGTGLDVNALALEVKKALN 583
 VL L+ +++L QA+DLR +E + K + + ++ L G++ L +
 Sbjct: 499 VLKLMSSSTYLVALCQAIDLRHLEENLKNVNRNTVNQVAKRTLTMGVNGE---LHPSRFCE 555

Query: 584 KRL-----EQTTTYDLEP--RWHDAFSYATGTVVE--LLSSSPSANVTLTAVNAWKVAS 633
 K L E Y +P + F +V+ L + NV+ +
 Sbjct: 556 KDLLRVVDREYVFAYADDPCSANYPFLQKLRQVLVDHALQNGEHEKNVSTSIFQKIAAFE 615

Query: 634 AEKAISLTREVRN-RFWQTPSSQAPAHAYLSRTRVLYSFVREELGVQARRGDVFGVQ 692
 E L +EV R + A + R+ LY FVREELG ++ G +
 Sbjct: 616 DELKAVLPKEVEGARSASAIENGNPAIPNRITECRSYPLYKFVREELGT-----EMLTGEKV 670

Query: 693 ETIGSNVSRIYEAIKDGRIHVLVKML 719
 ++ G +++ A+ DG I L++ L
 Sbjct: 671 KSPGEVCDKVFTAVCDGGIIDPLLECL 697

□>gi|3914262|sp|O49836|PAL2_LITER Phenylalanine ammonia-lyase 2 (PAL-2)
 gi|2911124|dbj|BAA24929.1| phenylalanine ammonia-lyase [Lithospermum erythrorhizo]
 Length = 705

Score = 343 bits (881), Expect = 8e-93
 Identities = 240/696 (34%), Positives = 355/696 (51%), Gaps = 36/696 (5%)

Query: 40 GLDGHAHQSQLEIVQELLSDPDVELSGYSLTXXXXXXXXXXXXXXXXXQNDDEIRAR 99
 G+ + S L+ V+++++ VV+L+G +LT + + R
 Sbjct: 19 GMAAESMKGSHLDEVKMKMAEFRKPVVQLAGKTLTIAQVAAIAARDDGVTVELAEAAREG 78

Query: 100 VDKSVDFLKAQLQNSV--YGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPTSVSSFS 157
 V S D++ + YGVTTGFG ++ RT+ +LQK LI G+ F
 Sbjct: 79 VKASSDWVMESMNKGTDSYGVTTGFGATSHRRTKQGGALQKELIRFLNAGI-----FG 131

Query: 158 VGRGLENLPLEVVRGAMVIRVNSLTRGHSVRLVLEALTNFLNHRITPIVPLRGSISA 217
 G +TLP R AM++R+N+L +G+S +R +LEA+T FLN ITP +PLRG+I+A
 Sbjct: 132 NGTETSHTLPHSATRAAMLVRINTLLQGYSGIRFEILEAITKFLNTNITPCLPLRGTTITA 191

Query: 218 SGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEA--VVLGPKEGLGLV 275
 SGDL PLSYIAG +TG P+ K T + + A EA L G+ + L PKEGL LV
 Sbjct: 192 SGDLVPLSYIAGLLTGRPNKAV---GPTGEKLNAAEFRLAGISSGFFELQPKGLALV 248

Query: 276 NGTAVSASMATXXXXXXXXXXXXXXXXXXVEAMVGQQGSFAPFIHDVCRPHPGQVEVA 335
 NGTAV + MA+ E M G+ F + + HPGQ+E A
 Sbjct: 249 NGTAVGSGMASMVLYEANILGVMSEVLSAVFAEVMNGKP-EFTDHLTHKLKHHPGQIEAA 307

Query: 336 RNIRTLGSSSFAXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLE 395
 + +L GS + +QDRY LRTSPQ+LGP +E + A + E
 Sbjct: 308 AIMEHILDGSGYVKAELLHEMDPLQKP-KQDRYALRTSPQWLGPQIEVIRSATKMIERE 366

Query: 396 NNTTTDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNR 455
 N+ DNPL+DV + HGGNFQ + + ++M+ TRLA+A IGKL F Q +EL+N N
 Sbjct: 367 INSVNDNPLIDVSRNKALHGGNFQGTPIGVAMDNTRLAIAAIGKLLFAQFSELVNDYYNN 426

Query: 456 GLPSCL-AAEDPSLNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVNSLALIS 514
 GLPS L + DPSL+Y KG +I +A+Y SEL LANPVT VQ AE NQ VNSL LIS
 Sbjct: 427 GLPSNLTGSRDPSLDYGFKGAEIAMASYCSELQFLANPVTNHVQSAEQHNQDVNSLGLIS 486

Query: 515 ARRTAEANDVLSLLASHLYCTLAQVDLRAMELDFKKQFDPLLPTLLQQHLGTGLDVNAL 574
 +R+T+EA ++L L+ +S L QAVDLR +E + + + + ++ L G+D
 Sbjct: 487 SRKTSEAVEILKLMSSSFLVALCQAVDLRHIEENVRLAVKKTVSQVAKKTLNIGVDG--- 543

Query: 575 ALEVKKALNKRLEQTTTYDLEPRWHDFAFSYATGTVE-----LLSSSPSANVTLT 624
 L + K L + + + D AT +++ L +S + + +
 Sbjct: 544 VLHPSRFSEKELLRVVDREYVFAYADDPSCATYPLMQKLREVLVSHALANSNEKDASTS 603

Query: 625 AVNAWKVASAEKAISLTREVRN-RFWQTPSSQAPAHAYLSRTRVLYSFVREELGVQARR 683
 + V E L +EV N R + A + R+ LY FVR ELG

Sbjct: 604 IFHKIGVFEEELKGILPKEVENARASVENGTAPAIPNKIEECRSYPLYKFVRGELGT---- 659

Query: 684 GDVFGVGVQQETIGSNVSRIYEAIKDGRINHVLVKML 719

++ G + + G + +++ A+ +G++ L+ L

Sbjct: 660 -ELLTGEKVRSPGEELDQVFNALCEGKLVDPDLLACL 694

☐ >gi|18001007|gb|AAL55242.1| phenylalanine ammonia-lyase [Lactuca sativa]
Length = 711

Score = 343 bits (880), Expect = 1e-92

Identities = 244/699 (34%), Positives = 364/699 (52%), Gaps = 40/699 (5%)

Query: 40 GLDGHAHQSQLEIVQELLSPTDDVVELSGYSLTXXXXXXXXXXXXXXXXXQND--DEIR 97
G+ A S L+ V+++++ VV+L G +LT + + + R

Sbjct: 23 GVAAEALTGSHLDEVKKMVAEFRKPVVKLGGETLTVSQVAGIAAANDSDTVKVELSEAAAR 82

Query: 98 ARVDKSVDFLKAQLQNSV--YGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPTSVSS 155
A V S D++ + YGVTTGFG ++ RT+ +LQK LI G+

Sbjct: 83 AGVKASSDWVMESMNKGTDSYGVTTGFGATSHRRTKQGGALQKELIRFLNAGI----- 135

Query: 156 FSVGRGLENLTPLEVVRGAMVIRVNSLTRGHSVRLVVLEALTNFLNHRITPIVPLRGS 215
F G +TLP R AM++R+N+L +G+S +R +LEA+T FLN+ ITP +PLRG+I

Sbjct: 136 FGNGTETSHTLPHSATRAAMIVRINTLLQGYSGIRFEILEAITKFLNNNITPCLPLRGTI 195

Query: 216 SASGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIMFAEAISLFGLEA--VVLGPKEGLG 273
+ASGDL PLSYIAG +TG P+ K T +++ A +A + G+E L PKEGL

Sbjct: 196 TASGDLVPLSYIAGLLTGRPNKAV---GPTGEVLNAEKAFAAAGVEGGFFELQPKEGLA 252

Query: 274 LVNGTAVSASMATXXXXXXXXXXXXXXXXXXVEAMVGQQGSFAPFIHDVCRPHPGQVE 333
LVNGTAV + MA+ E M G+ F + + HPGQ+E

Sbjct: 253 LVNGTAVSGMASMVLFDANVLALLSEVLSAIFAEVMQKGP-EFTDHLTHKLKHHPGQIE 311

Query: 334 VARNIRTLGSSFAXXXXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLS 393
A + +L GS + +QDRY LRTSPQ+LGP +E + + +

Sbjct: 312 AAAIMEYILDGSDYVKAQKVHEMDPLQKP-KQDRYALRTSPQWLGPQIEVIRSSSTKMIE 370

Query: 394 LENNTTTDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAM 453
E N+ DNPL+DV + HGGNFQ + + +SM+ TRLA+A IGKL F Q +EL+N

Sbjct: 371 REINSVNDNPLIDVSRNKALHGGNFQGTPIGVSMDNTRLAIAAIGKLMFAQFSELVNDFY 430

Query: 454 NRGLPSCLA-AEDPSLNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVNSLAL 512
N GLPS L+ +PSL+Y KG +I +A+Y SEL LANPVT VQ AE NQ VNSL L

Sbjct: 431 NNGLPSNLSSGRNPSLDYGFKGGEIAMASYCSELQFLANPVTNHVQSAEQHNQDVNSLGL 490

Query: 513 ISARRTAEANDVLSLLASHLYCTLQAVDLRAMELDFKKQFDPDLLPTLLQQHLGTGLDVN 572
ISAR+TAEA D+L L+ +++L Q++DLR +E + K + + ++ L G++

Sbjct: 491 ISARKTAEAVDILKLMSSSTYLVALCQSIDLRHLEENMKSTVKNTVSQVAKKVLTMGVNGE 550

Query: 573 ALALEVKKALNKRLEQTTTYDLEPRWHDFAFSYATGTVE-----LLSSSPSANVTL 623
L + K L + + + D T +++ L++ + T

Sbjct: 551 ---LHPSRFCEKDLLRVVDREYVFAYIDDVCSGTYPMLQKLRQVLVDHALNNGETEKNTN 607

Query: 624 TAVNAWKVASAEKAIS--LTREVRN-RFWQTPSSQAPAHAYLSPRTRVLYSFVREELGVQ 680
T++ K+A+ E+ + L +EV R + + + + R+ LY FVREELG

Sbjct: 608 TSI-FQKIATFEEELKVLLPKEVEGVRIAYENDTSLIPNRIKACRSYPLYRFVREELG-- 664

Query: 681 ARRGDVFGVGVQQETIGSNVSRIYEAIKDGRINHVLVKML 719

RG G + + G R++ A+ G+I L++ L

Sbjct: 665 --RG-FLTGEKVTSPGEEFDRVFTAMCKGQIIDPLLECL 700

☐ >gi|28316386|dbj|BAC56977.1| phenylalanine ammonia-lyase [Daucus carota]
Length = 715

Score = 343 bits (880), Expect = 1e-92

Identities = 252/728 (34%), Positives = 365/728 (50%), Gaps = 50/728 (6%)

Query: 16 FTNGSHAAPTKSAAGPTSALRRTP---GLDGHAAHQSQLEIVQELLSDPTDDVVELSGY 71
+TNG H ++ G +++ G+ A S LE V+ ++++ VV+L G
Sbjct: 3 YTNGHH----ENGNGVDLCMKKEDPLSWGVAEEALKGSHLEEVKRMVAEYRKPVVKLGGE 58

Query: 72 SLTXXXXXXXXXXXXXXXXXX-QNDDEIRARVDKSVDFLKAQLQNSV--YGVTTGFGGSADT 128
+LT + + RA V S D++ + YGVTTGFG ++
Sbjct: 59 TLTISQVA AISARDDSGVKVELSEARAGVKASSDWVMESMNKGTDSYGVTTGFGATSHR 118

Query: 129 RTEDAVSLQKALIEHQLCGVTPTSVSSFSVGRGLE---NTLPLEVVRGAMVIRVNSLTRG 185
RT+ +LQK LI G+ G G E NTLP R AM++R+N+L +G
Sbjct: 119 RTKQGGALQKELIRFLNAGI-----FGSGAEAGNNTLPHSATRAAMLVRINTLLQG 169

Query: 186 HSAVRLVVLEALTNFLNHRITPIVPLRGSISASGDLSPLSYIAGAITGHPDVKVHVLHEG 245
+S +R +LEA+T FLNH ITP +PLRG+I+ASGDL PLSYIAG +TG P+ K
Sbjct: 170 YSGIRFEILEAITKFLNHNITPCLPLRGITITASGDLVPLSYIAGLLTGRPNKAV---GP 226

Query: 246 TEKIMFAREAISLFGLEA--VVLGPKEGLGLVNGTAVSASMATXXXXXXXXXXXXXXXXXXXX 303
T + EA L G+E L PKEGL LVNGTAV + MA+
Sbjct: 227 TGVTLSPPEEAFKLAGVEGGFFELQPKEGLALVNGTAVGSGMASMVLFEANILAVLAEVMS 286

Query: 304 XXXVEAMVGQQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGSSFAXXXXXXXXXXXXXXGI 363
E M G+ F + + HPGQ+E A + +L GS++
Sbjct: 287 AIFAEVMQGKP-EFTDHLTHKLKHHPGQIEAAIMEHILDGSAYVKAQKLHEMDPLQKP 345

Query: 364 LRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTNDNPLLDVENKQTAHGGNFQASAV 423
+QDRY LRTSPQ+LGP +E + + + E N+ DNPL+DV + HGGNFQ + +
Sbjct: 346 -KQDRYALRTSPQWLGPQIEVIRSSTKMIEREINSVNDNPLIDVSRNKAIHGGNFQGTPI 404

Query: 424 SISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCLA-AEDPSLNYHGKGLDIHIAAY 482
+SM+ TRLA+A IGKL F Q +EL+N N GLPS L+ +PSL+Y KG +I +A+Y
Sbjct: 405 GVSMDNTRLAIAAIGKLMFAQFSELVNDFYNNGLPSNLSGGRNPSLDYGFKGAEIAMASY 464

Query: 483 ASELGHLANPVTTTFVQPAEMGNQAVNSLALISARRTAEANDVLSLLLASHLYCTLQAVDL 542
SEL LANPVT VQ AE NQ VNSL LIS+R+T+EA ++L L+ + L QA+DL
Sbjct: 465 CSELQFLANPVTNHVQSAEQHNQDVNSLGLISSRKTSEAVEILKLMSTTFLVGLCQAIDL 524

Query: 543 RAMELDFKKQFDPLLPDLLQQLHGTGLDVNALALEVKKALNKRLEQTTTYDLEPRWHDFAF 602
R +E + K + + ++ L G++ L + K L + + + D
Sbjct: 525 RHLEENLKSTVKNTVSQVAKRVLTMGVNGE---LHPSRFCEKDLLRVVDREYIFAYIDDP 581

Query: 603 SYAT-----GTVVELLSSSPSANVTLTAVNAWKVASAEKAIS--LTREVRN-RFWQT 651
AT T+VE ++ L+ K+A+ E + L +EV + R
Sbjct: 582 CSATYPLMQKLRETLVEHALNNGDKERNLSTSIFQKIAAFEDELKALLPKEVESARA AVE 641

Query: 652 PSSQAPAHAYLSPRTRVLYSFVREELGVQARRGDVFGVQQETIGSNVSRIYEAIKDGR I 711
+ A + R+ LY FVREELG + G + + G +++ A+ G I
Sbjct: 642 SGNPAIPNRIKECRSYPLYKFVREELGT-----EYLTGEKVTSPGEEFDKVTAMTKGEI 696

Query: 712 NHVLVKML 719
L++ L

Sbjct: 697 IDPLLECL 704

☐ >gi|12240240|gb|AAG49585.1| phenylalanine ammonia-lyase [Ipomoea nil]
Length = 711

Score = 343 bits (879), Expect = 1e-92

Identities = 250/693 (36%), Positives = 356/693 (51%), Gaps = 48/693 (6%)

Query: 49 SQLEIVQELLSDPTDDVVELSGYSLTXXXXXXXXXXXXXXXXXQNDDEIRARVDKSVDFLK 108
S L+ V+ ++++ V+L G +LT + +E RA V S D++

Sbjct: 34 SHLDEVKVMVAEFRKPAVKLGGETLTVAQVAIASRDNAVTVELSEESRAGVKASSDWVM 93

Query: 109 AQLQNSV--YGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPTSVSSFSVGRGLEN-- 164
+ YGVTTGFG ++ RT+ +LQK LI G+ G G E+

Sbjct: 94 DSMNKGTD SYGVTTGFGATSHRRTKQGGALQKELIRFLNAGI-----FGNGTESCH 144

Query: 165 TLPLEVVRGAMVIRVNSLTRGHSAVRLVVLEALTNFLNHRITPIVPLRGSISASGDLSP 224
TLP R AM++R+N+L +G+S +R +LEA+T LNH ITP +PLRG+I+ASGDL PL

Sbjct: 145 TLPHSATRAAMLVRINTLLQGYSGIRFEILEAITKLLNHNITPCLPLRGTTITASGDLVPL 204

Query: 225 SYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEA--VVLGPKEGLGLVNGTAVSA 282
SYIAG ITG P+ K + T + A EA+ L G+ L PKEGL LVNGTAV +

Sbjct: 205 SYIAGLITGRPNKAVGPNGET---LNAAEALRLAGVNGGFFELQPKEGLALVNGTAVGS 261

Query: 283 SMATXXXXXXXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQVEVARNIRTLL 342
MA+ E M G+ F + + HPGQ+E A + +L

Sbjct: 262 GMASMLFEANVLAVLSEVLSAIFAEVMNGKP-EFTDHLTHKLKHHHPGQIEAAIMEHIL 320

Query: 343 SGSSFAXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTDN 402
GSS+ +QDRY LRTSPQ+LGP +E + A + E N+ DN

Sbjct: 321 DGSSYVKAQKMHMDPLQKP-KQDRYALRTSPQWLGPQIEVIRAATKMIEREINSVNDN 379

Query: 403 PLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRLPSCL- 461
PL+DV + HGGNFQ + + +SM+ +RLALA IGKL F Q +EL+N N GLPS L

Sbjct: 380 PLIDVARSKALHGGNFQGTPIGVSMDNSRLALASIGKLLFAQFSELVNDYNNGLPSNLT 439

Query: 462 AAEDPSLNYHGKGLDIHIAAYASELGHLANPVTTTFVQPAEMGNQAVNSLALISARRTAEA 521
A +PSL+Y KG +I +A+Y SEL LANPVT VQ AE NQ VNSL LISAR+TAEA

Sbjct: 440 AGRNPSLDYGFKAIEIAMASYCSELQFLANPVTNHVQSAEQHNQDVNSLGLISARKTAEA 499

Query: 522 NDVLSLLLASHLYCTLQAVDLRAMELDFKKQFDPLLPTLLQQHLGTGLDVNA-LALEVKK 580
DVL L+ +++L QA+DLR +E + + + + ++ L G + A +K

Sbjct: 500 VDVLKLMSSSTYLVALCQAIDLRFLEENLRNAVKNVAVTQVAKRTLTMGANGELHPARFCEK 559

Query: 581 ALNKRLEQ-----TTTTYDLEPRWHDASFYATGTVVVELLSSSPSANVTLTAVNAW 629
L + +++ + Y L + A V L + S T T++

Sbjct: 560 DLLRVVDREYVFAYADDPCSANYPLMQKLRQAL-----VDHALQNGESEKNTGTSTI-FL 612

Query: 630 KVASAEKAIS--LTREVR-NRFWQTPSSQAPAHAYLSPRTRVLYSFVREELGVQARRGDV 686
KVA+ E + L +EV R + A + R+ LY FVRE LG ++

Sbjct: 613 KVAAFEDELKAVLPKEVEAARIAVESGNPAIPNRIKECRSYPLYKFVREGLGT-----EL 667

Query: 687 FVGVOQETIGSNVSRIYEAIKDGRINHVLVKML 719

G + + G +++ A+ +G I L++ L

Sbjct: 668 LTGEKVRSPGEECDKVFTAMCEGSIIDPLLECL 700

☐ >gi|1524313|emb|CAA68938.1| PAL1 protein [Petroselinum crispum]
gi|129582|sp|P24481|PAL1_PETCR Phenylalanine ammonia-lyase 1
Length = 716

Score = 342 bits (878), Expect = 2e-92

Identities = 244/697 (35%), Positives = 355/697 (50%), Gaps = 39/697 (5%)

Query: 40 GLDGHAHQSQLEIVQELLSDPDQVVELSGYSLTXXXXXXXXXXXXXXXXXX-QNDDEIRA 98
G+ A S L+ V+++++ VV+L G +LT + + RA
Sbjct: 31 GIAAEAMTGSHLDEVKMKMAEYRKPVVKLGGETLTISQVAASARDGSGVTVELSEAARA 90

Query: 99 RVDKSVDFLKAQLQNSV--YGVTTGFGGSADTRTEDAVSLQKALIEHQICGVTPTSVSSF 156
V S D++ + YGVTTGFG ++ RT+ +LQK LI G+
Sbjct: 91 GVKASSDWVMDSMNKGTDSYGVTTGFGATSHRRTKQGGALQKELIRFLNAGI----- 142

Query: 157 SVGRGLENLTPLEVVVRGAMVIRVNSLTRGHSVRLVLEALTNFLNHRITPIVPLRGSIS 216
G G +NTLP R AM++R+N+L +G+S +R +LEA+T FLN ITP +PLRG+I+
Sbjct: 143 -FGNGSDNTLPHSATRAAMLVRINTLLQGYSGIRFEILEAITKFLNQNTITPCLPLRGTIT 201

Query: 217 ASGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIMFAEAISLFGLEA--VVLGPKEGLGL 274
ASGDL PLSYIAG +TG P+ K T I+ EA L G+E L PKEGL L
Sbjct: 202 ASGDLVPLSYIAGLLTGRPNKAV---GPTGVILSPEEAFKLAGVEGGFFELQPEGLAL 258

Query: 275 VNGTAVSASMATXXXXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQVEV 334
VNGTAV + MA+ E M G+ F + + HPGQ+E
Sbjct: 259 VNGTAVGSGMASMVLFEANILAVLAEVMSAIFAEMVQKGP-EFTDHLTHKLKHHPGQIEA 317

Query: 335 ARNIRTLTSGSSFAXXXXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSL 394
A + +L GS++ +QDRY LRTSPQ+LGP +E + + +
Sbjct: 318 AAIMEHILDGSAYVKAQKLHEMDPLQKP-KQDRYALRTSPQWLGPQIEVIRSSTKMIER 376

Query: 395 ENNTTTDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMN 454
E N+ DNPL+DV + HGGNFQ + + +SM+ TRLA+A IGKL F Q +EL+N N
Sbjct: 377 EINSVNDNPLIDVSRNKAIHGGNFQGTPIGVSMNDNRLAIAAIGKLMFAQFSELVNDNFYN 436

Query: 455 RGLPSCLA-AEDPSLNHYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVNSLALI 513
GLPS L+ +PSL+Y KG +I +A+Y SEL LANPVT VQ AE NQ VNSL LI
Sbjct: 437 NGLPSNLSGGRNPSLDYGFKAIEAMASYCSELQFLANPVTNHVQSAEQHNQDVNSLGLI 496

Query: 514 SARRTAEANDVLSLLLASHLYCTLQAVDLRAMELDFKKQFDPLLPTLLQQHLGTGLDVNA 573
S+R+T+EA ++L L+ + L QA+DLR +E + K + ++ ++ L G++
Sbjct: 497 SSRKTSEAVEILKLMSTTFLVGLCQAIDLRHLEENLKSTVKNTVSSVAKRVLTMGVNGE- 555

Query: 574 LALEVKKALNKRLEQTTTYDLEPRWHDAFSYAT-----GTVVELLSSSPSANVTTLTA 625
L + K L + + + D AT T+VE + L+
Sbjct: 556 --LHPSRFCEKDLLRVVDREYIFAYIDDPSCSATYPLMQKLRQTLVEHALKNGDNERNLST 613

Query: 626 VNAWKVASAEKAIS--LTREVRN-RFQWTPSSQAPAHAYLSPRTRVLYSFVREELGVQAR 682
K+A+ E + L +EV + R + A + R+ LY FVR+ELG
Sbjct: 614 SIFQKIATFEDELKALLPKEVESARAALESNGPAIPNRIECSRYPYKVFVRKELGT--- 670

Query: 683 RGDVFGVGVQETIGSNVSRIYEAIKDGRINHLVKML 719
+ G + + G +++ A+ G I L++ L
Sbjct: 671 --EYLTGEKVTSPGEEFEKVFIAMSKGEIIDPLLECL 705

☐ >gi|58618140|gb|AAW80636.1| phenylalanine ammonia lyase [Lycopodium tristachyum]
Length = 722

Score = 342 bits (878), Expect = 2e-92

Identities = 245/688 (35%), Positives = 350/688 (50%), Gaps = 42/688 (6%)

Query: 48 QSQLEIVQELSDPTD-DVVELSGYSLTXXXXXXXXXXXXXXXXXQNDDEIRARVDKSVDF 106
 QS L+ V+E+ D V + G +LT + + RVD+S ++
 Sbjct: 52 QSHLDEVREMAKAFNSLDEVSIQGTNLTVAQVAASRRQGVKVCCLDSSAAKHRVDESSNW 111

Query: 107 LKAQLQNSV--YGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPTSVSSFSVGRGLEN 164
 + + YGVTTGFG ++ RT V LQ+ LI GV G N
 Sbjct: 112 VLQNVMRGTDITYGVTTGFGATSHRRTNQGVELQQELIGFLNAGVMEAG-----GGSN 163

Query: 165 TLPLEVVRGAMVIRVNSLTRGHSVRLVLEALTNFLNHRITPIVPLRGSISASGDLSP 224
 LP R AM++R N+L +G+S +R +LEA+ LN ITP +PLRGS+ASGDL PL
 Sbjct: 164 LLPASATRAAMLVRTNTLMQGYSGIRWQILEAMAKLLNAGITPKLPLRGSITASGDLVPL 223

Query: 225 SYIAGAITGHPDKVHVLHEGTEKIMFAEAI SLFGL- AVVLGPKEGLGLVNGTAVSAS 283
 SYIAG +TG + K VL +G E + EA+ L G+E VL PKEGL +VNGT+V A
 Sbjct: 224 SYIAGLVTGRKNSKA-VLADGRE--VSGEAMKLVGVENPFVLQPKEGLAMVNGTSVGAG 280

Query: 284 MATXXXXXXXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQVEVARNIRTL 343
 +A EAM G+ P H + + HPGQ+E A + +L
 Sbjct: 281 LAATVCYDANVLAVFAEVASALFCEAMQKGPEFADPLTHRL-KHHPGQIEAAIMEFILQ 339

Query: 344 GSSFAXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTDNP 403
 GSS+ +QDRY LRTSPQ+LGP +E + A ++ E N+ DNP
 Sbjct: 340 GSSYMKAAAKLHETDPLKKP-KQDRYALRTSPQWLGPQIEVIRSATQSIQREINSVNDNP 398

Query: 404 LLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCLA- 462
 L+DV HGGNFQ + + +SM+ TRLALA IGKL F Q +EL+N N GLPS L+
 Sbjct: 399 LIDVSRDLALHGGNFQGTPIGVSMNTRLALASIGKLMFAQFSELVNDFYNNGLPSNL 458

Query: 463 AEDPSLNYHGKGLDIHIAAYASELGHLANPVTTTFVQPAEMGNQAVNSLALISARRTAEAN 522
 +PSL+Y KG +I +A+Y SEL LANPVT VQ AE NQ VNSL LISAR+TAEA
 Sbjct: 459 GPNPSLDYGFKAIEAMASYTSELQFLANPVTNHVQSAEQHNQDVNSLGLISARKTAEAI 518

Query: 523 DVL SLLASHLYCTLQAVDLRAMELDFKKQFDPLLP TLLQQHLGTGLDVNALALEVKKAL 582
 ++L L+ ++L QA+DLR +E + + + + ++ L TG D L +
 Sbjct: 519 EILKLMTTTTYLVALCQAIDLRHLEENMQAVVKQAVSLVAKKTLTTGSDG---VLSPSRFC 575

Query: 583 NKRLEQTT-----TYDLEP--RWHDAFSYATGTVVELLSSSPSANVTLTAVNAWKVA-- 632
 K L Q TY +P + +VE A V + ++
 Sbjct: 576 EKDLLQLVDHQPIFTYIDDP TSAAYPLLQKLRQIMVEHALHDKDAAVIFNKITVFEEELK 635

Query: 633 -SAEKAI SLTREVRNRFWQTPSSQAPAHAYLSPRTRVLYS FVREELGVQARRGDV FVG 691
 + ++LTR+ ++ A + ++ LY FVR+EL Q + +G +
 Sbjct: 636 NHLQAEVTLTRDNFDK-----DIAAVPNRIKDCSYPLYEFVRKELNTQ-----ILIGSR 685

Query: 692 QETIGSNVSRIYEAIKGRINHLVKML 719
 ++ G ++++AI +G++ L+K L
 Sbjct: 686 TQSPGEVFEKVFDAISEGKLVAPLLKCL 713

☐ >gi|1171998|sp|P45726|PALY_CAMSI Phenylalanine ammonia-lyase
 gi|662271|dbj|BAA05643.1| phenylalanine ammonia-lyase [Camellia sinensis]
 Length = 714

Score = 342 bits (878), Expect = 2e-92

Identities = 241/698 (34%), Positives = 354/698 (50%), Gaps = 40/698 (5%)

Query: 40 GLDGHAHQSQLEIVQELLSDPTDDVVELSGYSLTXXXXXXXXXXXXXXXXXQNDDEIRAR 99
 G+ A S LE V+ ++ + VV L G +LT + + R

Sbjct: 28 GVAAEAMKGSHEEVKGMVEEFRKPVVRLGGETLTISQVAAIAVRGSEVAVELSESAREG 87

Query: 100 VDKSVDFLKAQLQNSV--YGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPPTSVSFS 157
 V S D++ + YGVTTGFG ++ RT++ +LQK LI G+

Sbjct: 88 VKASSDWVMESMNKGTD SYGVTTGFGATSHRRTKEGGALQKELIRFLNAGI----- 138

Query: 158 VGRGLEN--TLPLEVVRGAMVIRVNSLTRGHSVAVRLVVLEALTNFLNHRITPIVPLRGS 215
 G G E+ TLP R AM++R+N+L +G+S +R +LEA++ FLN+ ITP +PLRG+I

Sbjct: 139 FGNGTESCHTL PQSATRAAMLVRINTLLQGYSGIRFEILEAISKFLNNNITPCLPLRGTI 198

Query: 216 SASGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEA--VVLGPKEGLG 273
 +ASGDL PLSYIAG +TG + K T +I+ +EA L G+E L PKEGL

Sbjct: 199 TASGDLVPLSYIAGLLTGRHNSKAV---GPTGEILHPKEAFRLAGVEGGFFELQPKEGLA 255

Query: 274 LVNGTAVSASMATXXXXXXXXXXXXXXXXXXVEAMVGQQGSFAPFIHDVCRPHPGQVE 333
 LVNGTAV + +A+ E M G+ F + + HPGQ+E

Sbjct: 256 LVNGTAVGSGLASMLFEANILAVLSEVLSAIFAEVMQKGP-EFTDHLTHKLKHHPGQIE 314

Query: 334 VARNIRTLTSGSSFAXXXXXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLS 393
 A + +L GSS+ +QDRY LRTSPQ+LGPL+E + + ++

Sbjct: 315 AAAIMEHILDGSSYVKAQKLHEMDPLQKP-KQDRYALRTSPQWLGPLIEVIRSSSTKSIE 373

Query: 394 LENNTTTDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAM 453
 E N+ DNPL++V + HGGNFQ + + +SM+ TRLA+A IGKL F Q +EL+N

Sbjct: 374 REINSVNDNPLINVS RNKALHGGNFQGTPIGVSMNTRLAVASIGKLMFAQFSELVNDFY 433

Query: 454 NRGLPSCLA-AEDPSLNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVNSLAL 512
 N GLPS L+ +PSL+Y KG +I +AAY SEL LANPVT VQ AE NQ VNSL L

Sbjct: 434 NNGLP SNL SGGRNPSLDYGFKA EIAMAAYCSELQFLANPVTNHVQSAEQHNQDVNSLGL 493

Query: 513 ISARRTAEANDVLSLLLASHLYCTLQAVDLRAMELDFKKQFDPLLPTLLQQHLGTGLDVN 572
 IS+R+TAEA D+L L+ +++L QAVDLR E + + + ++ L G++

Sbjct: 494 ISSRKTA EAVDILKLMSS TYLVALCQAVDLRHFEENLRNTVKSTVSQVAKRVLTMGVNGE 553

Query: 573 ALALEVKKALNKRLEQTTTYDLEPRWHDASFYATGTVVE-----LLSSSPSANVT 622
 L + K L + + + D AT +++ L + N++

Sbjct: 554 ---LHPSRFCEKDLLRVVDREYIFAYIDDP CSATYPLMQKLRQVLVEHALKNGESEKNLS 610

Query: 623 LTAVNAWKVASAEKAI SLTREVRN-RFWQTPSSQAPAHAYLSPRTRVLYSFVREELGVQA 681
 + + E L +EV + R + A + R+ LY FVREELG

Sbjct: 611 TSIFQKIRAFEEEIKTLLPKEVESTRAAIENGNSAIPNRIKECRSYPLYK FVREELGT-- 668

Query: 682 RRGDV FVG VQ QETIGSNVSRIYEAIKDGRINHLVKML 719
 ++ G + + G +++ A+ G + L+ L

Sbjct: 669 ---ELLTGEKVRSPGEEFDKVF TALCKGEMIDPLMDCL 703

☐ >gi|50926498|ref|XP_473196.1| ☒ OSJNBa0073E02.18 [Oryza sativa (japonica cultivar-
 gi|32487855|emb|CAE05623.1| ☒ OSJNBb0061C13.5 [Oryza sativa (japonica cultivar-gr
 gi|38568069|emb|CAE05458.3| ☒ OSJNBa0073E02.18 [Oryza sativa (japonica cultivar-g
 Length = 714

Score = 342 bits (877), Expect = 2e-92

Identities = 245/716 (34%), Positives = 363/716 (50%), Gaps = 39/716 (5%)

Query: 18 NGSHAAPTksAAGPTsALRRTPGLDGHAHQsQLEIVQELLSdPTDDVVELSGYSLTxxx 77
NGS K A P + + L G S L+ V+ ++ + VV + G SLT

Sbjct: 13 NGSSLCVAKPRADPLNWGKAEEELSG-----SHLDAVKRMVEEYRRPVVTIEGASLTIAQ 67

Query: 78 xxxxxxxxxxxxxQNDDEIRARVDKsVDFLKAQLQNSV--YGVTTGFGGSADTRTEDAVS 135
+ D+ R RV S D++ + N YGVTTGFG ++ RT++ +

Sbjct: 68 VAAVASAGAARV-ELDESARGRVKASSDWMNSMMNGTDSYGVTTGFGATSHRRTKEGGA 126

Query: 136 LQKALIEHQLCGVTPtSVSSFSVGRGLE-NTLPLEVVRGAMVIRVNSLTRGHSAVRLVVL 194
LQ+ LI G + G G + + LP R AM++R+N+L +G+S +R +L

Sbjct: 127 LQRELIRFLNAG-----AFGNDDGHVLPAAATRAAMLVRINTLLQGYSGIRFEIL 177

Query: 195 EALTNFLNHRITPIVPLRGSISASGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIMFARE 254
E + LN +TP +PLRG+I+ASGDL PLSYIAG +TG P+ V V +G + + A E

Sbjct: 178 ETIATLLNANVTPLPLRGITITASGDLVPLSYIAGLVTGRPN-SVAVTPDGRK--VDAAE 234

Query: 255 AISLFGLEA--VVLGPKEGLGLVNGTAVSASMATxxxxxxxxxxxxxxxxxxxxxVEAMVG 312
A + G++ L PKEGL +VNGTAV + +A+ E M G

Sbjct: 235 AFKIAGIQHGFFELQPKEGLAMVNGTAVGSGLASMVLFEANVLGVLAEVL SAVFCEVMNG 294

Query: 313 QQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGSSFAXXXXXXXXXXXXXXGILRQDRYPLR 372
+ H + + HPGQ+E A + +L GSS+ +QDRY LR

Sbjct: 295 KPEYTDHLTHKL-KHHPGQIEAAAIMHILEGSSYMLAKKLGEldPLMKP-KQDRYALR 352

Query: 373 TSPQFLGPLVEDMMHAYSTLSLENNTTTDNPLLDVENKQTAHGGNFQASAVSISMEKTRL 432
TSPQ+LGP +E + A ++ E N+ DNPL+DV + HGGNFQ + + +SM+ TRL

Sbjct: 353 TSPQWLGPQIEVIRAATKSIEREINSVNDNPLIDVSRGKALHGGNFQGTPIGVSMDNTRL 412

Query: 433 ALALIGKLNFTQCTELLNAAMNRGLPSCLA-AEDPSLNYHGKGLDIHIAAYASELGHAN 491
A+A IGKL F Q +EL+N N GLPS L+ +PSL+Y KG +I +A+Y SEL LAN

Sbjct: 413 AIAAIGKLMFAQFSELVNDFYNNGLPSNLSGGRNP SLDYGFKGAEIAMASYCSELQFLAN 472

Query: 492 PVTTFVQPAEMGNQAVNSLALISARRTAEANDVLSLLLASHLYCTLQAVDLRAMELDFKK 551
PVT VQ AE NQ VNSL LIS+R+TAEA DVL L+ ++ L QA+DLR +E + +

Sbjct: 473 PVTNHVQSAEQHNQDVNSLGLISSRKTAEAIDVLKLMSSFLIALCQAIDLRHLEENVRs 532

Query: 552 QFDPLLPTLLQQHLGTGL--DVNALAL---EVKKALNKRLEQTTTYDLEPRWHDafSYAT 606
+ T+ ++ L T D++ ++ +A+++ D +

Sbjct: 533 AVKGCVTTVARKTLSTSATGDLHKARFCEKDLLQAIDREAVFAYADDPcsANYPLMQKMR 592

Query: 607 GTVVE--LLSSSPSANVTLTAVNAWKVASAEKAI SLTREVR-NRFWQTPSSQAPAHAYLS 663
++E L + NV + E ++L REV R + A A+

Sbjct: 593 AVLIEHALANGEAERNVDTSVFAKVATFEEELRVALPREVEAARA AVENGTAAKANRITE 652

Query: 664 PRTRVLYSFVREELGVQARRGDVFGVQQETIGSNVSRIYEAIKDGRINHVLVKML 719
R+ LY FVREELG + G + + G V++++ A+ G+ L++ L

Sbjct: 653 CRSYPLYRFVREELGT-----EYLtGEKTRSPGEEVNKVFVAMNQKHIDALLECL 703

☐ >gi|741010|prf||2006271A Phe ammonia lyase
Length = 725

Score = 342 bits (877), Expect = 2e-92
Identities = 244/700 (34%), Positives = 360/700 (51%), Gaps = 45/700 (6%)

Query: 40 GLDGHAHQsQLEIVQELLSdPTDDVVELSGYSLTxxxxxxxxxxxxxxxxxxQNDDEIRAR 99
G+ A S L+ V+ ++ + VV L G +LT + + RA

Sbjct: 40 GVAAEAMKGSHLDEVKRMVEEYRKPVVRLGGETLTISQVAAIAAHDGATV-ELSESARAG 98

Query: 100 VDKSVDFLKAQLQNSV--YGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPTSVSSFS 157
 V S D++ + YGVTTGFG ++ RT+ +LQK LI G+ F
 Sbjct: 99 VKASSDWVMESMNKGTDSYGVTTGFGATSHRRTKQGGALQKELIRFLNAGI-----FG 151

Query: 158 VGRGLENLPLEVVRGAMVIRVNSLTRGHSVRLVLEALTNFLNHRITPIVPLRGSISA 217
 G +TL R AM++R+N+L +G+S +R +LEA+T LN+ ITP +PLRG+I+A
 Sbjct: 152 NGTESNHTLFHTATRAAMLVRINTLLQGYSGIRFEILEAITKLLNNNITPCLPLRGITITA 211

Query: 218 SGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEAVV--LGPKEGLGLV 275
 SGDL PLSYIAG +TG + K H + +++ A+EA L G+ A L PKEGL LV
 Sbjct: 212 SGDLVPLSYIAGLLTGPSNSKAH---GPSGEMLNAKEAFQLAGINAEFFELQPKEGLALV 268

Query: 276 NGTAVSASMATXXXXXXXXXXXXXXXXXXXXXVEAMVGQQGSFAPFIHDVCRPHPGQVEVA 335
 NGTAV + +A+ E M G+ F + + HPGQ+E A
 Sbjct: 269 NGTAVGSGLASIVLFEANILAVLSEVLSAIFAEVMQKGP-EFTDHLTHKLKHHHPGQIEAA 327

Query: 336 RNIRTLTSGSSFAXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLE 395
 + +L GS++ +QDRY LRTSPQ+LGPL+E + + ++ E
 Sbjct: 328 AIMEHILHGSAYVKDAKKLHEMDPLQKP-KQDRYALRTSPQWLGPLIEVIRFSTKSIERE 386

Query: 396 NNTTTDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNR 455
 N+ DNPL+DV + HGGNFQ + + +SM+ TRLLALA IGKL F Q +EL+N N
 Sbjct: 387 INSVNDNPLIDVSRNKALHGGNFQGTPIGVSMNTRLALASIGKLLFAQFSELVNDFYNN 446

Query: 456 GLPSCL-AAEDPSLNYHGKGLDIHIAAYASELGHLANPVTTTFVQPAEMGNQAVNSLALIS 514
 GLPS L A+ +PSL+Y KG +I +A+Y SEL +LANPVTT VQ AE NQ VNSL LIS
 Sbjct: 447 GLPSNLSASRNPSLDYGFKGSEIAMASYCSELQYLANPVTTTHVQSAEQHNQDVNSLGLIS 506

Query: 515 ARRTAEANDVLSLLASHLYCTLQAVDLRAMELDFKKQFDPLLPTLLQQHLGTGLDVNAL 574
 +R+T EA ++L L+ ++ L QA+DLR +E + K + + ++ L G+
 Sbjct: 507 SRKTKEAIEILQLMSSTFLIALCQAIDLRHLEENLKNSVKNTVSQVAKKTLTIGVSGE-- 564

Query: 575 ALEVKKALNKRLEQTTTYDLEPRWHDAFSYATGTVVELL-----SSSPSANVT 622
 L + K L + + + D AT + + L S ++N +
 Sbjct: 565 -LHPSRFCEKDLLKVVDREHVF SYIDDPSCATYPLAQKLRLQVLVDHALVNGESEKNSNTS 623

Query: 623 LTAVNAWKVASAEKAIS--LTREVRN-RFWQTPSSQAPAHAYLSPRTRVLYSFVREELGV 679
 + K+A+ E+ + L +EV + R + A+ R+ LY FVREELG
 Sbjct: 624 IFQ----KIATFEEELKTLTPKEVESARTAYENGNSTIANKINGCRSYPLYKFVREELGT 679

Query: 680 QARRGDVFGVQQETIGSNVSRIYEAIKGRINHVLVKML 719
 G+ + + G +++ A+ G+I L+K L
 Sbjct: 680 SLLTGERVI-----SPGEECDKLFTAMCQKIIDPLLKCL 714

☐ >gi|13195320|gb|AAK15640.1| phenylalanine ammonia-lyase [Agastache rugosa]
 Length = 716

Score = 342 bits (876), Expect = 3e-92

Identities = 247/723 (34%), Positives = 360/723 (49%), Gaps = 42/723 (5%)

Query: 13 ANGFTNGSHAAPTKSAAGPTSALRRTPGLDGHAAHQSOLEIVQELLSIPTDDVVELSGYS 72
 +NG NG++ K P + L G S LE V+ ++ + VV+L G +
 Sbjct: 9 SNGHNNGANGFCVKQN-DPLNWAAAESLKG-----SHLEEVKRMVEEFRKPVVKLGGET 62

Query: 73 LTXXXXXXXXXXXXXXXXXQNDDEIRARVSKSVDFLKAQLQNSV--YGVTTGFGGSADTRT 130
 LT + + RA V S D++ + YGVTTGFG ++ RT
 Sbjct: 63 LTISQVAAIAAKDNAVAVELAESARAGVKASSDWVMSMSKGTDSYGVTTGFGATSHRRRT 122

Query: 131 EDAVSLQKALIEHQLCGVTPTSVSSFSVGRGLENLTLPLEVVRGAMVIRVNSLTRGHSAVR 190
 + +LQK LI G+ + S +TLP R AM++R+N+L +G+S +R
 Sbjct: 123 KQGGALQKELIRFLNAGIFGNATES-----NHTLPHTATRAAMLVRINTLLQGYSGIR 175

Query: 191 LVVLEALTNFLNHRITPIVPLRGSISASGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIM 250
 +LEA+T FLN +TP +PLRG+I+ASGDL PLSYIAG +TG P+ K + E +
 Sbjct: 176 FEILEAITKFLNQNVTPCLPLRGTTITASGDLVPLSYIAGLLTGRPNSKA--VGPAGEPLT 233

Query: 251 FAREAISLFGLEAVV--LGPKEGLGLVNGTAVSASMATXXXXXXXXXXXXXXXXXXXXXVE 308
 A +A L G+ L PKEGL LVNGTAV + +A+ E
 Sbjct: 234 -AEQAFKLAGVTGGFFDLQPKLEGLALVNGTAVSGSLASIALFDANVLAVLSVVMSPVFAE 292

Query: 309 AMVGQQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGSSFAXXXXXXXXXXXXXXXXXGILRQDR 368
 M G+ F + + HPGQ+E A + +L GS + +QDR
 Sbjct: 293 VMNGKP-EFTDHLTHKLKHHPGQIEAAAMEHILDGSGYVKAAQKLHEIDPLQKP-KQDR 350

Query: 369 YPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTNDNPLLDVENKQTAHGGNFQASAVSISME 428
 Y LRTSPQ+LGP +E + A + E N+ DNPL+DV + HGGNFQ + + +SM+
 Sbjct: 351 YALRTSPQWLGPQIEVIRTATKMIEREINSVNDNPLIDVSRNKAIHGGNFQGTPIGVSM 410

Query: 429 KTRLALALIGKLNFTQCTELLNAAMNRGLPSCLA-AEDPSLNYHGKGLDIHIAAYASELG 487
 TRLA+A IGKL F Q +EL+N N GLPS L+ +PSL+Y KG +I +A+Y SEL
 Sbjct: 411 NTRLAIASIGKLLFAQFSELVNDNFYNNGLPSNLSGGRNPSTDYGFKGSEIAMASYCSELQ 470

Query: 488 HLANPVTTTFVQPAEMGNQAVNSLALISARRTAEANDVLSLLLASHLYCTLQAVDLRAMEL 547
 L NPVT VQ AE NQ VNSL LIS+R+T EA D+L L+ +++L QAVDLR +E
 Sbjct: 471 FLVNPVTNHVQSAEQHNQDVNSLGLISSRKTEALDILKLMSSTYLVALCQAVDLRHVEE 530

Query: 548 DFKKQFDPLLPTLLQQHLGTGLDVNALALEVKKALNKRLEQTTTYDLEPRWHDAFSYATG 607
 + K + + ++ L G++ L + K L + + + D AT
 Sbjct: 531 NMKLAVKNTVSQVAKRTLTMGVNGE---LHPSRFCEKELIRVVDREYVFYIDDPCLATY 587

Query: 608 TVVE-----LLSSSPSANVTLTAVNAWKVASAEKAISLTREVRN-RFWQTPSSQA 656
 +++ L + NV+ + + + E L +EV + R S A
 Sbjct: 588 PLMQKLRQVLVDHALKNGESEKNVSTSIFHKIEAFEEELKALLPKEVESARIALESGPSA 647

Query: 657 PAHAYLSPRTRVLYSFVREELGVQARRGDVFGVQQETIGSNVSRIYEAIKDGRINHVLV 716
 A+ R+ LY F+REELG G+ V + G +++ A+ +G I L+
 Sbjct: 648 VANRIEECRSFPLYKFIREELGTGFLTGEKAV-----SPGEECEKVFAALSNGLIIDPLL 702

Query: 717 KML 719
 + L
 Sbjct: 703 ECL 705

☐ >gi|534893|emb|CAA57056.1| phenylalanine ammonia-lyase 2 [Petroselinum crispum]
 gi|1171994|sp|P45728|PAL2_PETCR Phenylalanine ammonia-lyase 2
 Length = 716

Score = 341 bits (875), Expect = 4e-92

Identities = 243/697 (34%), Positives = 354/697 (50%), Gaps = 39/697 (5%)

Query: 40 GLDGHAHQSQLEIVQELLSDPTDDVVELSGYSLTXXXXXXXXXXXXXXXXXX-QNDDEIRA 98
 G+ A S L+ V+++++ VV+L G +LT + + RA
 Sbjct: 31 GIAAEAMTGSHLDEVKKMVAEYRKPVVKLGGETLTISQVAAISARDGSGVTVELSEAAARA 90

Query: 99 RVDKSVDFLKAQLQNSV--YGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPTSVSSF 156
 V S D++ + YGVTTGFG ++ RT+ +LQK LI G+
 Sbjct: 91 GVKASSDWVMDSMNKGTD SYGVTTGFGATSHRRTKQGGALQKELIRFLNAGI----- 142

Query: 157 SVGRGLENLTPLEVVIRGAMVIRVNSLTRGHSAVRLVLEALTNFLNHRITPIVPLRGSIS 216
 G G +NTLP R AM++R+N+L +G+S +R +LEA+T FLN ITP +PLRG+I+
 Sbjct: 143 -FGNGSDNTLPHSATRAAMLVRINTLLQGYSGIRFEILEAITKFLNQNITPCLPLRGITIT 201

Query: 217 ASGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEA--VVLGPKEGLGL 274
 ASGDL PLSYIAG +TG P+ K T I+ EA L G+E L PKEGL L
 Sbjct: 202 ASGDLVPLSYIAGLLTGRPNKAV---GPTGVILSPEEAFKLAGVEGGFFELQPKEGLAL 258

Query: 275 VNGTAVSASMATXXXXXXXXXXXXXXXXXXXXXVEAMVGQQGSFAPFIHDVCRPHPGQVEV 334
 VNGTAV + MA+ E M G+ F + + HPGQ+E
 Sbjct: 259 VNGTAVSGMASMVLFEANILAVLAEVMSAIFAEMVQKQP-EFTDHLTHKLKHHHPGQIEA 317

Query: 335 ARNIRTLTSGSSFAXXXXXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSL 394
 A + +L GS++ +QDRY LRTSPQ+LGP +E + + +
 Sbjct: 318 AAIMEHILDGSAYVKAQKLHEMDPLQKP-KQDRYALRTSPQWLGPQIEVIRSSTKMIER 376

Query: 395 ENNTTTDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMN 454
 E N+ DNPL+DV + HGGNFQ + + +SM+ TRLA+A IGKL F Q +EL+N N
 Sbjct: 377 EINSVNDNPLIDVSRNKAIHGGNFQGTPIGMSMDNTRLAIAAIGKLMFAQFSELVNDNFYN 436

Query: 455 RGLPSCLA-AEDPSLNYHGKGLDIIHIAAYASELGHLANPVTTFVQPAEMGNQAVNSLALI 513
 GLPS L+ +PSL+Y KG +I +A+Y SEL LANPVT VQ AE NQ VNSL LI
 Sbjct: 437 NGLPSNLSGGRNPSLDYGFKAIEAMASYCSELQFLANPVTNHVQSAEQHNQDVNSLGLI 496

Query: 514 SARRTAEANDVLSLLASHLYCTLQAVDLRAMELDFKKQFDPLLPTLLQQHLGTGLDVNA 573
 S+R+T+EA ++L L+ + L QA+DLR +E + K + ++ ++ L G++
 Sbjct: 497 SSRKTSEAVEILKLMSTTFLVGLCQAIDLRHLEENLKSTVKNTVSSVAKRVLTMGVNGE- 555

Query: 574 LALEVKKALNKRL-----EQTTTYDLEP--RWHDAFSYATGTVVELLSSSPSANVTLTA 625
 L + K L E Y +P + T+VE + +
 Sbjct: 556 --LHPSRFCEKDLLRFVDREYIFAYIDDPSCATYPLMQKLRQTLVEHALKNGDNERNMNT 613

Query: 626 VNAWKVASAEKAIS--LTREVRN-RFWQTPSSQAPAHAYLSPRTRVLYSFVREELGVQAR 682
 K+A+ E + L +EV + R + A + R+ LY FVR+ELG+
 Sbjct: 614 SIFQKIATFEDELKALLPKEVESARAALESNPAPNRIECSRYPYKFKVRKELGI--- 670

Query: 683 RGDVFGVQQETIGSNVSRIYEAIKDGRINHVLVKML 719
 + G + + G +++ A+ G I L++ L
 Sbjct: 671 --EYLTGEKVTSPGEEFDKVFIAMSKGEIIDPLLECL 705

☐ >gi|24266655|gb|AAN52279.1| phenylalanine ammonia-lyase [Populus tremuloides]
 Length = 714

Score = 341 bits (875), Expect = 4e-92

Identities = 249/739 (33%), Positives = 371/739 (50%), Gaps = 63/739 (8%)

Query: 8 LATTLANGFTNGSHAAPTksAAGPTSALRRTP---GLDGHAHQSQLEIVQELLSDPDPTDD 64
 + T NG+ NGS + +R P G+ A S L+ V+ ++++
 Sbjct: 1 METITKNGYQNGS-----SESLCTQRDPLSWGVAEAMKGSHLDEVKRMVAEYRKP 51

Query: 65 VVELSGYSLTXXXXXXXXXXXXXXXXXX-QNDDEIRARVDKSVDFLKAQLQNSV--YGVTTG 121
 VV L+G +LT + + R RV S D++ + YGVTTG
 Sbjct: 52 VVNLGQNLTIQVASIAGHDASNVKVELSESARPRVKASSDWVMDKGTDSYGVTTG 111

Query: 122 FGGSADTRTEDAVSLQKALIEHQLCGVTPTSVSSFSVGRGLENLTPLEVVIRGAMVIRVNS 181
 FG ++ RT+ +LQK LI G+ F G +TLP R AM++R+N+
 Sbjct: 112 FGATSHRRTKQGALQKELIRFLNAGI-----FGNGTETCHTLPHSATRAAMLVRINT 164

Query: 182 LTRGHSVRLVLEALTNFLNHRITPIVPLRGSISASGDLSPLSYIAGAITGHPDVKVHV 241
 L +G+S +R +LEA+T LN+ ITP +PLRG+I+ASGDL PLSYIAG +TG P+ K
 Sbjct: 165 LLQGYSGIRFEILEAITKLLNNITPCLPLRGITITASGDLVPLSYIAGLLTGSPNSKAT- 223

Query: 242 LHEGTEKIMFAREAISLFGLEA--VVLGPKEGLLVNGTAVSASMATXXXXXXXXXXXXX 299
 +++ A EA G+++ L PKEGL LVNGTAV + +A+
 Sbjct: 224 --GPNGEVLDAVEAFKAAGIDSGFFELQPKEGLLVNGTAVGSGGLASMLVFTNVLA VLS 281

Query: 300 XXXXXXXXVEAMVGQQGSFAPFIHDCRPHPGQVEVARNIRTLLSGSSFAXXXXXXXXXXXXXX 359
 E M G+ F + + HPGQ+E A + +L GS++
 Sbjct: 282 ELISAIFAEVMNGKP-EFTDHLTHKLKHHPGQIEAAAIMEHILDGSAYMKAACKLHEMDP 340

Query: 360 XXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTNDNPLLDVENKQTAHGGNFQ 419
 +QDRY LRTSPQ+LGP +E + + ++ E N+ DNPL+DV + HGGNFQ
 Sbjct: 341 LQKP-KQDRYALRTSPQWLGPQIEVIRFSTKSIEREINSVNDNPLIDVSRNKALHGGNFQ 399

Query: 420 ASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCL-AAEDPSLNYHGKGLDIH 478
 + + +SM+ RLA+A IGKL F Q +EL+N N GLPS L A+ +PSL+Y KG +I
 Sbjct: 400 GTPIGVSMNDNVRLAIASIGKLLFAQFSELVNDFYNNGLPSNLTASRNPSLDYGFKGAEIA 459




Query: 479 IAAYASELGHLANPVTTFVQPAEMGNQAVNSLALISARRTAEANDVLSLLLASHLYCTLQ 538
 +A+Y SEL +LANPVT+ VQ AE NQ VNSL LIS+R+TAEA D+L L+ + L Q
 Sbjct: 460 MASYCSELQYLANPVTSHVQSAEQHNQDVNSLGLISSRKTAEAVDILKLMSTTFLVALCQ 519

Query: 539 AVDLRAMELDFKKQFDPLLPDLLQQLHGTGLDVNALALEVKKALNKRLEQTTTYDLEPRW 598
 A+DLR +E + + + + ++ L TG + L + K L + +
 Sbjct: 520 AIDLRHLEENLRSAVKNTVSHVSKRVLTGTANGE---LHPSRFCEKELLKVVDRE----- 571

Query: 599 HDAFSYATG-----TVVELLSSSPSANVTLTAVNAWKVASAEKAIS--LT 641
 D F+YA V L++ + T+V K+A+ E + L
 Sbjct: 572 -DVFAADDPCSATYPLMQKLQVLVDHALANGENEKNASTSV-FQKIAAFEDELKALLP 629

Query: 642 REVRN-RFWQTPSSQAPAHAYLSPRTRVLYSFVREELGVQARRGDVFGVQQETIGSNVS 700
 +EV + R + A + R+ LY FVREELG + G + G
 Sbjct: 630 KEVESARAAAYDSGNSAIENKIKECRSYPLYKFVREELGT-----GLLTGENVRSPGEEFD 684

Query: 701 RIYEAIKDGRINHLVKML 719
 +++ A+ +G+I +++ L
 Sbjct: 685 KVFTAMCEGKIIDPMLECL 703

☐ >gi|50910709|ref|XP_466843.1|  putative phenylalanine ammonia-lyase [Oryza sativa cultivar-group)]
 gi|48716546|dbj|BAD23149.1|  putative phenylalanine ammonia-lyase [Oryza sativa cultivar-group)]
 gi|48716258|dbj|BAD23794.1|  putative phenylalanine ammonia-lyase [Oryza sativa cultivar-group)]
 Length = 701

Score = 340 bits (873), Expect = 7e-92

Identities = 236/678 (34%), Positives = 358/678 (52%), Gaps = 35/678 (5%)

Query: 49 SQLEIVQELLSDPDDEVELSGYSLTXXXXXXXXXXXXX--XXQNDDEIRARVDKSVDF 106
 S L+ V+ +++ + +V++ G +L + D+E R RV S ++
 Sbjct: 25 SHLDEVKRMVAQFREPLVKIQGATLRVGQVAAVAQAKDAAGVAVELDEEARPRVKASSEW 84

Query: 107 LKAQLQNS--VYGVTTGFGGSADTRTEDAVSLQKALIEHQICGVTPTSVSSFSVGRGLEN 164

Sbjct: 85 + + + +YGVTTGFGG++ RT+D +LQ L+ H G+ T +
ILNCIAHGGDIYGVTTGFGGTSHRRTKDGPALQVELLRHLNAGIFGTGSDG-----H 136

Query: 165 TLPLEVVIRGAMVIRVNSLTRGHSVRLVLEALTNFLNHRITPIVPLRGSISASGDLSP 224
TLP E VR AM++R+N+L +G+S +R +LEA+T LN +TP +PLRG+I+ASGDL PL

Sbjct: 137 TLPSETVRAAMLVRINTLLQGYSGIRFEILEAITKLLNTGVTPCLPLRGTITASGDLVPL 196

Query: 225 SYIAGAITGHPDKVHVLHEGTEKIMFAREAISLFGLEA--VVLGPKEGLGLVNGTAVSA 282
SYIAG ITG P+ + + +G + + A EA L G+E L PKEGL +VNGT+V +

Sbjct: 197 SYIAGLITGRPNAQA-ISPDRK--VDAAEAFKLAGIEGGFFTLNPKEGLAIVNGTSVGS 253

Query: 283 SMATXXXXXXXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQVEVARNIRTLL 342
++A E M G+ H + + HPG +E A + +L

Sbjct: 254 ALAATVMFDANILAVLSEVL SAVFCEVMNGKPEYTDHLTHKL-KHHPGSIEAAIMEHIL 312

Query: 343 SGSSFAXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTND 402
+GSSF +QDRY LRTSPQ+LGP +E + A ++ E N+ DN

Sbjct: 313 AGSSFMSHAKKVNEMDPLLKP-KQDRYALRTSPQWLGPQIEVIRAATKSIEREVNSVNDN 371

Query: 403 PLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRLPSCLA 462
P++DV + HGGNFQ + + +SM+ RLA+A IGKL F Q +EL+N N GL S LA

Sbjct: 372 PVIDVHRGKALHGGNFQGTPIGVSMNARLAIANIGKLMFAQFSELVNEFYNNGLTSNLA 431

Query: 463 -AEDPSLNHYHGKGLDIHIAAYASELGHLANPVTTTFVQPAEMGNQAVNSLALISARRTAEA 521
+ +PSL+Y KG +I +A+Y SEL +LANP+T VQ AE NQ VNSL L+SAR+T EA

Sbjct: 432 GSRNPSLDYGFKGTEIAMASYCSELQYLANPITNHVQSAEQHNQDVNSLGLVSARKTLEA 491

Query: 522 NDVLSLLLASHLYCTLQAVDLRAMELDFKKQFDPDLLPTLLQQHL---GTGLDVNALALEV 578
D+L L+ ++++ QAVDLR +E + K + + ++ L TG D+++

Sbjct: 492 VDILKLMSTYIVALCQAVDLRHLLENIKSSSVKNCVTQVAKKVLTMNPTG-DLSSARFSE 550

Query: 579 KKALNK-RLEQTTTYDLEP--RWHDAFSYATGTVVELLSSSPSANVTLTAVNAWKVASAE 635
K L E +Y +P + +VE +S A + + E

Sbjct: 551 KNLLTAIDREAVFSYADDPSCANYPLMQKLRAVLVEHALTSGDAEPEASVFSKITKFEEE 610

Query: 636 KAISLTREVRNRFWQTPSSQAP-AHAYLSPRTRVLYSFVREELGVQARRGDVFFV-GVQQE 693
+L RE+ + AP A+ + R+ LY FVREELG VF+ G + +

Sbjct: 611 LRSALPREIEAARVAVANGTAPVANRIVESRSFPLYRFVREELGC-----VFLTGEK 664

Query: 694 TIGSNVSRIYEAIKDGRI 711
+ G ++++ I G++

Sbjct: 665 SPGEECNKVFGLGISQGKL 682

☐ >gi|58533149|gb|AAW78932.1| phenylalanine-ammonia lyase [Rhodiola sachalinensis]
Length = 710

Score = 340 bits (873), Expect = 7e-92
Identities = 238/702 (33%), Positives = 359/702 (51%), Gaps = 48/702 (6%)

Query: 40 GLDGHAHQSQLEIVQELLSPTDDVVELSGYSLTXXXXXXXXXXXXXXXXXQNDDEIRAR 99
GL A S L+ V+ ++ + V+L G +LT + + R

Sbjct: 24 GLAAEAMKGSHLDEVKRMVEEYRKPAVKLGGETLTIAQVAAIAGRGSDVRVELSESAREG 83

Query: 100 VDKSVDFLKAQLQNSV--YGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPTSVSSFS 157
V S D++ + YGVTTGFG ++ RT+ +LQK LI G+ F

Sbjct: 84 VKASSDWME SMGKGTDSYGVTTGFGATSHRRTKQGGALQKELIRFLNAGI-----FG 136

Query: 158 VGRGLENLPLEVVIRGAMVIRVNSLTRGHSVRLVLEALTNFLNHRITPIVPLRGSISA 217

G+ +TL R AM++R+N+L +G+S +R +LEA+T+ LN ITP +PLRG+I+A
 Sbjct: 137 SGKDTCHTSLQSATRAAMLVRINTLLQGYSIRFEILEAITSLNSDITPCLPLRGITITA 196

Query: 218 SGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEAVV--LGPKEGLGLV 275
 SGDL PLSYIAG +TG P+ K V G +++ EA G+E L PKEGL LV
 Sbjct: 197 SGDLVPLSYIAGLLTGRPNKA-VAENG--EVITPDEAFKRAGIEGGFFNLQPKEGLALV 253

Query: 276 NGTAVSASMATXXXXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQVEVA 335
 NGTAV + +A+ E M ++ F + + HPGQ+E A
 Sbjct: 254 NGTAVGSGLASMVLFDANVLAVLAEIMSAVFSEVMQ-RKPEFTDHLTHKLKHHPGQIEAA 312

Query: 336 RNIRTLLSGSSFAXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLE 395
 + +L GS + +QDRY LRTSPQ+LGP VE + + ++ E
 Sbjct: 313 AIMEHILDGSEYVKAACKLHETDPPQKP-KQDRYALRTSPQWLGPQVEVIRFSTKSIERE 371

Query: 396 NNTTTDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNR 455
 N+ DNPL+DV + HGGNFQ + + +SM+ TRLA+A IGKL F Q +EL+N N
 Sbjct: 372 VNSVNDNPLIDVSRNKAIHGGNFQGTPIGVSMDNTRLAIAAIGKLMFAQFSELVNDFYNN 431

Query: 456 GLPSCLA-AEDPSLNYHGKGLDIHIAAYASELGHANPVTTFVQPAEMGNQAVNSLALIS 514
 GLPS L+ + +PSL+Y KG +I +A+Y SEL L NPVT VQ AE NQ VNSL LIS
 Sbjct: 432 GLPSNLGSRNPSLDYGFKAIEAMASYCSELQFLGNPVTNHVQSAEQHNQDVNSLGLIS 491

Query: 515 ARRTAEANDVLSLLASHLYCTLQAVDLRAMELDFKKQFDPLLPTLLQQHLGTGLDVNAL 574
 +R+TA+A D+L L+ +++L QA+DLR ME + + + + ++ L TG +
 Sbjct: 492 SRKTAKAVDILKMSSTYLVALCQAIDLRHMEENLRMTVKTTISQVAKRTLTTGANGE-- 549

Query: 575 ALEVKKALNKRLEQTTTYDLEPRWHDFAFSYATGTVVELL-----SSSPSAN 620
 L + K L + + + D AT +++ L +P+++
 Sbjct: 550 -LHASRLCEKDLLKVVDREYVFAYIDDPCLATYPLMQKLQVLVDHALTKGENEKNPNSS 608

Query: 621 VTLTAVNAWKVASAEKAIS--LTREVRNRFWQTPSSQAP-AHAYLSPRTRVLYSFVREEL 677
 + L K+A+ + + L +EV N + AP A+ R+ LY F+REEL
 Sbjct: 609 IFL-----KIAAFKDELKTLTPKEVENMRLLIENGAPMANQIKECRSYPLYRFIREEL 662

Query: 678 GVQARRGDVFGVQQETIGSNVSRIYEAIKDGRIHVLVKML 719
 G G+ + + G +++ A+ +G+I +++ L
 Sbjct: 663 GTALLSGE-----KTRSPGEEFDKVFVAMCEGKIIDPMLECL 699

☐ >gi|266731|sp|Q01861|PAL1_PEA Phenylalanine ammonia-lyase 1
 gi|217982|dbj|BAA00886.1| phenylalanine ammonia-lyase [Pisum sativum]
 gi|217980|dbj|BAA00885.1| phenylalanine ammonia-lyase [Pisum sativum]
 Length = 723

Score = 340 bits (872), Expect = 9e-92

Identities = 240/697 (34%), Positives = 355/697 (50%), Gaps = 39/697 (5%)

Query: 40 GLDGHAHQSQLEIVQELLSDPDDEVELSGYSLTXXXXXXXXXXXXXXXXXQNDDEIRAR 99
 G+ A S L+ V+ ++ + VV L G +LT + + RA
 Sbjct: 38 GVAAEAMKGSHLDEVKRMVEEYRKPVVRLLGGETLTISQVAAIAAHDHGVKVELSESARAG 97

Query: 100 VDKSVDFLKAQLQNSV--YGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPTSVSSFS 157
 V S D++ + YGVTTGFG ++ RT+ +LQK LI G+ F
 Sbjct: 98 VKASSDWVMESMNKGTDSYGVTTGFGATSHRRTKQGGALQKELIRFLNAGI-----FG 150

Query: 158 VGRGLENLPLEVVRGAMVIRVNSLTRGHSVRLVLEALTNFLNHRITPIVPLRGSISA 217
 G +TLP R AM++R+N+L +G+S +R +LEA+T +N+ +TP + LRG+I+A
 Sbjct: 151 NGTESSHTLPHTATRAAMLVRINTLLQGYSIRFEILEAITKLINNVTPCL-LRGITITA 209

Query: 218 SGDLSPLSYIAGAITGHPDVKVHVLHEGTE-KIMFAREAISLFGLEA--VVLGPKEGLGL 274
 SGDL PLSYIAG +TG P+ K H GT +I+ A+EA + L PKEGL L
 Sbjct: 210 SGDLVPLSYIAGLLTGRPNKHAH----GTSGEILNAKEAFQSAEINDGFFELQPKEGLAL 265

Query: 275 VNGTAVSASMATXXXXXXXXXXXXXXXXXXXXXVEAMVGQQGSFAPFIHDVCRPHPGQVEV 334
 VNGTAV + +A+ E M G+ F + + HPGQ+E
 Sbjct: 266 VNGTAVGSGLASIVLFEANILAVLSEVLSAIFAEMVQKGP-EFTDHLTHKLKHHPGQIEA 324

Query: 335 ARNIRTLLSGSSFAXXXXXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSL 394
 A + +L GS++ +QDRY LRTSPQ+LGPL+E + + ++
 Sbjct: 325 AAIMEHILDGSAYVKAACKLHEMDPLQKP-KQDRYALRTSPQWLGPLIEVIRFSTKSIER 383

Query: 395 ENNTTTDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMN 454
 E N+ DNPL+DV + HGGNFQ + + +SM+ TRLLA IGKL F Q +EL+N N
 Sbjct: 384 EINSVNDNPLIDVSRNKALHGGNFQGTPIGVSMNTRLALASIGKLLFAQFSELVNDNFYN 443

Query: 455 RGLPSC-LAEDPSLNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVNSLALI 513
 GLPS L A+ +PSL+Y KG +I +A+Y SEL +LANPVT VQ AE NQ VNSL LI
 Sbjct: 444 NGLPSNLSASRNPSLDYGFKGSEIAMASYCSELQYLANPVTTHVQSAEQHNQDVNSLGLI 503

Query: 514 SARRTAEANDVLSLLLASHLYCTLQAVDLRAMELDFKKQFDPLLPTLLQQHLGTGLDVNA 573
 S+R+T EA ++L L+ ++ L QAVDLR +E + K ++ + ++ L TG++
 Sbjct: 504 SSRKTYEAIEILQLMSSTFLIALCQAVDLRHLEENLKNVKNIVSQVAKRTLTTGVNGE- 562

Query: 574 LALEVKKALNKRLEQTTTYDLEPRWHDASYATGTVVE-----LLSSSPSANVTL 623
 L + K L + + + D AT +++ L++ N+
 Sbjct: 563 --LHPSRFCEKDLLRVVDREHVFAYIDDPSCATYPLMQKLRQVLVDHALVNGESEKNLNT 620

Query: 624 TAVNAWKVASAEKAISLTREVRN-RFWQTPSSQAPAHAYLSPRTRVLYSFVREELGVQAR 682
 + E L +EV + R + + R+ LY FVR+ELG
 Sbjct: 621 SIFQKIATFEDELKTLPLKEVESTRAAYESGNPTVPNKINGCRSYPLYRFRVQELGTGLL 680

Query: 683 RGDVFGVGVQETIGSNVSRIYEAIKDGRINHVLVKML 719
 G+ + + G +++ AI G+I L++ L
 Sbjct: 681 TGEKVI-----SPGEECDKLFTAICQGKIIDPLLQCL 712

☐ >gi|633597|emb|CAA55075.1| phenylalanine ammonia-lyase [Nicotiana tabacum]
 gi|1171997|sp|P45733|PAL3_TOBAC Phenylalanine ammonia-lyase
 Length = 712

Score = 340 bits (871), Expect = 1e-91

Identities = 242/691 (35%), Positives = 353/691 (51%), Gaps = 42/691 (6%)

Query: 49 SQLEIVQELLSIPTDDVVELSGYSLTXXXXXXXXXXXXXXXXXQND--DEIRARVDKSVDF 106
 S L+ V+++++ VV+L G +LT + + + RA V S D+
 Sbjct: 33 SHLDEVKKMVAEFRKPVVKGGETLTVAQVAAIAAKDNAKTVKVELSEGARAGVKASSDW 92

Query: 107 LKAQLQNSV--YGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPTSVSSFSVGRGLEN 164
 + + YGVTTGFG ++ RT++ +LQK LI GV G G E+
 Sbjct: 93 VMDSMSKGTDSYGVTTGFGATSHRRTKNGGALQKELIRFLNAGV-----FGNGTES 143

Query: 165 --TLPLEVVRGAMVIRVNSLTRGHSVRLVLEALTNFLNHRITPIVPLRGSISASGDLS 222
 TLP R AM++R+N+L +G+S +R +LEA+T LNH +TP +PLRG+I+ASGDL
 Sbjct: 144 CHTLPQSGTRAAMLVRINTLLQGYSGIRFEILEAITKLLNHNVTPLPLRGITITASGDLV 203

Query: 223 PLSYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEA--VVLGPKEGLGLVNGTAV 280
 PLSYIAG +TG P+ K + T + A EA + G+ + L PKEGL LVNGTAV

Sbjct: 204 PLSYIAGLLTGRPNSKAIGPNGET---LNAEEAFRVAGVNSGFFELQPKEGLALVNGTAV 260

Query: 281 SASMATXXXXXXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQVEVARNIRT 340
+ +A+ E M G+ F + + HPGQ+E A +

Sbjct: 261 GSGGLASMVLFDANILAVFSEVLSAIFAEMVNGKP-EFTDHLTHKLKHHPGQIEAAAIMMEH 319

Query: 341 LLSGSSFAXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTT 400
+L GSS+ +QDRY LRTSPQ+LGP +E + A + E N+

Sbjct: 320 ILDGSSYVKAPQKLHETDPLQKP-KQDRYALRTSPQWLGPQIEVIRSATKMIEREINSVN 378

Query: 401 DNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSC 460
DNPL+DV + HGGNFQ + + +SM+ RLALA IGKL F Q +EL+N N GLPS

Sbjct: 379 DNPLIDVSRNKALHGGNFQGTPIGVSMNARLALASIGKLMFAQFSELVNDYYNGLPSN 438

Query: 461 L-AAEDPSLNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVNSLALISARRTA 519
L A +PSL+Y KG +I +A+Y SEL LANPVT VQ AE NQ VNSL LISAR+TA

Sbjct: 439 LTAGRNPSLDYGFKGSEIAMASYCSELQFLANPVTNHVQSAEQHNQDVNSLGLISARKTA 498

Query: 520 EANDVLSLLLASHLYCTLQAVDLRLAMELDFKKQFDPLLPTLLQQHLGTGLDVNALALEVK 579
EA D+L L+ +++L QA+DLR +E + + + + ++ L G + L

Sbjct: 499 EAVDILKLMSSSTYLVALCQAIIDLRLHLEENLRNAVKNVTSQVAKRTLTMGANGE---LHPS 555

Query: 580 KALNKRLEQTTTYDLEPRWHDFAFSYATGTVVELL-----SSSPSANVTLTAVNAW 629
+ K L + + R+ D A +++ L + N +

Sbjct: 556 RFCEKDLLRVVDREYVFRYADDACSANYPLMQKLRQVLVDHALENGENEKNANSSIFQKI 615

Query: 630 KVASAEKAISLTREVRN-RFQWTPSSQAPAHAYLSPRTRVLYSFVREELGVQARRGDV FV 688
E L +EV + R + A A+ R+ LY FVREELG ++

Sbjct: 616 LAFEGELKAVLPKEVESARISLENGNPAIANRIKECRSYPLYRFVREELG-----AELLT 670

Query: 689 GVQQETIGSNVSRIYEAIKDGRINHVLVKML 719
G + + G +++ A+ +G+I L++ L

Sbjct: 671 GEKVRSPGEECDKVFTAMCNGQIIDSLECL 701

☐ >gi|6433808|emb|CAB60719.1| phenylalanine ammonia-lyase [Cicer arietinum]
gi|9910836|sp|Q9SMK9|PAL2_CICAR Phenylalanine ammonia-lyase 2
Length = 718

Score = 340 bits (871), Expect = 1e-91

Identities = 241/715 (33%), Positives = 352/715 (49%), Gaps = 36/715 (5%)

Query: 12 LANGFTNGSHAAPTKSAAGPTSALRRTPGLDGHAHQSQLEIVQELLSDPTDDVVELSGY 71
L NG NGS ++ G+ + S L+ V+ ++ + VV L G

Sbjct: 4 LPNGNCNGSSLNVCNGNGNLSNNDLSLWGMADSMRGSHLDEVKRMVEEYRKAVVPLGGK 63

Query: 72 SLTXXXXXXXXXXXXXXXXXQNDDEIRARVDKSVDFLKAQLQNSV--YGVTTGFGGSADTR 129
LT + +E R V S D++ + YGVTTGFG ++ R

Sbjct: 64 GLTISQVAAVATQNTGVAVELAEETRYAVKASSDWVVDSDMNKGTDSYGVTTGFGATSHRR 123

Query: 130 TEDAVSLQKALIEHQLCGVTPTSVSSFSVGRGLENLPLEVVIRGAMVIRVNSLTRGHSAV 189
T+ +LQ LI G+ F G TLP R AM++R+N+L +G+S +

Sbjct: 124 TKQGGALQNELIRFLNAGI-----FGNGTESTQTLPHATRAAMLVRINTLLQGYSGI 176

Query: 190 RLVVLEALTNFLNHRITPIVPLRGSISASGDLSPLSYIAGAITGHPDVKVHVLHEGTEKI 249
R ++EA+ FLNH ITP +PLRG+I+ASGDL PLSY+AG + G P+ K + G +I

Sbjct: 177 RFEIMEIAIAKFLNHNITPCLPLRGITITASGDLVPLSYVAGLLIGRPNSK-SIGPNG--QI 233

Query: 250 MFAREAISLFGLEA--VVLGPKEGLGLVNGTAVSASMATXXXXXXXXXXXXXXXXXXXXV 307

+ A+EA L G+E L PKEGL LVNGTAV + +A+
 Sbjct: 234 LNAKEAFQLAGIETGFFELQPK EGLALVNGTAVGSGLASLALFETNLLVVLSEILSAIFA 293
 Query: 308 EAMVGQQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGSSFAXXXXXXXXXXXXXXXXXGILRQD 367
 E M G+ F + + HPGQ+E A + +L GS + +QD
 Sbjct: 294 EVMQKGP-EFTDHLTHKLKHHPGQIEAAAIMEHILDGSSYYVKAQKVHDIDPLQKP-KQD 351
 Query: 368 RYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTNDNPLLDVENKQTAHGGNFQASAVSISM 427
 RY LRTSPQ+LGP +E + +A + E N+ DNPL+DV + HGGNFQ + + +SM
 Sbjct: 352 RYALRTSPQWLGPQIEVIRNATKMIEREINSVNDNPLIDVSRNKALHGGNFQGTPIGVSM 411
 Query: 428 EKTRLALALIGKLNFTQCTELLNAAMNRGLPSCS-AAEDPSLNYHGKGLDIHIAAYASEL 486
 + TRLA+A IGKL F Q +EL+N N GLPS L + +PSL+Y KG +I +A+Y SEL
 Sbjct: 412 DNTRLAIASIGKLMFAQFSELVNDNFYNNGLPSNLTGSRNPSLDYGFKGAEIAMASYCSEL 471
 Query: 487 GHLANPVTTFVQPAEMGNQAVNSLALISARRTAEANDVLSLLASHLYCTLQAVDLRAME 546
 +LANPVT VQ AE NQ VNLS LIS+R+TAEA ++L L+ ++ L QA+DLR +E
 Sbjct: 472 QYLANPVTNHVQSAEQHNQDVNSLGLISSRKTAEAVEILKLMSSTFLVALCQAIDLRHIE 531
 Query: 547 LDFKKQFDPLLPDLLQQLHGLTGLDVNALALEVKKALNKRLEQTTTYDLEPRWHDAFSYAT 606
 + K + + ++ L G++ L + K L + + D AT
 Sbjct: 532 ENLKSVMKNTVSQVAKRVLTVGVNGE---LHPSRFCEKDLLNVVEREYVFAYIDDPSCSAT 588
 Query: 607 GTVVELL-----SSSPSANVTLTAVNAWKVASAEKAISLTREVRN-RFWQTPSSQ 655
 +++ L + N + + E L +EV + R +
 Sbjct: 589 YPLMQKLRHVLVDHALENGDREGNSSTSIFQKIGAFEQELKTLPLPKEVESVRVDVENGNP 648
 Query: 656 APAHAYLSPRTRVLYSFVREELGVQARRGDVFGVQVQETIGSNVSRIYEAIKDG 710
 A + + R+ LY FVRE LG + G + + G +++ A+ DGR
 Sbjct: 649 AVPNRIIECRSYPLYKFVRENLTG-----SLLTGEKIRSPGEECDKVFAALCDGR 698

>gi|3914261|sp|O49835|PAL1_LITER Phenylalanine ammonia-lyase 1 (PAL-1)
 gi|2911122|dbj|BAA24928.1| phenylalanine ammonia-lyase [Lithospermum erythrorhizo]
 Length = 710

Score = 340 bits (871), Expect = 1e-91

Identities = 239/687 (34%), Positives = 351/687 (51%), Gaps = 36/687 (5%)

Query: 49 SQLEIVQELLSDPDPTDDVVELSGYSLTXXXXXXXXXXXXXXXXXQNDDEIRARVDKSVDFLK 108
 S L+ V+ ++++ VV+L+G +LT + + R V S D++
 Sbjct: 33 SHLDEVKNMVAEFRKPVVQLAGKTLTIGQVAAIAARDDGVTVELAEAAAREGVKASSDWVM 92
 Query: 109 AQLQNSV--YGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPTS SVSSFSVGRGLENTL 166
 + YGVTTGFG ++ RT+ +LQK LI G+ F G +TL
 Sbjct: 93 DSMNKGTD SYGVTTGFGATSHRRTKQGGALQKELIRFLNAGI-----FGNGTETSHTL 145
 Query: 167 PLEVVRGAMVIRVNSLTRGHSAVRLVVLEALTNFLNHRITPIVPLRGSISASGDLSPLSY 226
 P R AM++R+N+L +G+S +R +LEA+T FLN ITP +PLRG+I+ASGDL PLSY
 Sbjct: 146 PHSATRAAMLVRINTLLQGYSGIRFEILEAITKFLNTNITPCLPLRGTITASGDLVPLSY 205
 Query: 227 IAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEA--VVLGPKEGLGLVNGTAVSASM 284
 IAG +TG P+ K + EKI A EA L G+ L PKEGL LVNGTAV + M
 Sbjct: 206 IAGLLTGRPNKA--VGPTGEKIN-AEEAFRLAGISTGFFELQPK EGLALVNGTAVGSGM 262
 Query: 285 ATXXXXXXXXXXXXXXXXXXXXXVEAMVGQQGSFAPFIHDVCRPHPGQVEVARNIRTLLSG 344
 A+ E M G+ F + + HPGQ+E A + +L G
 Sbjct: 263 ASMVLYEANILAVLSEVISAIFA EVMNGKP-EFTDHLTHKLKHHPGQIEAAAIMEHILDG 321

Query: 345 SSFAXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTDNPL 404
 S + +QDRY LRTSPQ+LGP +E + A + E N+ DNPL
 Sbjct: 322 SGYVKAQKLHEMDPLQKP-KQDRYALRTSPQWLGPQIEVIRSATKMIEREINSVNDNPL 380

Query: 405 LDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRLPSCL-AA 463
 +DV + HGGNFQ + + ++M+ TRLA+A IGKL F Q +EL+N N GLPS L +
 Sbjct: 381 IDVSRNKALHGGNFQGTPIGVAMDNTRLAIASIGKLLFAQFSELVNDYNNGLPSNLTGS 440

Query: 464 EDPSLNYHGKGLDIHIAAYASELGHLANPVTTTFVQPAEMGNQAVNSLALISARRTAEAND 523
 +PSL+Y KG +I +A+Y SEL LANPVT VQ AE NQ VNSL LIS+R+T+EA +
 Sbjct: 441 RNPSLDYGFKAIEAMASYCSELQFLANPVTNHVQSAEQHNQDVNSLGLISSRKTSEAVE 500

Query: 524 VLSLLLASHLYCTLQAVDLRAMELDFKKQFDPLLPTLLQQHLGTGLDVNALALEVKKALN 583
 +L L+ +S L QAVDLR +E + + + + ++ L TG++ L +
 Sbjct: 501 ILKLMSSSFLVALFQAVDLRHIEENVRLAVKNVTSQVAKRTLTTGVNGE---LHPSRFSE 557

Query: 584 KRLEQTTTYDLEPRWHDFAFSYATGTVVELL-----SSSPSANVTLTAVNAWKVAS 633
 K L + + + D T +++ L + +V + + +
 Sbjct: 558 KDLLRVVDREYVFAYADDPCLTTYPLMQKLRETLVGHALDNGENEKDVNTSIFHKIAIFE 617

Query: 634 AEKAISLTREVRN-RFQWTPSSQAPAHAYLSPRTRVLYSFVREELGVQARRGDVFGVQ 692
 E L +EV N R A ++ R+ LY FVREELG ++ G +
 Sbjct: 618 EELKAILPKEVENARASVENGIPAISNRIEECRSYPLYKFVREELGT-----ELLTGEKV 672

Query: 693 ETIGSNVSRIYEAIKDGRINHVLVKML 719
 + G + +++ A+ +G++ L+ L
 Sbjct: 673 RSPGEELDKVFTAMCEGKLVDPDLLACL 699

☐ >gi|50910713|ref|XP_466845.1| ☒ putative phenylalanine ammonia-lyase [Oryza sativa
 cultivar-group)]
 gi|48716548|dbj|BAD23151.1| ☒ putative phenylalanine ammonia-lyase [Oryza sativa
 cultivar-group)]
 Length = 718

Score = 339 bits (869), Expect = 2e-91
 Identities = 242/684 (35%), Positives = 350/684 (51%), Gaps = 53/684 (7%)

Query: 49 SQLEIVQELLSIPTDDVVELSGYSLTXXXXXXXXXXXXXXXXXQNDDEIRARVDKSVDFLK 108
 S L+ V+ ++ D +V++ G SLT + D+ R RV S D++
 Sbjct: 42 SHLDEVKRMVEDFRQPLVKIEGASLTIAQVAAVAAGAGDARVELDESARGRVKASSDWVM 101

Query: 109 AQLQNSV--YGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPTSVSSFSVGRGLENTL 166
 + N YGVTTGFG ++ RT++ +LQ+ LI G T + L
 Sbjct: 102 NSMMNGTDSYGVTTGFGATSHRRTKEGGALQRELIRFLNAGAFGTGTDG-----HVL 153

Query: 167 PLEVVRGAMVIRVNSLTRGHSVRLVLEALTNFLNHRITPIVPLRGSISASGDLSPLSY 226
 P E R AM++R+N+L +G+S +R +LEA+T LN +TP +PLRG+I+ASGDL PLSY
 Sbjct: 154 PAEATRAAMLVRINTLLQGYSGIRFEILEAITKLLNANVTPLPLRGTITASGDLVPLSY 213

Query: 227 IAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEA--VVLGPKEGLGLVNGTAVSASM 284
 IAG ITG + V V +G + + A EA + G+E L PKEGL +VNGTAV + +
 Sbjct: 214 IAGLITGRQN-SVAVAPDGRK--VTAAEAFKIAIEHGFELQPKGLAMVNGTAVGSGL 270

Query: 285 ATXXXXXXXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQVEVARNIRTLLSG 344
 A+ E M G+ H + + HPGQ+E A + +L G
 Sbjct: 271 ASTVLFEANVLAILAEVLSAVFCEVMTGKPEYTDHLTHKL-KHHPGQIEAAIMEHILEG 329

Query: 345 SSFAXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTNDNPL 404
 SS+ +QDRY LRTSPQ+LGP +E + A ++ E N+ DNPL
 Sbjct: 330 SSYMKLAKKLGEPLMKP-KQDRYALRTSPQWLGPQIEVIRFATKSIEREINSVNDNPL 388

Query: 405 LDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCLA-A 463
 +DV + HGGNFQ + + +SM+ TRLALA IGKL F Q +EL+N N GLPS L+
 Sbjct: 389 IDVSRGKALHGGNFQGTPIGVSMNTRLALAAIGKLMFAQFSELVNDFYNNGLPSNLSSG 448

Query: 464 EDPSLNYHGKGLDIHIAAYASELGHLANPVTTTFVQPAEMGNQAVNSLALISARRTAEAND 523
 +PSL+Y KG +I +A+Y SEL L NPVT VQ AE NQ VNSL LIS+R+TAEA D
 Sbjct: 449 RNPSLDYGFKAIEAMASYCSELQFLGNPVNTNHVQSAEQHNQDVNSLGLISSRKTAEAID 508

Query: 524 VLSLLLASHLYCTLQAVDLRAMELDFKKQFDPLLPTLLQQHLGTGLDVNAL-ALEVKKAL 582
 +L L+ ++ L QA+DLR +E + K + + Q L +N + L + +
 Sbjct: 509 ILKLMSSSTFLIALCQAIDLRHLEENMK-----TAVKNCVMQVAKKSLSMNHMGGLHIARFC 564

Query: 583 NKRLEQTTTYDLEPRWHDASYATG-----TVVELLSSSPSANVTLTAVN 627
 K L T D E F+YA + L++ + V T++
 Sbjct: 565 EKDL--LTAIDREA----VFAYADDPCSANYPLMQKLRAVLIEHALANGDAERVLETSIF 618

Query: 628 AWKVASAEKAI--SLTREVR-NRFWQTPSSQAPAHAYLSPRTRVLYSFVREELGVQARRG 684
 A KVA E+ + +L +EV R + + R+ LY FVREE+G
 Sbjct: 619 A-KVAEFEQHVRAALPKEVEAARAAVENGTPLPVNRIKECRSYPLYRFVREEVGT----- 672

Query: 685 DVFGVQQETIGSNVSRIYEAID 708
 + G + + G ++++ AI +
 Sbjct: 673 EYLTGEKTRSPGEELNKVLVAINE 696

☐ >gi|34541972|gb|AA074878.1| phenylalanine ammonia lyase [Populus balsamifera subsp. deltoides]
 Length = 711

Score = 339 bits (869), Expect = 2e-91

Identities = 243/698 (34%), Positives = 353/698 (50%), Gaps = 40/698 (5%)

Query: 40 GLDGHAHQSQLEIVQELLSDPTDDVVELSGYSLTXXXXXXXXXXXXXXXXXQNDDEIRAR 99
 G+ + S L+ V+ ++ + VV+L G +LT + +E RA
 Sbjct: 25 GMAAESLKGSHLDEVKRMIEEYRKPVVKLGGETLTIGQVTAIASRDVGVMVELSEEARAG 84

Query: 100 VDKSVDFLKAQLQNSV--YGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPPTSVSSFS 157
 V S D++ + YGVTTGFG ++ RT+ LQK LI G+ S
 Sbjct: 85 VKASSDWMDSMSKGTDSYGVTTGFGATSHRRTKQGGELQKELIRFLNAGIFGNDTES-- 142

Query: 158 VGRGLENLPLEVVRGAMVIRVNSLTRGHSVRLVLEALTNFLNHRITPIVPLRGSISA 217
 +TLP R AM++R N+L +G+S +R +LEA+T LNH ITP +PLRG+I+A
 Sbjct: 143 -----SHTLPRSATRAAMLVRFNLTLLQGYSGIRFEMLEAITKLLNHNITPCLPLRGITITA 197

Query: 218 SGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEA--VVLGPKEGLGLV 275
 SGDL PLSYIAG +TG P+ K + E + A EA + G++ L PKEGL LV
 Sbjct: 198 SGDLVPLSYIAGLLTGRPNKA--VGPNGEPLSPA-EAFTQAGIDGGFFELQPKGLALV 254

Query: 276 NGTAVSASMATXXXXXXXXXXXXXXXXXXXXXVEAMVGQQGSFAPFIHDVCRPHPGQVEVA 335
 NGTAV + +A+ E M G+ F + + HPGQ+E A
 Sbjct: 255 NGTAVGSGGLAMVLFETNVLAILSEVLSAIFAEVMQKPK-EFTDHLTHKLKHHPGQIEAA 313

Query: 336 RNIRTLSSGSSFAXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLE 395
 + +L GS++ +QDRY LRTSPQ+LGPL+E + + + E
 Sbjct: 314 AIMEHILDGSAYVKEAQKLHEIDPLQKP-KQDRYALRTSPQWLGPLIEVIRTSTKMIERE 372

Query: 396 NNTTTDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNR 455
 N+ DNPL+DV + HGGNFQ + + +SM+ TRLA+A IGKL F Q +EL+N N
 Sbjct: 373 INSVDNPLIDVSRNKALHGGNFQGTPIGVSMONTRLAIASIGKLMFAQFSELVNDYFNN 432

Query: 456 GLPSCL-AAEDPSLNYHGKGLDIHIAAYASELGHLANPVTTTFVQPAEMGNQAVNSLALIS 514
 GLPS L +PSL+Y KG +I +A+Y SEL LANPVT VQ AE NQ VNSL LIS
 Sbjct: 433 GLPSNLTGGRNPSTLDYGFKAIEAMASYCSELQFLANPVTNHVQSAEQHNQDVNSLGLIS 492

Query: 515 ARRTAEANDVLSLLLASHLYCTLQAVDLRAMELDFKKQFDPLLPTLLQQHLGTGLDVNAL 574
 +R+TAEA D+L L+ + L QAVDLR +E + K + + ++ L G +
 Sbjct: 493 SRKTAEAVDILKLMSTTFLVGLCQAVDLRHIEENLKSTVKNTVSQVAKRVLTMGFNGE-- 550

Query: 575 ALEVKKALNKRLEQTTTYDLEPRWHDAFSYATGTVVE-----LLSSSPSANVTIT 624
 L + K L + + + D AT +++ L++ N T +
 Sbjct: 551 -LHPSRFCEKDLLKVVDRHVFYSYIDDPSCATYPLMQKLRQVLVEHALVNGERETNSTTS 609

Query: 625 AVNAWKVASAEKAIS--LTREVRN-RFWQTPSSQAPAHAYLSPRTRVLYSFVREELGVQA 681
 K+ S E+ + L +EV + R + A + R+ LY FVREELG
 Sbjct: 610 IFQ--KIGSFEEELKTLTPKEVESARLEVENGNPAPNRIKECRSYPLYKFVREELGT-- 665

Query: 682 RRGDVFGVGVQETIGSNVSRIYEAIKDGRINHVLVKML 719
 + G + ++ G +++ AI G++ L++ L
 Sbjct: 666 ---SLLTGEKVKSPGEEFDKVFATAICAGKLIDPLLECL 700

☐ >gi|39777534|gb|AAR31107.1| phenylalanine ammonia-lyase [Quercus suber]
 Length = 709

Score = 339 bits (869), Expect = 2e-91
 Identities = 239/695 (34%), Positives = 351/695 (50%), Gaps = 34/695 (4%)

Query: 40 GLDGHAHQSQLEIVQELSDPTDDVVELSGYSLTXXXXXXXXXXXXXXXXXQNDDEIRAR 99
 GL S L+ V+ ++ + +V+ G SLT + +E RA
 Sbjct: 23 GLAAEGLKGSHLDEVKRMVDEFKPLVKPGGKSLTIAQVAAIASQDGAIKVELAEERAG 82

Query: 100 VDKSVDFLKAQLQNSV--YGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPTSVSSFS 157
 V S D++ + YGVTTGFG ++ RT+ +LQ+ LI G+
 Sbjct: 83 VKASSDWVMGSMKDGKDSYGVTTGFGATSHRRTKQGGALQRELIRFLNAGI----- 133

Query: 158 VGRGLEN--TLPLEVVRGAMVIRVNSLTRGHSAVRLVVLEALTNFLNHRITPIVPLRSGI 215
 G G E+ TLP R AM++R+N+L +G+S +R ++EA+T FLNH ITP +PLRG+I
 Sbjct: 134 FGNGTESCHTLPHATRAAMLVRINTLLQGYSGIRFEIMEAITKFLNHNITPCLPLRGTI 193

Query: 216 SASGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEA--VVLGPKEGLG 273
 +ASGDL PLSYIAG +TG P+ K V G + A +A L G++ L PKEGL
 Sbjct: 194 TASGDLVPLSYIAGLLTGRPNKA-VGPNGES--LDATKAFELAGIDGGFFELQPEGLA 250

Query: 274 LVNGTAVSASMATXXXXXXXXXXXXXXXXXXVEAMVGQQGSFAPFIHVDVCRPHPGQVE 333
 LVNGTAV + +A+ E M G+ F + + HPGQ+E
 Sbjct: 251 LVNGTAVGSLASMLFEANVQAVFAEVLSAIFAEVMQKGP-EFTDHLTHKLKHHPGQIE 309

Query: 334 VARNIRTLLSGSSFAXXXXXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLS 393
 A + +L GS++ +QDRY LRTSPQ+LGP +E + A +
 Sbjct: 310 AAAIMEHILDGSAYIKAAQKLHEIDPLQKP-KQDRYALRTSPQWLGPQIEVIRTATKMIE 368

Query: 394 LENNTTTDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAM 453
 E N+ DNPL+DV + HGGNFQ + + +SM+ TRLA+A +GKL F Q ++L+N
 Sbjct: 369 REINSVDNPLIDVARNKALHGGNFQGTPIGVSMONTRLAIASVGKLMFAQFSKLVNDYY 428

Query: 454 NRGLPSCL-AAEDPSLNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVNSLAL 512
 N GLPS L A+ +PSL+Y KG +I +A+Y SEL LANPVT VQ AE NQ VNSL L
 Sbjct: 429 NNGLPSNLTASRNPSLDYGFKGAEIAMASYCSELQFLANPVTNHVQSAEQHNQDVNSLGL 488

Query: 513 ISARRTAEANDVLSLLLASHLYCTLQAVDLRAMELDFKKQFDPLLPTLLQQHLGTGLD-- 570
 IS+R+TAEA D+L L+ + L QAVDLR ME + K + + ++ L G +
 Sbjct: 489 ISSRKTAEAVDILKLMSTTFLVALCQAVDLRHMEENLKN TVKN TVSQVAKRVLTMGSNGE 548

Query: 571 ---VNALALEVKKALNKRLEQTTTYDLEPRWHDASFYATGTVVELLSSSPSANVTLTAVN 627
 ++ K +N+ D + +VE ++ L+
 Sbjct: 549 LHPSRFCEKDLLKVVNREYVFAYIDDPSCSATYPLMQKLRQVLVEHALNNGDKETNLSTSI 608

Query: 628 AWKVASAEKAIS--LTREVRNRFWQTPSSQAP-AHAYLSPRTRVLYSFVREELGVQARRG 684
 K+ + E+ + L +EV + + +A + R+ LY FVREELG
 Sbjct: 609 FQKIGAFEEELKTLLPKEVEGARIEIENGKAAIPNPIKECRSYPLYRFVREELGT----- 663

Query: 685 DVFGVGQQETIGSNVSRIYEAIKDGRINHVLVKML 719
 + G + + G +++ A+ G++ L+ L
 Sbjct: 664 SLLTGERIRSPGEEFDKVFSAACAGKLIDPLLDCL 698

☐ >gi|4808126|emb|CAB42793.1| phenylalanine-ammonia lyase [Citrus clementina x Cit
 Length = 721

Score = 338 bits (868), Expect = 3e-91

Identities = 240/688 (34%), Positives = 351/688 (51%), Gaps = 37/688 (5%)

Query: 49 SQLEIVQELLSIPTDDVVELSGYSLTXXXXXXXXXXXXXXXXXXXX---QNDDEIRARVDKSVD 105
 S LE V+ ++++ VV L G +LT + + R V S D
 Sbjct: 43 SHLEEVKRMVAEYRKPVVNLGGETLTVAQVAAIATAGDVNAQVKVELSESAREGVKASSD 102

Query: 106 FLKAQLQNSV--YGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPTSVSSFSVGRGLE 163
 ++ + YGVTTGFG ++ RT++ +LQK LI+ G+ F G
 Sbjct: 103 WVMDSMNKGTDSYGVTTGFGATSHRRTQNGGALQKELIKFLNAGI-----FGNGTKSS 155

Query: 164 NTLPLEVVRGAMVIRVNSLTRGHSVRLVLEALTNFLNHRITPIVPLRGSISASGDLSP 223
 +TLP R AM++RVN+L +G+S +R +L+A+T LNH ITP +PLRG+I+ASGDL P
 Sbjct: 156 HTLPHSATRAAMLVRVNTLLQGYSGIRFEILDITKLLNHSITPCLPLRGITITASGDLVP 215

Query: 224 LSYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEAVVLGPKEGLGLVNGTAVSAS 283
 LSYIAG +TG P+ K +I+ A+EA G L PKEGL LVNGTAV +
 Sbjct: 216 LSYIAGLLTGRPNKAT---GPNGEIIDAQEASKQAGFGFFELQPKEGLALVNGTAVGSG 272

Query: 284 MATXXXXXXXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQVEVARNIRTLLS 343
 +A+ E M G+ F + + HPGQ+E A + +L
 Sbjct: 273 LASMVLFDANNLALLSEILSAIFAEVMQGKP-EFTDHLTHKLKHHPGQIEAAAIMEHILD 331

Query: 344 GSSFAXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTDNP 403
 GSS+ +QDRY LRTSPQ+LGP +E + A ++ E N+ DNP
 Sbjct: 332 GSSYVKAACKLHEIDPLQKP-KQDRYALRTSPQWLGPQIEVIRFATKSIEREINSVNDNP 390

Query: 404 LLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCLA- 462
 L+DV + HGGNFQ + + +SM+ TRLA+A IGKL F Q +EL+N N GLPS L+
 Sbjct: 391 LIDVSRNKALHGGNFQGTPIGVSMNTRLAIAAIGKLMFAQFSELVNDFYNNGLPSNLG 450

Query: 463 AEDPSLNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVNSLALISARRTAEAN 522
 +PSL+Y KG +I +A+Y SEL LANPVT VQ AE NQ VNSL LIS+R+TAEA
 Sbjct: 451 GRNPSLDYGFKGAEIAMASYCSELQFLANPVTNHVQSAEQHNQDVNSLGLISSRKTAEA 510

Query: 523 DVLSLLLASHLYCTLQAVDLRAMELDFKKQFDPDLLPTLLQQHLGTGLD-----VNALALE 577
D+L L+ ++ L QA+DLR +E + K + + ++ L G + +
Sbjct: 511 DILKLMSSSTFLVALCQAIDLRHLEENLKHTVKDTVSVQVARKVLTVGANGELHPSRFCEKD 570

Query: 578 VKKALNKRLEQTTTYDLEP--RWHDAFSYATGTVVELLSSSPSANVTLTAVNAWKVASAE 635
+ KA ++ E Y +P + +VE ++ + K+A+ E
Sbjct: 571 LLKAADR--EHVFAYIDDPSCSATYPLMQKLRQVLVEHALNNGENEKNANSSIFQKIAAFE 628

Query: 636 KAIS--LTREVRNRFWQTPSSQAPA--HAYLSPRTRVLYSFVREELGVQARRGDVFGVQ 691
+ + L +EV N QT + P + R+ LY VREELG + G +
Sbjct: 629 EELKAVLPKEVENA-RQTVENGNTIPNRIKECRSYPLYRLVREELGT-----NFLTGEK 682

Query: 692 QETIGSNVSRIYEAIKDGRINHVLVKML 719
+ G +++ A+ G+I +++ L
Sbjct: 683 VTSPGEKFDKVFTAMCQGKIIDPMLECL 710

☐ >gi|14486430|gb|AAK62030.1| phenylalanine ammonia-lyase 1 [Manihot esculenta]
Length = 710

Score = 338 bits (868), Expect = 3e-91
Identities = 242/714 (33%), Positives = 361/714 (50%), Gaps = 41/714 (5%)

Query: 22 AAPTKSAAGPTSALRRTPGLDGHAHQSQLEIVQELLSDPTDDVVELSGYSLTXXXXXXX 81
A+P S+A P + G+ + S L+ V+ ++ + VV L G +LT
Sbjct: 11 ASPGFSSADPLNW-----GMAAESLKGSHLDEVKRMVDEYRKPVVRLGGETLTIAQVTAI 65

Query: 82 XXXXXXXXXXXQNDDEIRARVDKSVDFLKAQLQNSV--YGVTTGFGGSADTRTEDAVSLQKA 139
+ +E RA V S D++ + YGVTTGFG ++ RT+ +LQ+
Sbjct: 66 ANHDSGVKVELSEEARAGVKASSDWLDSMNKGTDSYGVTTGFGATSHRRTKQGGALQRE 125

Query: 140 LIEHQLCGVTPTSVSSFSVGRGLENLPLEVVIRGAMVIRVNSLTRGHSAVRLVVLEALTN 199
LI G+ F G+ +TL R AM++R+N+L +G+S +R +LEA+T
Sbjct: 126 LIRFLNAGI-----FGNGQESCHTSLHTATRAAMLVRINTLLQGYSGIRFEILEAITK 178

Query: 200 FLNHRITPIVPLRGSISASGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLF 259
F+N+ +TP +PLRG+I+ASGDL PLSYIAG +TG P+ K L E + A EA L
Sbjct: 179 FINNVNTPRLPLRGTTITASGDLVPLSYIAGLLTGRPNKSKS--LGPNGESLD-AAEAFKLA 235

Query: 260 GLEA--VVLGPKEGLGLVNGTAVSASMATXXXXXXXXXXXXXXXXXXXXVEAMVGQQGSF 317
G+ L PKEGL LVNGTAV + +A+ E M+G+ F
Sbjct: 236 GINGGFFELQPKEGLALVNGTAVGSGGLASMLFEANVLAVLSEVLSAIFAEVMLGKP-EF 294

Query: 318 APFIHDVCRPHPGQVEVARNIRTLLSGSSFAXXXXXXXXXXXXXXGILRQDRYPLRTSPQF 377
+ + HPGQ+E A + +L GSS+ +QDRY LRTSPQ+
Sbjct: 295 TDHLTHKLKHHPGQIEAAAIMHVLDGSSYIKAAQKVHEIDPLQKP-KQDRYALRTSPQW 353

Query: 378 LGPLVEDMMHAYSTLSLENNTTTDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALI 437
LGP +E + A + E N+ DNPL+DV HGGNFQ + + +SM+ TRLA+A I
Sbjct: 354 LGPQIEVIRTATKMIEREINSVNDNPLIDVSRNIALHGGNFQGTPIGVSMNDTRLAIASI 413

Query: 438 GKLNFTQCTELLNAAMNRGLPSCL-AAEDPSLNYHGKGLDIHIAAYASELGHLANPVTTF 496
GKL F Q +EL+N N GLPS L +PSL+Y KG +I +A+Y SEL LANPVT
Sbjct: 414 GKLMFAQFSELVNDFYNNGLPSNLTGGRNPISLDYGFKAELIAMASYCSELQFLANPVTNH 473

Query: 497 VQPAEMGNQAVNSLALISARRTAEANDVLSLLLASHLYCTLQAVDLRAMELDFKKQFDPL 556
VQ AE NQ VNSL LIS+R+TAEA D+L L+ +++L QA+DLR +E + K+
Sbjct: 474 VQSAEQHNQDVNSLGLISSRKTAEAVDILKLMSSSTYLVALCQAIDLRHLEENLKQTVKNT 533

Query: 557 LPTLLQQHLGTGLDVNALALEVKKALNKRLEQTTTYDLEPRWHDAFSYATGTVVE----- 611
 + + ++ L G++ L + K L + + + D AT +++
 Sbjct: 534 VSQVAKRVLTMGINGE---LHPSRFCEKDLLKVVDREYVYAYVDDPCSATYPLMQKLRQV 590

Query: 612 -----LLSSSPSANVTLTAVNAWKVASAEKAISLTREVRN-RFWQTPSSQAPAHAYLSPR 665
 +++ N + + E L +EV + R + A ++ R
 Sbjct: 591 LVDHAMMNGEKEKNSSTSIFQKIGAFEEELKTLLPKEVESARTEYENGNPAINKIKI ECR 650

Query: 666 TRVLYSFVREELGVQARRGDVFGVGVQQTIGSNVSRIYEAIKDGRINHVLVKML 719
 + LY FVREELG + G + + G +++ AI G++ +++ L
 Sbjct: 651 SYPLYK FVREELGC-----SLLTGEKIRSPGEEFDKVFSAICAGKLIDPML ECL 699

☐ >gi|129594|sp|P25872|PAL1_TOBAC Phenylalanine ammonia-lyase
 gi|2564057|dbj|BAA22948.1| phenylalanine ammonia-lyase [Nicotiana tabacum]
 gi|170350|gb|AAA34122.1| phenylalanine ammonia lyase
 Length = 715

Score = 338 bits (868), Expect = 3e-91

Identities = 250/727 (34%), Positives = 366/727 (50%), Gaps = 45/727 (6%)

Query: 13 ANGFTNGSHAAPT-KSAAGPTSALRRTPGLDGHAHQSQLEIVQELLSDPTDDVVELSGY 71
 +NG NG K +A P + L G S L+ V++++S+ +V+L G
 Sbjct: 3 SNGHVNGGENFELCKKSADPLNWEMAAESLRG-----SHLDEVKKMVSEFRKPMVKLGGE 57

Query: 72 SLTXXXXXXXXXXXXXXXXX---QNDDEIRARVDKSVDFLKAQLQNSV--YGVTTGFGGSA 126
 SLT + +E RA V S D++ + YGVTTGFG ++
 Sbjct: 58 SLTVAQVAIAVRDKSANGVKVELSEEARAGVKASSDWVMDSMNKGTD SYGVTTGFGATS 117

Query: 127 DTRTEDAVSLQKALIEHQLCGVTPTSVSSFSVGRGLENLTPLEVVRGAMVIRVNSLTRGH 186
 RT++ +LQK LI GV F G +TLP R AM++R+N+L +G+
 Sbjct: 118 HRRTKNGGALQKELIRFLNAGV-----FGNGTETSHLPHSATRAAMLVRINTLLQGY 170

Query: 187 SAVRLVVLEALTNFLNHRITPIVPLRGSISASGDLSPLSYIAGAITGHPDVKVHVLHEGT 246
 S +R +LEA+T +N ITP +PLRG+I+ASGDL PLSYIAG +TG P+ K + T
 Sbjct: 171 SGIRFEILEAITKLINSNITPCLPLRGITITASGDLVPLSYIAGLLTGRPNKAVGPNGET 230

Query: 247 EKIMFAEAISLFGLEA--VVLGPKEGLGLVNGTAVSASMATXXXXXXXXXXXXXXXXXXXX 304
 + A EA + G+ L PKEGL LVNGTAV + MA+
 Sbjct: 231 ---LNAEEAFRVAGVNGGFFELQPK EGLALVNGTAVGSGMASMVLFD SNILAVMSEVLSA 287

Query: 305 XXVEAMVGQQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGSSSFAXXXXXXXXXXXXXXXXXX 364
 E M G+ F + + HPGQ+E A + +L GSS+
 Sbjct: 288 IFAEVMNGKP-EFTDHLTHKLKHHPGQIEAAAIMEHILDGSSYVKAQKLHEMDPLQKP- 345

Query: 365 RQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTNDNPLLDVENKQTAHGGNFQASAVS 424
 +QDRY LRTSPQ+LGP +E + A + E N+ DNPL+DV + HGGNFQ + +
 Sbjct: 346 KQDRYALRTSPQWLGPQIEVIRAATKMIEREINSVNDNPLIDVSRNKALHGGNFQGTPIG 405

Query: 425 ISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCL-AAEDPSLNYHGKGLDIHIAAYA 483
 +SM+ RLALA IGKL F Q +EL+N N GLPS L A+ +PSL+Y KG +I +A+Y
 Sbjct: 406 VSMDNARLALASIGKLMFAQFSELVNDYYNGLPSNLTA SRNP SLDYGFKA EIAMASYC 465

Query: 484 SELGHLANPVTTTFVQPAEMGNQAVNSLALISARRTAEANDVLSLLLASHLYCTLQAVDLR 543
 SEL LANPVT VQ AE NQ VNSL LISAR+TAEA D+L L+ +++L QA+DLR
 Sbjct: 466 SELQFLANPVTNHVQSAEQHNQDVNSLGLISARKTAEAVDILKLMSSTYLVALCQAIDLR 525

Query: 544 AMELDFKKQFDPLLP TLLQQHLGTGLDVNALALEVKKALNKRLE-----EQTTTYDLEPR 597

+E + K + + ++ L G + L + K L E Y +P
 Sbjct: 526 HLEENLKNVAVKNTVSQVAKRTLTMGANGE---LHPARFCEKELLRIVDREYLFAYADDPC 582
 Query: 598 W--HDAFSYATGTVVELLSSSPSANVTLTAVNAWKVASAEKAIS--LTREVRN-RFWQTP 652
 + +V+ ++ + + + K+ + E + L +EV + R
 Sbjct: 583 SCNYPLMQKLRQVLVDHAMNGESEKNVNSSIFQKIGAFEDLKAVLPKEVESARAALES 642
 Query: 653 SSQAPAHAYLSPRTRVLYSFVREELGVQARRGDVFGVQQETIGSNVSRIYEAIKDGRIN 712
 + A + R+ LY FVR+ELG ++ G + + G +++ A+ +G+I
 Sbjct: 643 GNPAIPNRITECRSYPLYRFVRKELGT-----ELLTGEKVRSPGEECDKVFTAMCNGQII 697
 Query: 713 HVLVKML 719
 +++ L
 Sbjct: 698 DPMLECL 704

☐ >gi|417444|sp|Q04593|PAL2_PEA Phenylalanine ammonia-lyase 2
 gi|217984|dbj|BAA00887.1| phenylalanine ammonia-lyase [Pisum sativum]
 Length = 724

Score = 338 bits (868), Expect = 3e-91
 Identities = 238/696 (34%), Positives = 354/696 (50%), Gaps = 37/696 (5%)

Query: 40 GLDGHAHQSQLEIVQELLSDPTDDVVELSGYSLTXXXXXXXXXXXXXXXXXQNDDEIRAR 99
 G+ A S L+ V+ ++ + VV L G +LT + + RA
 Sbjct: 39 GVAAEAMKGSHLDEVKRMVDEYRKPVRLGGETLTISQVAAIAAHDHGVKVELSESARAG 98
 Query: 100 VDKSVDFLKAQLQNSV--YGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPTSVSSFS 157
 V S D++ + YGVTT G ++ RT+ +LQK LI G+ F
 Sbjct: 99 VKASSDWVMESMNKGTDSYGVTTVHGATSHRRTKQGGALQKELIRFLNAGI-----FG 151
 Query: 158 VGRGLENLPLEVVIRGAMVIRVNSLTRGHSVRLVLEALTNFLNHRITPIVPLRGSISA 217
 G +TLP R AM++R+N+L +G+S +R +LEA+T +N+ +TP + LRG+I+A
 Sbjct: 152 NGSESTHTLPHATRAAMLVRINTLLQGYSGIRFEILEAITKLINNNVTPCL-LRGTITA 210
 Query: 218 SGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEA--VVLGPKEGLGLV 275
 SGDL PLSYIAG +TG P+ K H + +I+ AREA G+ L PKEGL LV
 Sbjct: 211 SGDLVPLSYIAGLLTGRPNKAH---GPSGEILNAREAFQSAGINDGFFELQPKEGLALV 267
 Query: 276 NGTAVSASMATXXXXXXXXXXXXXXXXXXVEAMVGQQGSFAPFIHDVCRPHPGQVEVA 335
 NGTAV + +A+ E M G+ F + + HPGQ+E A
 Sbjct: 268 NGTAVGSLASIVLFEANILAVLSEVLSAIFAEMVQKGP-EFTDHLTHKLKHHPGQIEAA 326
 Query: 336 RNIRTLGSSSFAXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLE 395
 + +L GS++ +QDRY LRTSPQ+LGPL+E + + ++ E
 Sbjct: 327 AIMEHILDGSAYVKAACKLHEMDPLQKP-KQDRYALRTSPQWLGPLIEVIRFSTKSIERE 385
 Query: 396 NNTTTDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNR 455
 N+ DNPL+DV + HGGNFQ + + +SM+ TRLALA IGKL F Q +EL+N N
 Sbjct: 386 INSVDNPLIDVSRNKALHGGNFQGTPIGVSMNTRLALASIGKLLFAQFSELVNDFFYNN 445
 Query: 456 GLPSCL-AAEDPSLNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVNSLALIS 514
 GLPS L A+ +PSL+Y KG +I +A+Y SEL +LANPVTTF VQ AE NQ VNSL LIS
 Sbjct: 446 GLPSNLSASRNPSLDYGFKGSEIAMASYCSELQYLANPVTTHVQSAEQHNQDVNSLGLIS 505
 Query: 515 ARRTAEANDVLSLLLASHLYCTLQAVDLRAMELDFKKQFDPLLPTLLQQHLGTGLDVNAL 574
 +R+T EA ++L L+ ++ L QA+DLR +E + K ++ + ++ L TG++
 Sbjct: 506 SRKTYEAIEILQLMSSTFLIALCQAIDLRHLEENLKNVKNMVSHVAKRTLTTGINGE-- 563

Query: 575 ALEVKKALNKRLEQTTTYDLEPRWHDFAFSYATGTVVE-----LLSSSPSANVTLT 624
 L + K L + + + D AT +++ L++ N+ +
 Sbjct: 564 -LHPSRFCEKDLLRVVDREHVFSYIDDPSCATYPLMQKLRQVLVDHALVNGESEKLNLS 622

Query: 625 AVNAWKVASAEKAISLTREVRN-RFWQTPSSQAPAHAYLSRPRTRVLYSFVREELGVQARR 683
 E L +EV + R + ++ R+ LY FVREELG
 Sbjct: 623 IFQKIATFEDELKTLPLKEVESARGAYENGNTTISNKIKECRSYPLYKFVREELGTSLLT 682

Query: 684 GDVFGVQQETIGSNVSRIYEAIKDGRINHVLVKML 719
 G+ + + G +++ AI G+I L++ L
 Sbjct: 683 GEKVI-----SPGEECDKLFTAICQGKIIDPLECL 713

☐ >gi|50926490|ref|XP_473192.1| ☒ OSJNBa0073E02.14 [Oryza sativa (japonica cultivar-gr)]
 gi|32487851|emb|CAE05619.1| ☒ OSJNBb0061C13.1 [Oryza sativa (japonica cultivar-gr)]
 gi|38568065|emb|CAE05454.3| ☒ OSJNBa0073E02.14 [Oryza sativa (japonica cultivar-gr)]
 Length = 707

Score = 338 bits (867), Expect = 3e-91

Identities = 243/690 (35%), Positives = 371/690 (53%), Gaps = 41/690 (5%)

Query: 49 SQLEIVQELLSDPTDDVVELSGYSLTXXXXXXXXXXXXXXXXXX--QNDDEIRARVDKSVDF 106
 S L+ V+ +++ + VV++ G SL + D+E R RV S ++
 Sbjct: 29 SHLDEVKRMVAQSREAVVKIEGSSLRVGQVAASAAKDASGVVVELDEEARPRVKASSEW 88

Query: 107 LKAQLQNS--VYGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPTSVSSFSVGRGLE- 163
 + + + +YGVTTGFGG++ RT+D +LQ L+ H G+ G G +
 Sbjct: 89 ILNCIAHGGDIYGVTTGFGGTSRRRTKDGQALQVELLRHLNAGI-----FGNGSDG 139

Query: 164 NTLPLEVVRGAMVIRVNSLTRGHSVRLVVLEALTNFLNHRITPIVPLRGSISASGDLSP 223
 N+LP EV R AM++R+N+L +G+S +R +LEA+T +N ++P +PLRG+I+ASGDL P
 Sbjct: 140 NSLPSEVSRAAMLVRINTLLQGYSGIRFEILEAITKLINTGVSPCLPLRGITITASGDLVP 199

Query: 224 LSYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEAVV--LGPKEGLGLVNGTAVS 281
 LSYIAG ITG P+ + V +G K + A EA + G++ L PKEGL +VNGT+V
 Sbjct: 200 LSYIAGLITGRPNAQA-VTVDG--KKVDAAEAFKIAGIQGGFFRLEPKEGLAIVNGTSVG 256

Query: 282 ASMATXXXXXXXXXXXXXXXXXXXXXVEAMVGQQGSFAPFIHDVCRPHPGQVEVARNIRTL 341
 +++A E M G+ H + + HPG +E A + +
 Sbjct: 257 SALAAMVLYDANVLAVLSEVLSAVFCEVMNGKPEYTDHLTHKL-KHHPGSIEAAAIMEHI 315

Query: 342 LSGSSFAXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTDD 401
 L+GS+F +QDRY LRTSPQ+LGP +E + A ++ E N+ D
 Sbjct: 316 LAGSAFMPHAQKVNEVDPLLKP-KQDRYALRTSPQWLGPQIEVIRAATKSIEREVNSVND 374

Query: 402 NPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCL 461
 NP++DV + HGGNFQ + + +SM+ TRLA+A IGKL F Q +EL+N N GL S L
 Sbjct: 375 NPVIDVHRGKALHGGNFQGTPIGVSMNTRLAIANIGKLMFAQFSELVNEFYNNGLTSNL 434

Query: 462 A-AEDPSLNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVNSLALISARRTAE 520
 A + +PSL+Y KG +I +A+Y SEL LANPVT VQ AE NQ VNSL L+SAR+TAE
 Sbjct: 435 AGSRNPSLDYGFKGTEIAMASYCSELQFLANPVTNHVQSAEQHNQDVNSLGLVSAKRTAE 494

Query: 521 ANDVLSLLLASHLYCTLQAVDLRAMELDFKKQFDPLLPDLLQQLHGTGLDVNAL--ALEV 578
 A D+L L+ +++L QAVDLR +E + K + T+ ++ L TG L A
 Sbjct: 495 AVDILKLMSSTYLVALCQAVDLRHLLENLKSARKNCVTTVAKKVLTTG-PAGGLHSARFS 553

Query: 579 KKALNKRLEQTTTYDLEPRWHDFAFSYATGT-----VVELLSSSPSANVTLTAVNAWKVA 632

+KAL +++ Y A +Y T V L++ P+ ++V + K+

Sbjct: 554 EKALLTAIDREAVYSYADDPCSA-NYPLMTKIRAVLVEHALANGPAEKDDGSSVFS-KIT 611

Query: 633 SAEKAI--SLTREVRNRFWQTPSSQAP-AHAYLSPRTRVLYSFVREELGVQARRGDVFG 689

+ E+ + +L RE+ + AP + R+ LY FVREELG G

Sbjct: 612 AFEEELREALPREMEAARVAFETGTAPITNRIKESRSFPLYRFVREELGCV-----YLTG 666

Query: 690 VQQETIGSNVSRIYEAIKDGRINHVLVKML 719

+ ++ G ++++ AI + ++ +++ L

Sbjct: 667 EKLKSPGEECNKVFLAISERKLIDPMLECL 696

☐ >gi|738926|prf||2001451A Phe ammonia lyase
Length = 723

Score = 337 bits (865), Expect = 6e-91
Identities = 239/697 (34%), Positives = 354/697 (50%), Gaps = 39/697 (5%)

Query: 40 GLDGHAHQSQLEIVQELSDPTDDVVELSGYSLTXXXXXXXXXXXXXXXXXQNDDEIRAR 99

G+ A S L+ V+ ++ + VV L G +LT + + RA

Sbjct: 38 GVAAEAMKGSHLDEVKRMVEEYRKPVVRLGGETLTISQVAAIAAHDHGVKVELSESARAG 97

Query: 100 VDKSVDFLKAQLQNSV--YGVTTFGFGSADTRTEDAVSLQKALIEHQLCGVTPTSVSSFS 157

V S D++ + YGVTTFGFG ++ RT+ +LQK LI G+ F

Sbjct: 98 VKASSDWVMESMNKGTDSYGVTTGFGATSHRRTKQGGALQKELIRFLNAGI-----FG 150

Query: 158 VGRGLENLPLEVVRGAMVIRVNSLTRGHSVRLVLEALTNFLNHRITPIVPLRGSISA 217

G +TLP R AM++R+N+L +G+S +R +LEA+T +N+ +TP + LRG+I+A

Sbjct: 151 NGTESSHTLPHTATRAAMLVRINTLLQGYSGIRFEILEAITKLINNNVTPCL-LRGTITA 209

Query: 218 SGDLSPLSYIAGAITGHPDVKVHVLHEGTE-KIMFAREAISLFGLEA--VVLGPKEGLGL 274

SGDL PLSYIAG +TG P+ K H GT +I+ A+EA + L PKEGL L

Sbjct: 210 SGDLVPLSYIAGLLTGRPNKAH----GTSGEILNAKEAFQSAEINDGFFELQPKEGLAL 265

Query: 275 VNGTAVSASMATXXXXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQVEV 334

VNGTAV + +A+ E G+ F + + HPGQ+E

Sbjct: 266 VNGTAVGSGLASIVLFEANILAVLSEVLSAIFAEVHQGP-EFTDHLTHKLKHHPGQIEA 324

Query: 335 ARNIRTLLSGSSFAXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSL 394

A + +L GS++ +QDRY LRTSPQ+LGPL+E + + ++

Sbjct: 325 AAIMEHILDGSAYVKAACKLHEMDPLQKP-KQDRYALRTSPQWLGPLIEVIRFSTKSIER 383

Query: 395 ENNTTTDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMN 454

E N+ DNPL+DV + HGGNFQ + + +SM+ TRLALA IGKL F Q +EL+N N

Sbjct: 384 EINSVNDNPLIDVSRNKALHGGNFQGTPIGVSMNTRLALASIGKLLFAQFSELVNDNFYN 443

Query: 455 RGLPSC-LAEDPSLNYHGKGLDIHIAAYASELGHLANPVTTTFVQPAEMGNQAVNSLALI 513

GLPS L A+ +PSL+Y KG +I +A+Y SEL +LANPVTT VQ AE NQ VNSL LI

Sbjct: 444 NGLPSNLSASRNPSLDYGFKGSEIAMASYCSELQYLANPVTTTHVQSAEQHNQDVNSLGLI 503

Query: 514 SARRTAEANDVLSLLLASHLYCTLQAVDLRAMELDFKKQFDPLLPTLLQQHLGTGLDVNA 573

S+R+T EA ++L L+ ++ L QAVDLR +E + K ++ + ++ L TG++

Sbjct: 504 SSRKTYEAIEILQLMSSTFLIALCQAVDLRHLEENLKNVKNIVSQVAKRTLTTGVNGE- 562

Query: 574 LALEVKKALNKRLEQTTTYDLEPRWDAFSYATGTVE-----LLSSSPSANVTL 623

L + K L + + + D AT +++ L++ N+

Sbjct: 563 --LHPSRFCEKDLLRVVDREHVFAYIDDPCSATYPLMQKLRQVLVDHALVNGESEKNLNT 620

Query: 624 TAVNAWKVASAEKAIISLTREVRN-RFWQTPSSQAPAHAYLSPRTRVLYSFVREELGVQAR 682

+ E L +EV + R + + R+ LY FVR+ELG
 Sbjct: 621 SIFQKIATFEDELKTLKPKEVESTRAAYESGNPTVPNKINGCRSYPLYRFVRQELGTGLL 680
 Query: 683 RGDVFGVGVQQETIGSNVSRIYEAIKDGRINHLVKML 719
 G+ + + G +++ AI G+I L++ L
 Sbjct: 681 TGEKVI-----SPGEECDKLFTAICQGKIIDPLLQCL 712

>gi|27436243|gb|AA013347.1| phenylalanine ammonia-lyase2; PAL [Lactuca sativa]
 Length = 713

Score = 337 bits (864), Expect = 8e-91
 Identities = 237/687 (34%), Positives = 352/687 (51%), Gaps = 36/687 (5%)

Query: 40 GLDGHAHQSQLEIVQELLSDPD VVELSGYSLTXXXXXXXXXXXXXXXXX-QNDDEIRA 98
 G+ + S L+ V+ +++ VV L G +LT + + RA
 Sbjct: 29 GMAAESLKGSHLDEVKRMVAEFRKPVVRLGGETLTVSQVAAIAASDNAGVKVELSETARA 88
 Query: 99 RVDKSVDFLKAQLQNSV--YGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPTSVSSF 156
 V S D++ + YGVTTGFG ++ RT++ +LQK LI G+ F
 Sbjct: 89 GVKASSDWMESMNKGTDSYGVTTGFGATSHRRTKEGGALQKELIRFLNAGI-----F 141
 Query: 157 SVGRGLENTLPLEVVRGAMVIRVNSLTRGHSVRLVLEALTNFLNHRITPIVPLRGSIS 216
 G +TLP R AM++R+N+L +G+S +R +LEA+T FLNH +TP +PLRG+I+
 Sbjct: 142 GNGTESTHTLPHSATRAAMLVRINTLLQGYSGIRFEILEAITKFLNHNVTPLPLRGIT 201
 Query: 217 ASGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEA--VVLGPKEGLGL 274
 ASGDL PLSYIAG +TG + K T +++ A +A + G+E L PKEGL L
 Sbjct: 202 ASGDLVPLSYIAGLLTGRANSKAV---GPTGEVLNAEKAFAGVEGGFFELQKEGLAL 258
 Query: 275 VNGTAVSASMATXXXXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQVEV 334
 VNGTAV + MA+ E M G+ F + + HPGQ+E
 Sbjct: 259 VNGTAVGSGMASMVLFDANVLALLSEVLSAIFAEVMQGKP-EFTDHLTHKLKHHPGQIEA 317
 Query: 335 ARNIRTLGSSSFAXXXXXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSL 394
 A + +L GS + +QDRY LRTSPQ+LGP +E + + +
 Sbjct: 318 AAIMEYILDGSDYVKAQKVHEMDPLQKP-KQDRYALRTSPQWLGPQIEVIRSSTKMIE 376
 Query: 395 ENNTTTDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMN 454
 E N+ DNPL+DV + HGGNFQ + + +SM+ TRLA+A IGKL F Q +EL+N N
 Sbjct: 377 EINSVNDNPLIDVSRNKALHGGNFQGTPIGVSMNTRLAIAAIGKLMFAQFSELVNDNFYN 436
 Query: 455 RGLPSCLA-AEDPSLNHYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVNSLALI 513
 GLPS L+ +PSL+Y KG +I +A+Y SEL LANPVT VQ AE NQ VNSL LI
 Sbjct: 437 NGLPSNLSGGRNPGLDYGFKGAEIAMASYCSELQFLANPVTNHVQSAEQHNQDVNSLGLI 496
 Query: 514 SARRTAEANDVLSLLLASHLYCTLQAVDLRAMELDFKKQFDPLLPTLLQQHLGTGLDVNA 573
 SAR+TAE+ ++L L+ ++L Q++DLR +E + K + + ++ L TG++
 Sbjct: 497 SARKTAESVEILKLMSTTYLVALCQSIDLRHLEENLKSTVKNTVSLVAKKILTGTGVNGE- 555
 Query: 574 LALEVKKALNKRLEQTTTYDLEPRWDAFSYATGTVVELL-----SSSPSANVTLTAVN 627
 L + K L + + + D AT +++ L + + N T++
 Sbjct: 556 --LHPSRFCEKDLLRVVDREYVFAYIDDACSATYPLMQKLRQVIVDHALNNENDAGTSI- 612
 Query: 628 AWKVASAEKAIS--LTREVRN-RFQWTPSSQAPAHAYLSPRTRVLYSFVREELGVQARRG 684
 K++ E+ + L +EV R S+ + R+ LY FVREELG
 Sbjct: 613 FQKISEFEEELKAVLPKEVEGVRSAYESSTLTIPNRIKECRSYPLYRFVREELGT----- 667
 Query: 685 DVFGVGVQQETIGSNVSRIYEAIKDGRI 711

G + + G +++ A+ G I
 Sbjct: 668 GFLTGEVETSPGEEFDKVF TALCKGHI 694

>gi|3334285|sp|O23865|PAL1_DAUCA Phenylalanine ammonia-lyase 1
 gi|2618590|dbj|BAA23367.1| phenylalanine ammonia-lyase [Daucus carota]
 Length = 708

Score = 337 bits (864), Expect = 8e-91
 Identities = 238/693 (34%), Positives = 346/693 (49%), Gaps = 32/693 (4%)

Query: 40 GLDGHAHQSQLEIVQELLSDPTDDVVELSGYSLTXXXXXXXXXXXXXXXXXQNDDEIRAR 99
 G+ A S L+ V+ +++ +V+L G +LT + RA
 Sbjct: 24 GMAAEALTGSHLDEVKRMVAEFRKPMVQLGGETLTVSQVAAIAAGSVKVELA--ESARAG 81

Query: 100 VDKSVDFLKAQLQNSV--YGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPTSVSSFS 157
 V S D++ + YGVTTGFG ++ RT+ +LQK LI G+ F
 Sbjct: 82 VKASSDWVMESMNKGTDSYGVTTGFGATSHRRTKQGGALQKELIRFLNAGI-----FG 134

Query: 158 VGRGLENTLPLEVVRGAMVIRVNSLTRGHSVRLVLEALTNFLNHRITPIVPLRGSISA 217
 G N LP R AM++R+N+L +G+S +R +LEA+T FLN ITP +PLRG+I+A
 Sbjct: 135 SGNDSSNILPHSATRAAMLVRINTLLQGYSGIRFEILEAITKFLNQITPCLPLRGITITA 194

Query: 218 SGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEA--VVLGPKEGLGLV 275
 SGDL PLSYIAG +TG P+ K T + + A EA L G++ L PKEGL LV
 Sbjct: 195 SGDLVPLSYIAGLLTGRPNKAV---GPTGENLTAAEAFKLAGVDGGFFELQPKEGLALV 251

Query: 276 NGTAVSASMATXXXXXXXXXXXXXXXXXXVEAMVGQQGSFAPFIHDVCRPHPGQVEVA 335
 NGTAV + MA+ E M G+ F + + HPGQ+E A
 Sbjct: 252 NGTAVSGMASMVLFTETNILAVLAEVMSAIFAEVMQKGP-EFTDHLTHKLKHHPGQIEAA 310

Query: 336 RNIRTLTSGSSFAXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLE 395
 + +L GSS+ +QDRY LRTSPQ+LGP +E + + + E
 Sbjct: 311 AIMEHILDGSSYVKAEEKQHEMDPLQKP-KQDRYALRTSPQWLGPQIEVIRSSTKMIERE 369

Query: 396 NNTTTDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNR 455
 N+ DNPL+DV + HGGNFQ + + +SM+ TRLA+A IGKL F Q +EL+N N
 Sbjct: 370 INSVDNPLIDVSRNKAIHGGNFQGTPIGVSMONTRLAIAAIGKLMFAQFSELVNDFYNN 429

Query: 456 GLPSCLA-AEDPSLNYHGKGLDIIHIAAYASELGHLANPVTTFVQPAEMGNQAVNSLALIS 514
 GLPS L+ +PSL+Y KG +I +A+Y SEL L NPVT VQ AE NQ VNSL LIS
 Sbjct: 430 GLPSNLSGGRNP SLDYGFKGAEIAMASYCSELQFLGNPVTNHVQSAEQHNQDVNSLGLIS 489

Query: 515 ARRTAEANDVLSLLASHLYCTLQAVDLRAMELDFKKQFDPLLPTLLQQHLGTGLD---- 570
 +R+TAEA ++L L+ + L QAVDLR +E + K + + ++ L G++
 Sbjct: 490 SRKTAEAVEILKLMSTTFLVGLCQAVDLRHLEENLKSTVKNTVSQVAKKVLTMGVNGELH 549

Query: 571 -VNALALEVKKALNKRLEQTTTYDLEPRWHDFAFSYATGTVVVELLSSSPSANVTLTAVNAW 629
 L++ + +++ D + +VE + L+
 Sbjct: 550 PSRFCELDLLRVVDREYIFAYIDDP SATYPLMQKLRQVLVEHALKNGETEKNLSTSIFQ 609

Query: 630 KVASAEKAIS--LTREVRN-RFWQTPSSQAPAHAYLSRTRVLYSFVREELGVQARRGDV 686
 K+A+ E + L +EV + R + A + R+ LY F+REELG
 Sbjct: 610 KIAAFEDELKALLPKEVESARAVVESGNPAIPNRIKECRSYPLYKFIREELGTV-----Y 664

Query: 687 FVG VQQETIGSNVSRIYEAIKDGRINHVLVKML 719
 G + + G +++ A+ G I L+ L
 Sbjct: 665 LTGEKVTSPGEEFDKVF TAMSKGEIIDPLLACL 697

☐ >gi|24266658|gb|AAN52280.1| phenylalanine ammonia-lyase [Populus tremuloides]
Length = 711

Score = 337 bits (863), Expect = 1e-90

Identities = 243/693 (35%), Positives = 348/693 (50%), Gaps = 30/693 (4%)

Query: 40 GLDGHAHQSQLEIVQELLSDPTDDVVELSGYSLTXXXXXXXXXXXXXXXXXQNDDEIRAR 99
G+ + S L+ V+ ++ + VV+L G +LT + +E R
Sbjct: 25 GMAAESLKGSHLDEVKRMIDEYRKPVVKLGGETLTIGQVTAIASRDIGVKVELSEEARVG 84

Query: 100 VDKSVDFLKAQLQNSV--YGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPTSVSFS 157
V S D++ + YGVTTGFG ++ RT+ LQK LI G+ F
Sbjct: 85 VKASSDWVMDSMNKGTD SYGVTTGFGATSHRRTKQGELQKELIRFLNAGI-----FG 137

Query: 158 VGRGLENLPLLEVVRGAMVIRVNSLTRGHSVRLVLEALTNFLNHRITPIVPLRGSISA 217
G +TLP R AM++R+N+L +G+S +R +LEA+T LNH ITP +PLRG+I+A
Sbjct: 138 NGTESTHTLPHSASRAAMLVRINTLLQGYSGIRFEILEAITKLLNHNITPCLPLRGTTITA 197

Query: 218 SGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIMFAEAI SLFGLEA--VVLGPKEGLGLV 275
SGDL PLSYIAG +TG P+ K L E + A EA +L G+ L PKEGL LV
Sbjct: 198 SGDLVPLSYIAGLLTGRPNKA--LGPNGEPLT-AAEAFTLAGINGGFELQPKEGLALV 254

Query: 276 NGTAVSASMATXXXXXXXXXXXXXXXXXXVEAMVGQQGSFAPFIHDVCRPHPGQVEVA 335
NGTAV + +A+ E M G+ F + + HPGQ+E A
Sbjct: 255 NGTAVGSGLASMVL FETNVLAILSEVLSAIFAEVMQGKP-EFTDHLTHKLKHHPGQIEAA 313

Query: 336 RNIRTLGSSSFAXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLE 395
+ +L GSS+ QDRY LRTSPQ LG L+E + + + E
Sbjct: 314 AVMEHILDGSSYVKAQKLHEIDPLQKP-EQDRYALRTSPQGLGLLIEVIRTSTKMIERE 372

Query: 396 NNTTTDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNR 455
N+ DNPL+DV + HGGNFQ + + +SM+ TRLA+A IGKL F Q +EL+N N
Sbjct: 373 INSVNDNPLIDVSRNKALHGGNFQGTPIGVSMNTRLAIASIGKLMFAQFSELVNDYYNN 432

Query: 456 GLPSCL-AAEDPSLNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVNSLALIS 514
GLPS L +PSL+Y KG +I +A+Y SEL LANPVT VQ AE NQ VNSL LIS
Sbjct: 433 GLPSNLTGGRNP SLDYGFKGA EIAMASYCSELQFLANPVTNHVQSAEQHNQDVNSLGLIS 492

Query: 515 ARRTAEANDVLSLLASHLYCTLQAVDLRAMELDFKKQFDPLLPTLLQQHLGTGLDVNAL 574
AR+TAEA ++L L+ + L QA+DLR +E + K + + ++ L G +
Sbjct: 493 ARKTAEAVEILKLMSTTWLVALCQAIDLRHIEENLKN TVKNTVSQVAKRVLTMGFNGELH 552

Query: 575 ALEV-KKALNKRL--EQTTTYDLEP--RWHDAFSYATGTVE--LLSSSPSANVTLTAVN 627
+ +K L K + E TY +P + +V+ L++ N + +
Sbjct: 553 PSRICEKDLLKVVDREHVFTYIDDP SATYPLMQKL RQVLVDHALMNGEKEHNSSTSIFQ 612

Query: 628 AWKVASAEKAISLTREVRN-RFQWTPSSQAPAHAYLSPRTRVLYSFVREELGVQARRGDV 686
V E L +EV + R + A + R+ LY FVREELG +
Sbjct: 613 KIGVFEDELKALLPKEVESARLELENGNPAIPNRITECRSYPLYKFVREELGT-----IL 667

Query: 687 FVG VQ QETIGSNVSRIYEA IKDGRINHVLVKML 719
G + + G +++ AI G++ +++ L
Sbjct: 668 LTGEKVGSPGEEFDKVF TAICAGKLIDPMLECL 700

☐ >gi|50910721|ref|XP_466849.1| ☒ putative phenylalanine ammonia-lyase [Oryza sativa]

cultivar-group)]

gi|48716552|dbj|BAD23155.1| **G** putative phenylalanine ammonia-lyase [Oryza sativa
cultivar-group)]
Length = 713

Score = 337 bits (863), Expect = 1e-90

Identities = 245/712 (34%), Positives = 363/712 (50%), Gaps = 42/712 (5%)

Query: 13 ANGFTNGSHAAPTKSAAGPTSALRRTPGLDGHAAHQSQLEIVQELLSDPTDDVVELSGYS 72
ANG + AAP A P + + T + G S L+ V+ +++ +V++ G S
Sbjct: 10 ANGMSGLCVAAPR---ADPLNWGKATEEMTG-----SHLDEVKRMVAEYRQPLVKIEGAS 61

Query: 73 LTXXXXXXXXXXXXXXXXXXQNDDEIRARVDKSVDFLKAQLQNSV--YGVTTGFGGSADTRT 130
L + D+ R RV S D++ + N YGVTTGFG ++ RT
Sbjct: 62 LRQAQVAVAAGEARV-ELDESARERVKASSDWVMNSMMNGTDSYGVTTGFGATSHRRT 120

Query: 131 EDAVSLQKALIEHQLCGVTPTS SVSSFSVGRGLENTLPLEVVRGAMVIRVNSLTRGHSAVR 190
++ +LQ+ LI G T + LP E R AM++R+N+L +G+S +R
Sbjct: 121 KEGGALQRELIRFLNAGAFGTGTDG-----HVLPAEATRAAMLVRINTLLQGYSGIR 172

Query: 191 LVVLEALTNFLNHRITPIVPLRGSISASGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIM 250
+LEA+ LN +TP +PLRG+I+ASGDL PLSYIAG +TG + V V +G++ +
Sbjct: 173 FEILEAIAKLLNANVTPLPLRGITASGDLVPLSYIAGLVTGRENA-VAVAPDGSK--V 229

Query: 251 FAREAISLFGLEA--VVLGPKEGLGLVNGTAVSASMATXXXXXXXXXXXXXXXXXXXXXVE 308
A EA + G++ L PKEGL +VNGTAV + +A+ E
Sbjct: 230 NAAEAFKIAGIQGGFFELQPKEGLAMVNGTAVGSGLASTVLFEANILAILAEVLSAVFCE 289

Query: 309 AMVGQQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGSSFAXXXXXXXXXXXXXXGILRQDR 368
M G+ H + + HPGQ+E A + +L GSS+ +QDR
Sbjct: 290 VMNGKPEYTDHLTHKL-KHHPGQIEAAAIMHEILEGSSYMKHAKKLGEPLMKP-KQDR 347

Query: 369 YPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTNDNPLLDVENKQTAHGGNFQASAVSISME 428
Y LRTSPQ+LGP +E + A ++ E N+ DNPL+DV + HGGNFQ + + +SM+
Sbjct: 348 YALRTSPQWLGPQIEVIRAATKSIEREINSVNDNPLIDVSRGKALHGGNFQGTPIGVSM 407

Query: 429 KTRLALALIGKLNFTQCTELLNAAMNRLPSCLA-AEDPSLNYHGKGLDIHIAAYASELG 487
TRLA+A IGKL F Q +EL+N N GLPS L+ +PSL+Y KG +I +A+Y SEL
Sbjct: 408 NTRLAIAAIGKLMFAQFSELVNDFYNGLPSNLSSGRNPSLDYGFKAELAMASYCSELQ 467

Query: 488 HLANPVTTFVQPAEMGNQAVNSLALISARRTAEANDVLSLLLASHLYCTLQAVDLRAMEL 547
L NPVT VQ AE NQ VNSL LIS+R+T EA D+L L+ ++ L QAVDLR +E
Sbjct: 468 FLGNPVTNHVQSAEQHNQDVNSLGLISSRKTDIDAIDILKMSSTFLIALCQAVDLRHIEE 527

Query: 548 DFKKQFDPLLPTLLQQHLGTGLDVNA-LALEVKKALNKRL--EQTTTYDLEPRWHD--AF 602
+ K + T+ ++ L T + +A +K L K + E Y +P H+
Sbjct: 528 NVKSAVKSVCMTVAKKTLSTNSTGDLHVARFCEKDLLKEIDREAVFAYADDPCHNYPLM 587

Query: 603 SYATGTVVELLSSSPSANVTLTAVNAWKVASAEKAISLTR-----EVRNRFWQTPSSQAPA 658
+VE ++ +A KVA E+ + T E + ++ P+
Sbjct: 588 KKLRNVLVERALANGAAEFNADTSVFAKVAQFEEELRATLPGAIEAARAANGTAAIPS 647

Query: 659 HAYLSPRTRVLYSFVREELGVQARRGDVFGVQVQETIGSNVSRIYEAIKDGR 710
R+ LY FVREELG + G + + G +++ AI +G+
Sbjct: 648 R-ITECRSYPLYRFVREELGTK-----YLTGEKTRSPGEELNKVLVAINEGK 693

☐ >gi|3024360|sp|Q42667|PALY_CITLI Phenylalanine ammonia-lyase

gi|1276903|gb|AAB67733.1| phenylalanine ammonia-lyase
Length = 722

Score = 337 bits (863), Expect = 1e-90

Identities = 242/713 (33%), Positives = 353/713 (49%), Gaps = 43/713 (6%)

Query: 30 GPTSALRRTPGLD-----GHAHQSQLEIVQELLSDPTDDVVELSGYSLTXXXXXXXXX 82
G TS+L G D + S L+ V+ ++ + VV+L G SLT
Sbjct: 17 GGTSSLGLCTGTDPLNWTVAADSLKSHLDEVKRMIDEYRRPVVKLGGESLTIGQVTAIA 76

Query: 83 XXXXXXXXQNDDEIRARVDKSVDFLKAQLQNSV--YGVTTGFGGSADTRTEDAVSLQKAL 140
+ + RA V S D++ + YGVTTGFG ++ RT+ +LQK L
Sbjct: 77 AHDSGVKVELAEARAGVKASSDWVMDMMKGTDSYGVTTGFGATSHRRTKQGGALQKEL 136

Query: 141 IEHQLCGVTPTSVSSFSVGRGLENLPLEVVRGAMVIRVNSLTRGHSAVRLVVLEALTNF 200
I G+ F G +TLP R AM++RVN+L +G+S +R +LE +T F
Sbjct: 137 IRFLNSGI-----FGNGTESSHTLPHSATRAAMLVRVNTLLQGYSGIRFEILETITKF 189

Query: 201 LNHRTPIVPLRGSISASGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFG 260
LNH ITP +PLRG+I+ASGDL PLSYIAG +TG P+ K V G +++ EA +L G
Sbjct: 190 LNHNITPCLPLRGITASGDLVPLSYIAGLLTGRPNKA-VGSNG--QVLNPTEAFNLG 246

Query: 261 LEA--VVLGPKEGLGLVNGTAVSASMATXXXXXXXXXXXXXXXXXXXXVEAMVGQOGSFA 318
+ + L PKEGL LVNGTAV + +A E M G+ F
Sbjct: 247 VTSGFFELQPKEGLALVNGTAVGSGLAATVLFANILAIMSEVLSAIFAEMNGKP-EFT 305

Query: 319 PFIHDVCRPHPGQVEVARNIRTLLSGSSFAXXXXXXXXXXXXXXGILRQDRYPLRTSPQFL 378
+ + HPGQ+E A + +L GSS+ +QDRY LRTSPQ+L
Sbjct: 306 DHLTHKLKHHPGQIEAAIMEHILDGSSYVKAQKLHETDPLQKP-KQDRYALRTSPQWL 364

Query: 379 GPLVEDMMHAYSTLSLENNTTTDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIG 438
GP +E + A + E N+ DNPL+DV + HGGNFQ + + +SM+ TRLA+A IG
Sbjct: 365 GPQIEVIRAATKMIEREINSVNDNPLIDVSRNKALHGGNFQGTPIGVSMNTRLAIASIG 424

Query: 439 KLNFTQCTELLNAAMNRGLPSCL-AAEDPSLNYHGKGLDIHIAAYASELGHLANPVTTFV 497
KL F Q +EL+N N GLPS L +PSL+Y KG +I +A+Y SEL LANPVT V
Sbjct: 425 KLMFAQFSELVNDFYNNGLPSNLTGGRNPSLDYGFKAIEIAMASYCSELQFLANPVTNHV 484

Query: 498 QPAEMGNQAVNSLALISARRTAEANDVLSLLLASHLYCTLQAVDLRLAMELDFKKQFDPLL 557
Q AE NQ VNSL L S+R+TAEA D+L L+ ++ L QA+DLR +E + K +
Sbjct: 485 QSAEQHNQDVNSLGLNSSRKTAEAVIDILKLMSSSTFLVALCQAIDLRHLEENLKNTVKNTV 544

Query: 558 PTLLQQHGLGTGLDVNALALEVKKALNKRLEQTTTYDLEPRWHDASFYATGTVVELL---- 613
+ ++ L G++ L + K L + + + D A+ +++ L
Sbjct: 545 SQVAKRVLTMGVNGE---LHPSRFCEKDLIKVVDREYVFAYIDDPCSASSPLMQKLRQVL 601

Query: 614 -----SSSPSANVTLTAVNAWKVASAEKAI SLTREVRNRFWQTPSSQAPAHAYLSP-RT 666
+ N T + E L +EV + S A + R+
Sbjct: 602 VDHALDNGDREKNSTTSIFQKIGAFEDLKTLLPKEVEIARTELESGNAIIPNRIKECRS 661

Query: 667 RVLYSFVREELGVQARRGDVFGVQQTETIGSNVSRIYEAIKGRINHVLVKML 719
LY VRE++G + G + + G +++ A+ +G++ +++ L
Sbjct: 662 YPLYKIVREDIGT-----SLLTGEKVRSPGEEFDKVFTAMCEGKLIDPMLECL 709

>gi|14326457|gb|AAK60274.1| phenylalanine ammonia-lyase 1 [Manihot esculenta]
Length = 687

Score = 336 bits (862), Expect = 1e-90

Identities = 240/701 (34%), Positives = 354/701 (50%), Gaps = 41/701 (5%)

Query: 22 AAPTKSAAGPTSALRRTPGLDGHAHQSQLLEIVQELLSIPTDDVVELSGYSLTXXXXXXX 81
 A+P S+A P + G+ + S L+ V+ ++ + VV L G +LT
 Sbjct: 11 ASPGFSSADPLNW-----GMAAESLKGSHLDEVKRMVDEYRKPVVRLGGETLTIAQVTAI 65

Query: 82 XXXXXXXXXQNDDEIRARVDKSVDFLKAQLQNSV--YGVTTGFGGSADTRTEDAVSLQKA 139
 + +E RA V S D++ + YGVTTGFG ++ RT+ +LQ+
 Sbjct: 66 ANHDSGVKVELSEEARAGVKASSDWVLD SMNKGTD SYGVTTGFGATSHRRTKQGGALQRE 125

Query: 140 LIEHQLCGVPTPTSVSSFSVGRGLENLPLEVVRGAMVIRVNSLTRGHSVRLVLEALTN 199
 LI G+ F G+ +TL R AM++R+N+L +G+S +R +LEA+T
 Sbjct: 126 LIRFLNAGI-----FGNGQESCHTSLHTATRAAMLVRINTLLQGYSGIRFEILEAITK 178

Query: 200 FLNHRITPIVPLRGSISASGDLSPSYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLF 259
 F+N+ +TP +PLRG+I+ASGDL PLSYIAG +TG P+ K L E + A EA L
 Sbjct: 179 FINNNVTPRLPLRGITASGDLVPLSYIAGLLTGRPNKS--LGPNGESLD-AAEAFKLA 235

Query: 260 GLEA--VVLGPKEGLGLVNGTAVSASMATXXXXXXXXXXXXXXXXXXXXVEAMVGQQGSF 317
 G+ L PKEGL LVNGTAV + +A+ E M+G+ F
 Sbjct: 236 GINGGFELQPKEGLALVNGTAVGSGLASMVLFEANVLAVLSEVLSAIFAENVMLGKP-EF 294

Query: 318 APFIHDVCRPHPGQVEVARNIRTLTSGSSFAXXXXXXXXXXXXXXXXXGILRQDRYPLRTSPQF 377
 + + HPGQ+E A + +L GSS+ +QDRY LRTSPQ+
 Sbjct: 295 TDHLTHKLKHPGQIEAAIMEHVLGSSYIKAAQKVHEIDPLQKP-KQDRYALRTSPQW 353

Query: 378 LGPLVEDMMHAYSTLSLENNTTTNDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALI 437
 LGP +E + A + E N+ DNPL+DV HGGNFQ + + +SM+ TRLA+A I
 Sbjct: 354 LGPQIEVIRTATKMIEREINSVNDNPLIDVSRNIALHGGNFQGTPIGVSMNTRLAIASI 413

Query: 438 GKLNFTQCTELLNAAMNRGLPSCL-AAEDPSLNYHGKGLDIHIAAYASELGHLANPVTTF 496
 GKL F Q +EL+N N GLPS L +PSL+Y KG +I +A+Y SEL LANPVT
 Sbjct: 414 GKLMFAQFSELVNDFYNNGLPSNLTGGRNPSLDYGFKAELAMASYCSELQFLANPVTNH 473

Query: 497 VQPAEMGNQAVNSLALISARRTAEANDVLSLLASHLYCTLQAVDLRAMELDFKKQFDPL 556
 VQ AE NQ VNSL LIS+R+TAEA D+L L+ +++L QA+DLR +E + K+
 Sbjct: 474 VQSAEQHNQDVNSLGLISSRKTAEAVDILKLMSSSTYLVALCQAIDLRHLEENLKQTVKNT 533

Query: 557 LPTLLQQHLGTGLDVNALALEVKKALNKRLEQTTTYDLEPRWHDASFYATGTVE----- 611
 + + ++ L G++ L + K L + + + D AT +++
 Sbjct: 534 VSQVAKRVLTMGINGE---LHPSRFCEKDLLKVVDREYVYAYVDDPCSATYPLMQKLRQV 590

Query: 612 -----LLSSSPSANVTLTAVNAWKVASAEKAI SLTREVRN-RFWQTPSSQAPAHAYLSPR 665
 +++ N + + E L +EV + R + A ++ R
 Sbjct: 591 LVDHAMNGEKEKNSSTSIFQKIGAFEEELKTLLPKEVESARTEYENG NPAISNKIKECR 650

Query: 666 TRVLYSFVREELGVQARRGDVFGVQQETIGSNVSRIYEAI 706
 + LY FVREELG + G + + G +++ AI
 Sbjct: 651 SYPLYKFVREELGC-----SLLTGEKIRSPGEEFDKVFSAI 686

☐ >gi|56409806|emb|CAH17686.1| phenylalanine ammonia lyase [Beta vulgaris]
 Length = 719

Score = 335 bits (860), Expect = 2e-90

Identities = 244/723 (33%), Positives = 357/723 (49%), Gaps = 40/723 (5%)

Query: 16 FTNGSHAAPTKSAAGPTSALRRTPGLDGHAHQSQLLEIVQELLSIPTDDVVELSGYSLTX 75
 + NGS P A G A S L+ V+++++ + + L G +LT

Sbjct: 7 YQNGSSEMDLCIGGKPIQADPLNWGKAAEAITGSHLDEVKKMVAEYRNPAILRGGETLTV 66

Query: 76 XXXXXXXXXXXX--XXXXQNDDEIRARVDKSVDFLKAQLQNSV--YGVTTGFGGSADTRTE 131
+ + RA V S D++ + YGVTTGFG ++ RT+

Sbjct: 67 AQVAAVAAATGPHEAAVELAESARAGVKASSDWVMDSMNKGTD SYGVTTGFGATSHRRTK 126

Query: 132 DAVSLQKALIEHQLCGVTPPTS SVSSFSVGRGLENLPLEVVRGAMVIRVNSLTRGHS AVRL 191
+LQK LI GV F G +TLP R AM++R+N+L +G+S +R

Sbjct: 127 QGGALQKELIRFLNAGV-----FGNGTESSHTLPHTATRAAMLVRINTLLQGYSGIRF 179

Query: 192 VVLEALTNFLNHRITPIVPLRGSISASGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIMF 251
+LEA+T LN+ ITP +PLRG+I+ASGDL PLSYIAG +TG P+ K V G +++

Sbjct: 180 EILEAITGLLNNNITPCLPLRGITITASGDLVPLSYIAGLLTGRPNKA-VGPNG--EVLN 236

Query: 252 AREAISLFGLEA--VVLGPKEGLGLVNGTAVSASMATXXXXXXXXXXXXXXXXXXXXVEA 309
A +A + + L PKEGL LVNGTAV + MA+ E

Sbjct: 237 AEQAFKAAQISSGFELQPKGLALVNGTAVGSGMASIVLFETNILAVLAEVISAVFAEV 296

Query: 310 MVGQQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGSSFAXXXXXXXXXXXXXGILRQDRY 369
M G+ F + + HPGQ+E A + +L GSS+ +QDRY

Sbjct: 297 MNGKP-EFTDHLTHKLKHHPGQIEAAAIMEHILDGSSYMKAALHELDPLQKP-KQDRY 354

Query: 370 PLRTSPQFLGPLVEDMMHAYSTLSLENNTTTNDNPLLDVENKQTAHGGNFQASAVSISMEK 429
LRTSPQ+LGP +E + A ++ E N+ DNPL+DV + HGGNFQ + + +SM+

Sbjct: 355 ALRTSPQWLGPQIEVIRFATKSIEREINSVNDNPLIDVSRNKALHGGNFQGTPIGVSM DN 414

Query: 430 TRLALALIGKLNFTQCTELLNAAMNRGLPSCL-AAEDPSLNYHGKGLDIHIAAYASELGH 488
RLA+A IGKL F Q +EL+N N GLPS L A+ DPSL+Y KG +I +A+Y SEL

Sbjct: 415 ARLAIAAIGKLLFAQFSELVNDYNNGLPSNLTA SRDPSLDYGFKA EIAMASYCSELQF 474

Query: 489 LANPVTTFVQPAEMGNQAVNSLALISARRTAEANDVLSLLLASHLYCTLQAVDLRAMELD 548
L NPVT VQ AE NQ VNSL LISAR+TAEA D+L L+ ++ L QA+DLR +E +

Sbjct: 475 LGNPVTNHVQSAEQHNQDVNSLGLISARKTAEAVDILKLMSSFTFLVALCQAIDLRHLEEN 534

Query: 549 FKKQFDPLLPTLLQQHLGTGLDVNALALEVKKALNKRLEQTTTYDLEPRWHD AF SYATGT 608
K + + ++ L TG + L + K L + + + D T

Sbjct: 535 VKHAVKNTVSQVCRRVLITGSNGE---LHPGRFCEKELIRVVEREYVFAYADDPCSVTYP 591

Query: 609 VVE-----LLSSSPSANVTLTAVNAWKVASAEKAISLTREVR--NRFWQTPSSQA 656
+++ L + NV+ + E L +EV +++ +S

Sbjct: 592 LMQKLRQVLVDQALANGDSEKNVSTSIFQKIGAFEEELKARLPKEVEAARAAYESGNSVI 651

Query: 657 PAHAYLSPRTRVLYSFVREELGVQARRGDVFGVQQETIGSNVSRIYEAIKDGRINHV LV 716
P + R+ +Y F+REEL G+ + + G + +++ AI G+I L+

Sbjct: 652 P-NRIKECRSYPVYKFIREELNTNLLTG EKVI-----SPGEEIDKVFTAICQGKIIDPLL 705

Query: 717 KML 719
L

Sbjct: 706 DCL 708

☐ >gi|129587|sp|P26600|PAL5_LYCES Phenylalanine ammonia-lyase (PAL)
gi|170469|gb|AAA34176.1| phenylalanine ammonia-lyase
Length = 721

Score = 335 bits (860), Expect = 2e-90
Identities = 244/730 (33%), Positives = 364/730 (49%), Gaps = 41/730 (5%)

Query: 9 ATTLANGFTNGSHAAPTKSAAGPTSALRRTPGLDGHAHQSQLEIVQELLSIPTDDVVEL 68

Sbjct: 3 ++ + NG NG K + L + + S L+ V++++ + +V+L
SSIVQNGHVNGEAMDLCKKSINVNDPLNWE--MAESLRGSHLDEVKKMVDEFKPIVKL 60

Query: 69 SGYSLTXXXXXXXXXXXXXXXXX---QNDDEIRARVDKSVDFLKAQLQNSV--YGVTTGFG 123
G +LT + + RA V S D++ + YGVTTGFG

Sbjct: 61 GGETLTVAQVASIANVDNKSNGVKVELSESARAGVKASSDWVMDSMGKGTD SYGVTTGFG 120

Query: 124 GSADTRTEDAVSLQKALIEHQLCGVTPPTSVSSFSVGRGLENTLPLEVVRGAMVIRVNSLT 183
++ RT++ +LQK LI GV F G +TLP R AM++R+N+L

Sbjct: 121 ATSHRRRTKNGGALQKELIRFLNAGV-----FGNGTESSHTLPHSATRAAMLVRINTLL 173

Query: 184 RGHSAVRLVVLEALTNFLNHRITPIVPLRGSISASGDLSPLSYIAGAITGHPDVKVHVLH 243
+G+S +R +LEA+T +N ITP +PLRG+I+ASGDL PLSYIAG +TG P+ K +

Sbjct: 174 QGYSGIRFEILEAITKLINSNITPCLPLRGTTASGDLVPLSYIAGLLTGRPNKA--VG 231

Query: 244 EGTEKIMFAREAISLFGLEA--VVLGPKEGLGLVNGTAVSASMATXXXXXXXXXXXXXXXXX 301
EK+ A E + G+ + L PKEGL LVNGTAV + MA+

Sbjct: 232 PNGEKLN-AEERFRVAGVTS GFFELQPK EGLALVNGTAVGSGMASMVLFESNILAVMSEV 290

Query: 302 XXXXXVEAMVGQQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGSSFAXXXXXXXXXXXXXXXXXX 361
E M G+ F ++ + HPGQ+E A + +L GSS+

Sbjct: 291 LSAIFAEVMNGKP-EFTDYLTHKLKHHPGQIEAAAMEHILDGSSYVKAQKLHEMDPLQ 349

Query: 362 GILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTNDNPLLDVENKQTAHGGNFQAS 421
+QDRY LRTSPQ+LGP +E + A + E N+ DNPL+DV + HGGNFQ +

Sbjct: 350 KP-KQDRYALRTSPQWLGPQIEVIRAATKMIEREINSVNDNPLIDVSRNKALHGGNFQGT 408

Query: 422 AVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLP-SCLAAEDPSLNYHGKGLDIHIA 480
+ +SM+ TRLALA IGKL F Q +EL+N N GLP + A +PSL+Y KG +I +A

Sbjct: 409 PIGVSMDNTRLALASIGKLMFAQFSELVNDYNNGLPLNLTAGRNPSLDYGLKGAEIAMA 468

Query: 481 AYASELGHLANPVTTFVQPAEMGNQAVNSLALISARRTAEANDVLSLLLASHLYCTLQAV 540
+Y SEL LANPVT VQ AE NQ VNSL LISAR+TAEA D+L L+ +++L QA+

Sbjct: 469 SYCSELQFLANPVTNHVQSAEQHNQDVNSLGLISARKTAEAVDILKMSSTYLVALCQAI 528

Query: 541 DLRAMELDFKKQFDPLLP TLLQQHLGTGLDVNALALEVKKALNKRLEQT-----TYDL 594
DLR +E + K + + ++ L G + L + K L Q TY

Sbjct: 529 DLRHLEENLKNVKNNTVSQVAKKTLAMGANGE---LHPARFCEKELLQVVEREYLFITYAD 585

Query: 595 EP--RWHDAFSYATGTVVELLSSSPSANVTLTAVNAWKVASAEKAIS--LTREVRN-RFW 649
+P + +V+ + + L + K+ + E + L +EV + R

Sbjct: 586 DPCSSTYPLMQKLRLQVLVDHAMKNGESEKNLNSSIFQKIVAFEDELKAVLPKEVESARAV 645

Query: 650 QTPSSQAPAHAYLSPRTRVLYSFVREELGVQARRGDVFGVQVQETIGSNVSRIYEAIKDG 709
+ A + R+ LY VR+E+G ++ G + + G + +++ A +G

Sbjct: 646 VESGNPAIPNRITECRSYPLYRLVRQEVGT-----ELLTGKVRSPGEEIDKVFTAFENG 700

Query: 710 RINHVLVKML 719
+I L++ L

Sbjct: 701 QIIDPLLECL 710

☐ >gi|400725|sp|P31425|PAL1_SOLTU Phenylalanine ammonia-lyase 1
Length = 720

Score = 335 bits (859), Expect = 3e-90

Identities = 252/741 (34%), Positives = 372/741 (50%), Gaps = 54/741 (7%)

Query: 1 MAPSLDSLATTLANGFTNGS--HAAPTKSAAGPTSALRRTPGLDGHAHQSQLEIVQELL 58

Sbjct: 1 MAPS+ NG NG KS P + L G S L+ V+++
 MAPSIAQ-----NGHVNGEVEEVLWKKSIHDPLNWEMAVDLSLRG-----SHLDEVKKMV 49

Query: 59 SDPTDDVVELSGYSLTXXXXXXXXXXXXXXXXX---QNDDEIRARVDKSVDFLKAQLQNSV 115
 + +V+L G +LT + + RA V S D++ +

Sbjct: 50 DEFKRPIVKLWGETLTVAQVASIANADNKTSGFKVELSESARAGVKASSDWVMSMSKGT 109

Query: 116 --YGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPTSVSSFSVGRGLENTLPLEVVVRG 173
 YGVTTGF ++ RT++ +LQK LI+ GV F G +TLP R

Sbjct: 110 DSYGVTTGFCATSHRRTKNGGALQKELIKFLNAGV-----FGNGTESTHTLPHSATRA 162

Query: 174 AMVIRVNSLTRGHSVRLVLEALTNFLNHRITPIVPLRGSISASGDLSPLSYIAGAITG 233
 AM++R+N+L +G+S +R +LEA+T +N ITP +PLRG+++ASGDL PLSYIAG +TG

Sbjct: 163 AMLVRINTLLQGYSGIRFEILEAITKLINSNITPCLPLRGTVTASGDLVPLSYIAGLLTG 222

Query: 234 HPDVKVHVLHEGTEKIMFAREAISLFGLEA--VVLGPKEGLGLVNGTAVSASMATXXXXX 291
 P+ K V G++ + A EA + + L PKEGL LVNGTAV + MA+

Sbjct: 223 RPNSKA-VGPSGSK--LDADAEFRVAASGGFFELQPKEGLALVNGTAVGSGMASIVLYD 279

Query: 292 XXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGSSFAXXX 351
 E M G+ F ++ + HPGQ+E A + +L GSS+

Sbjct: 280 SNILAVMFEVLSAIFAEVMNGKP-EFTDYLTHKLKHHPGQIEAAAIMEHILDGSSYVCAA 338

Query: 352 XXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTDNPLLDVENKQ 411
 +QDRY LRTSPQ+LGP +E + A + E N+ DNPL+DV +

Sbjct: 339 QKLHEMDPLQKP-KQDRYALRTSPQWLGPQIEVIRAAATKMIEREINSVNDNPLIDVSRNK 397

Query: 412 TAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCL-AAEDPSLNY 470
 HGGNFQ + + +SM+ TRLALA IGKL F Q +EL+N N GLPS L A +PSL+Y

Sbjct: 398 AIHGGNFQGTPIGVSMNTRLALASIGKLMFAQFSELVNDYNNGLPSNLTAGRNPSLDY 457

Query: 471 HGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVNSLALISARRTAEANDVLSLLA 530
 KG +I +A+Y SEL LANPVT VQ AE NQ VNSL LISAR+TAEA D+L L+ +

Sbjct: 458 GFKGAELIAMASYCSELQFLANPVTNHVQSAEQHNQDVNSLGLISARKTAEAVDILKLMSS 517

Query: 531 SHLYCTLQAVDLRAMELDFKKQFDPLLPDLLQHLGTGLDVNALA-LEVKKALNKRL--- 586
 ++L QA+DLR +E + K ++ + Q L + A+ L + K L

Sbjct: 518 TYLVALCQAIDLRHLEENLKS----VVKNTVSQVAKRTLITIGAIGELHPARFCEKELLRV 573

Query: 587 ---EQTTTYDLEP--RWHDAFSYATGTVVELLSSSPSANVTLTAVNAWKVASAEKAIS-- 639
 E TY +P + +V+ + + + + K+ + E ++

Sbjct: 574 VDREYLFTYADDPSSSTYPLMQKLRLQVLVDHAMKNGESEKNINSSIFQKIGAFEDELNAV 633

Query: 640 LTREVRN-RFWQTPSSQAPAHAYLSPRTRVLYSFVREELGVQARRGDVFGVQQETIGSN 698
 L +EV + R + + + R+ LY VR+ELG ++ G + + G

Sbjct: 634 LPKEVESARALLESIGNPSIPNRITECRSYPLYRLVRQELGT-----ELLTGEKVRSPGEE 688

Query: 699 VSRIYEAIKDGRINHVLVKML 719
 + +++ A+ +G+IN L++ L

Sbjct: 689 IEKVFTAMCNGQINDPLLECL 709

☐ >gi|7798554|dbj|BAA95629.1| phenylalanine ammonia lyase [Catharanthus roseus]
 Length = 716

Score = 335 bits (859), Expect = 3e-90

Identities = 237/697 (34%), Positives = 352/697 (50%), Gaps = 37/697 (5%)

Query: 40 GLDGHAHQSQLEIVQELLSIPTDDVVELSGYSLTXXXXXXXXXXXXXXXXX---QNDDEIRA 98

G+ + S L+ V+ ++++ VV+L G +LT + ++ RA
 Sbjct: 29 GMAADSLKGSHLDEVKRMVAEFRKPVVKLGGETLTISQVAAIAARDYNAVKVELSEDARA 88

Query: 99 RVDKSVDFLKAQLQNSV--YGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPTSVSSF 156
 V S D++ + YGVTTGFG ++ RT+ +LQK LI G+ F
 Sbjct: 89 GVKASSDWVME SMNKGTD SYGVTTGFGATSHRRTKQGGALQKELIRFLNAGI-----F 141

Query: 157 SVGRGLENLTPLEVVRGAMVIRVNSLTRGHSVRLVLEALTNFLNHRITPIVPLRGSIS 216
 G +TLP R AM++R+N+L +G+S +R +LEA+T FLNH ITP +PLRG+I+
 Sbjct: 142 GNGTESSHTLPHSATRAAMLVRINTLLQGYSGIRFEILEAITKFLNHNITPCLPLRGITIT 201

Query: 217 ASGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEAVV--LGPKEGLGL 274
 ASGDL PLSYIAG +TG P+ K V G +I+ +A + G+ + L PKEGL L
 Sbjct: 202 ASGDLVPLSYIAGLLTGRPNKA-VGPNG--EIVNPEQAFKMAGVNDGLFELQPKEGLAL 258

Query: 275 VNGTAVSASMATXXXXXXXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQVEV 334
 VNGTAV + MA+ E M G+ F + + HPGQ+E
 Sbjct: 259 VNGTAVGSGMASMVLFEANILAVLSEVLSAIFAEMVNGKP-EFTDHLTHKLKHHHPGQIEA 317

Query: 335 ARNIRTLTSGSSFAXXXXXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSL 394
 A + +L GS + +QDRY LRTSPQ+LGP +E + A +
 Sbjct: 318 AAIMEHILDGSGYVKAHKLHEMDPLQKP-KQDRYALRTSPQWLGPQIEVIRSATKMIER 376

Query: 395 ENNTTTDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMN 454
 E N+ DNPL+DV + HGGNFQ + + +SM+ RLA+A IGKL F Q +EL+N N
 Sbjct: 377 EINSVNDNPLIDVSRNKALHGGNFQGTPIGVSMDNARLAIASIGKLMFAQISELVNDFYN 436

Query: 455 RGLPSCLA-AEDPSLNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVNSLALI 513
 GLPS L+ +PSL Y KG +I +A+Y SEL +LANPVT VQ AE NQ VNSL LI
 Sbjct: 437 NGLPSNLSGGRNPSLVYGFKAETAMASYCSELQYLANPVTNHVQSAEQHNQDVNSLGLI 496

Query: 514 SARRTAEANDVLSLLLASHLYCTLQAVDLRAMELDFKKQFDPLLPTLLQQHLGTGLDVNA 573
 S+R+TAEA ++L L+ +++L QA+DLR +E + K + + ++ L G++
 Sbjct: 497 SSRKTAEAVEILKMSSTYLVALCQAIDLRHLEENLKNVKNKTVSQVAKRTLTVGVNGE- 555

Query: 574 LALEVKKALNKRLEQTTTYDLEPRWHDFAFSYATGTVVE-----LLSSSPSANVTL 623
 L + K L + + + D T ++E L + NV
 Sbjct: 556 --LHPSRFCEKDLIRVVDREYVFAYVDDPCSGTYPLMEKLRQVIVDHALQNGESEKNVNT 613

Query: 624 TAVNAWKVASAEKAISLTREVRN-RFQWTPSSQAPAHAYLSPRTRVLYSFVREELGVQAR 682
 + E L +EV + R + A + R+ LY FVRE++G
 Sbjct: 614 SIFQKIAAFEDELKTVLPKEVESARTALENGNPAIPNRIKECRSYPLYKFVREDVG---- 669

Query: 683 RGDVFGVGVQQTIGSNVSRIYEAIKDGRINHVLVKML 719
 + G + + G +++ A+ + +I L++ L
 Sbjct: 670 -AEFLTGEKDRSPGEEFDKVF+TAMCNEKIIDPLLECL 705

☐ >gi|735957|emb|CAA53733.1| phenylalanine ammonia-lyase [Cucumis melo]
 gi|1076275|pir|S52632 phenylalanine ammonia-lyase (EC 4.3.1.5) - muskmelon
 Length = 619

Score = 335 bits (858), Expect = 4e-90

Identities = 223/615 (36%), Positives = 327/615 (53%), Gaps = 28/615 (4%)

Query: 116 YGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPTSVSSFSVGRGLENLTPLEVVRGAM 175
 YGVTTGFG ++ +RT+ +LQK LI G+ F G +TLP R AM
 Sbjct: 13 YGVTTGFGATSHSR TKQGGALQKELIRFLNAGI-----FGNGTESNHTLPHATRAAM 65

Query: 176 VIRVNSLTRGHSVRLVLEALTNFLNHRITPIVPLRGSISASGDLSPLSYIAGAITGHP 235
 ++R+N+L +G+S +R +LE++T LNH +TP +PLRG+I+ASGDL P SYIAG +TG P
 Sbjct: 66 LVRINTLLQGYSGIRFEILESITKLLNHNVTPLPLRGTTITASGDLVPFSYIAGFLTGRP 125

Query: 236 DVKVHVLHEGTEKIMFAREAISLFGLEAVV--LGPKEGLGLVNGTAVSASMATXXXXXXX 293
 + K T I+ A A G+++ V L PKEGL LVNGT V + +A+
 Sbjct: 126 NAKA----VPTGDILDAVAAFKYAGIDSGVFELQPKEGLALVNGTGVGSGLASIVLFEAN 181

Query: 294 XXXXXXXXXXXXXXXVEAMVGQQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGSSFAXXXXX 353
 E M G+ F + + HPGQ+E A + LL GS+
 Sbjct: 182 ILALLSEVISAIFAQVMQKGP-EFTDHLTHKLKHHHPGQIEAAAIMEHLLDGSASQKDAKR 240

Query: 354 XXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNNTTTDNPLLDVENKQTA 413
 +QDRY LRTSPQ+LGP +E + H+ ++ E N+ DNPL+DV +
 Sbjct: 241 LHELDPLQNSPKQDRYALRTSPQWLGPQIEVIRHSTKSIEREINSVNDNPLIDVSRNKAL 300

Query: 414 HGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRLPSCLA-AEDPSLNYHG 472
 HGGNFQ + + +SM+ TRLALA IGKL F Q +EL+N N GLPS L+ +PSL+Y
 Sbjct: 301 HGGNFQGTPIGVSMNTRLALASIGKLLFAQFSELVNDFYNNGLPSNLSGGSNPSLDYGF 360

Query: 473 KGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVNSLALISARRTAEANDVLSLLASH 532
 KG +I +A+Y SEL +LANPVT VQ AE NQ VNSL LIS+R+TAEA D+L L+ +
 Sbjct: 361 KGAEIAMASYCSELQYLANPVTNHVQSAEQHNQDVNSLGLISSRKTAEADILKLMSTTF 420

Query: 533 LYCTLQAVDLRAMELDFKKQFDPLLPTLLQQHLGTGLDVNA-LALEVKKALNKRLEQTTT 591
 L QA+DLR +E + K + + ++ L G++ L+ +K L K +++
 Sbjct: 421 LAALCQAIDLRHIEENLKSTVKNTVSQVAKKILTIGVNGELHLSRFCEKDLLKVIDREYC 480

Query: 592 Y----DLEPRWHDASFYATGTVVELLSSSPSANVTLTAVNAWKVASAEKAIS--LTREVR 645
 + D + +VE + L + K+ + E+ + L +EV
 Sbjct: 481 FAYIDDPCSMTYPLMQKLRLVVEHALKNNDLKNLNSIFLKIGAFEEELKTLLPKEVE 540

Query: 646 NRFWQTPSSQAPAHAYLSP-RTRVLYSFVREELGVQARRGDVFGVQQTIGSNVSRIYE 704
 + +A + R+ +Y FVREEL D+ G + ++ G +++
 Sbjct: 541 SGRQAISKGKAIPIRIKDCRSYPIYKFVREEL-----ETDILTGEKVKSPGEEFDKVS 595

Query: 705 AIKDGRINHVLVKML 719
 AI +G+I L++ L
 Sbjct: 596 AICEGKIIDPLLECL 610

☐ >gi|322743|pir||A44133 phenylalanine ammonia-lyase (EC 4.3.1.5) - tomato
 Length = 721

Score = 335 bits (858), Expect = 4e-90

Identities = 245/730 (33%), Positives = 363/730 (49%), Gaps = 41/730 (5%)

Query: 9 ATTLANGFTNGSHAAPTKSAAGPTSALRRTPGLDGHAAHQSQLEIVQELLSDPDDEVEL 68
 ++ + NG NG K + L + + S L+ V++++ + +V L
 Sbjct: 3 SSIVQNGHVNGEAMDLCCKKSINVNDPLNWE--MAAESLRGSHLDEVKKMVDEFKPIVFL 60

Query: 69 SGYSLTXXXXXXXXXXXXXXXXX---QNDDEIRARVDKSVDFLKAQLQNSV--YGVTTGFG 123
 G +LT + + RA V S D++ + YGVTTGFG
 Sbjct: 61 GGETLTVAQVASIANVDNKSNGVKVELSESARAGVKASSDWVMDSMGKGTDSYGVTTGFG 120

Query: 124 GSADTRTEDAVSLQKALIEHQLCGVTPTSVSSFSVGRGLENLPLEVVRGAMVIRVNSLT 183
 ++ RT++ +LQK LI GV F G +TLP R AM++R+N+L
 Sbjct: 121 ATSHRRRTKNGGALQKELIRFLNAGV-----FGNGTESSHTLPHSATRAAMLVRINTLL 173

Query: 184 RGHSAVRLVVLEALTNFLNHRITPIVPLRGSISASGDLSPLSYIAGAITGHPDVKVHVLH 243
 +G+S +R +LEA+T +N ITP +PLRG+I+ASGDL PLSYIAG +TG P+ K +
 Sbjct: 174 QGYSGIRFEILEAITKLINSNITPCLPLRGITITASGDLVPLSYIAGLLTGRPNKA--VG 231

Query: 244 EGTEKIMFAREAISLFGLEA--VVLGPKEGLGLVNGTAVSASMATXXXXXXXXXXXXXXXXX 301
 EK+ A E + G+ + L PKEGL LVNGTAV + MA+
 Sbjct: 232 PNGEKLN-AEERFRVAGVTSGFFELQPKEGLALVNGTAVGSGMASMVLFESENILAVMSEV 290

Query: 302 XXXXXVEAMVGQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGSSFAXXXXXXXXXXXXXXXXXX 361
 E M G+ F ++ + HPGQ+E A + +L GSS+
 Sbjct: 291 LSAIFAEVMNGKP-EFTDYLTHKLKHHPGQIEAAAIMEHILDGSSYVKAQKLHEMDPLQ 349

Query: 362 GILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNNTTTDNPLLDVENKQTAHGGNFQAS 421
 +QDRY LRTSPQ+LGP +E + A + E N+ DNPL+DV + HGGNFQ +
 Sbjct: 350 KF-KQDRYALRTSPQWLGPQIEVIRAATKMIEREINSVNDNPLIDVSRNKALHGGNFQGT 408

Query: 422 AVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLP-SCLAAEDPSLNHYHGKGLDIHIA 480
 + +SM+ TRLALA IGKL F Q +EL+N N GLP + A +PSL+Y KG +I +A
 Sbjct: 409 PIGVSMDNTRLALASIGKLMFAQFSELVNDYNNGLPLNLTAGRNPSLDYGLKGAEIAMA 468

Query: 481 AYASELGHLANPVTTTFVQPAEMGNQAVNSLALISARRTAEANDVLSLLLASHLYCTLQAV 540
 +Y SEL LANPVT VQ AE NQ VNSL LISAR+TAEA D+L L+ +++L QA+
 Sbjct: 469 SYCSELQFLANPVTNHVQSAEQHNQDVNSLGLISARKTAEAVDILKLMSSSTYLVALCQAI 528

Query: 541 DLRAELDFKKQFDPLLPDLLQHLGTGLDVNALALEVKKALNKRLEQTT-----TYDL 594
 DLR +E + K + + ++ L G + L + K L Q TY
 Sbjct: 529 DLRLHEENLKNVKNVTSQVAKKTLAMGANGE---LHPARFCEKELLQVVEREYLFYAD 585

Query: 595 EPRWHDAF--SYATGTVVELLSSSPSANVTLTAVNAWKVASAEKAIS--LTREVRN-RFW 649
 +P F +V+ + + L + K+ + E + L +EV + R
 Sbjct: 586 DPCSSTYFLMQKLRLQVLVDHAMKNGESEKLNSSSIFQKIVAFEDELKAVLPKEVESARAV 645

Query: 650 QTPSSQAPAHAYLSPRTRVLYSFVREELGVQARRGDVFGVQVQETIGSNVSRIYEAIKDG 709
 + A + R+ LY VR+E+G ++ G + + G + +++ A +G
 Sbjct: 646 VESGNPAIPNRITECRSYPLRLVRQEVGT-----ELLTGEKVRSPGEEIDKVFTAFENG 700

Query: 710 RINHVLVKML 719
 +I L++ L
 Sbjct: 701 QIIDPLLECL 710

☐ >gi|5332353|gb|AAA34179.2| phenylalanine ammonia lyase [*Lycopersicon esculentum*]
 Length = 704

Score = 335 bits (858), Expect = 4e-90

Identities = 237/688 (34%), Positives = 355/688 (51%), Gaps = 33/688 (4%)

Query: 48 QSQLEIVQELLSDPTDDVVELSGYSLTXXXXXXXXXXXXXXXXX---QNDDEIRARVDKSV 104
 QS L+ V++++ + +V+L G +L+ + + RA V S
 Sbjct: 23 QSHLDEVKKMVEFRKPIVKLGGETLSVAQVASIANVDDKSNGVKVELSESARAGVKASS 82

Query: 105 DFLKAQLQNSV--YGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPTSVSSFSVGRGL 162
 D++ + YGVT GFG ++ RT++ +LQK LI GV + SF
 Sbjct: 83 DWVMSMSKGTDSYGVTAGFGATSHRRTKNGGALQKELIRFLNAGVFGNGIESF----- 136

Query: 163 ENTLPLEVVRGAMVIRVNSLTRGHSVRLVVLEALTNFLNHRITPIVPLRGSISASGDL 222
 +TLP R AM++R+N+L +G+S +R +LEA+T +N ITP +PLRG+I+ASGDL
 Sbjct: 137 -HTLPHSATRAAMLVRINTLLQGYSGIRFEILEAITKLINSNITPCLPLRGITITASGDLV 195

Query: 223 PLSYIAGAITGHPDVKVHVLHEGTEKIMFAREAI SLFGLEA--VVLGPKEGLGLVNGTAV 280
 PLSYIAG +TG P+ K + EK+ A EA + G+ L PKEGL LVNGTAV
 Sbjct: 196 PLSYIAGLLTGRPNKA--VGPNGEKLN-AEEAF CVAGISGGFFELQPKEGLALVNGTAV 252

Query: 281 SASMATXXXXXXXXXXXXXXXXXXXXXVEAMVGQGSFAPFIH DVC RPHPGQVEVARNIRT 340
 ++MA+ E M G+ F ++ + HPGQ+E A +
 Sbjct: 253 GSAMASIVLFESNIFAVMSEVLSAIFTEVMNGKP-EFTDYLTHKLKHHHPGQIEAAAIM E H 311

Query: 341 LLSGSSFAXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTT 400
 +L GSS+ +QDRY LRTSPQ+LGP +E + A + E N+
 Sbjct: 312 ILDGSSYVKVAQKLHEMDPLQKP-KQDRYALRTSPQWLGPQIEVIRAATKMIEREINSVN 370

Query: 401 DNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRLPSC 460
 DNPL+DV + HGGNFQ + + +SM+ TRLALA IGKL F Q +EL+N N GLPS
 Sbjct: 371 DNPLIDVSRNKALHGGNFQGTPIGVSM D NTRLALASIGKLMFAQFSELVNDYYNGLPSN 430

Query: 461 L-AAEDPSLNYHGKGLDIHIAAYASELGH LANPV TTFVQPAEMGNQAVNSLALISARRTA 519
 L A +PSL+Y KG +I +A+Y SEL LANPVT VQ AE NQ VNSL LISAR+TA
 Sbjct: 431 LTAGRNP SLDYGFKGAEIAMASYCSELQFLANPVTNHVQSAEQHNQDVNSLGLISARKTA 490

Query: 520 EANDVLSLLLASHLYCTLQAVDLRAMELDFKKQFDP L LPTLLQQHL--GTGLDVNALALE 577
 +A D+L ++ +++L QA+DLR +E + K + + ++ L G +++
 Sbjct: 491 KAVDILKIMSSTYLVALCQAIDLRHLEENLKS VVKNTV S QVAKRTLTMGANGELH PARFS 550

Query: 578 VKKALN-KRLEQTTTYDLEP--RWHDAFSYATGT VVELLS SPSANVT LTAVNAWKVASA 634
 K+ L E Y +P + +V+ + + + + K+ +
 Sbjct: 551 EKELLRVVDREYLFAYADDP CSSNYPLMQKL RQVLVDQAMKNGESEKNVNSSIFQKIGAF 610

Query: 635 EKAI--SLTREVRN-RFWQTPSSQAPAHAYLS PRTRVLYSFVREELGVQARRGDV FVG VQ 691
 E + L +EV + R + + R+ LY VREELG ++ G +
 Sbjct: 611 EDELI AVL PKEVESVR AVFESGNPLIRNRIT ECRSYPLYRLVREELGT-----ELLTGEK 665

Query: 692 QETIGSNVSRIYEAIKDGRINHVLVKML 719
 + G + +++ AI +G+I L++ L
 Sbjct: 666 VRSPGEEIDKVFTAICNGQIIDPLECL 693

☐ >gi|58618156|gb|AAW80644.1| phenylalanine ammonia lyase [Pteridium aquilinum]
 Length = 678

Score = 335 bits (858), Expect = 4e-90

Identities = 238/686 (34%), Positives = 358/686 (52%), Gaps = 36/686 (5%)

Query: 49 SQLEIVQELLS DPTD-DVVELSGYSLTXXXXXXXXXXXXXXXXXQNDDEIRARVDKSVDFL 107
 S L+ +++++S T + +++ G +LT ++ + RVD+S ++
 Sbjct: 3 SFLDDIKQMISTFTAEE LKIEGKTLTVAEVA AFARSKEMVLC LDEAAAKQRVDESALWV 62

Query: 108 KAQLQNS--VYGVTTFGG SADRTE DAVSLQKALIEHQ LCGVTP TSVSSFSVGRGLENT 165
 + ++ VYGVTTG+G ++ RT + LQ+ LI G+ G+ N
 Sbjct: 63 QNKIMKGCDVYGVT TGYGATSHRR TNQID LQRELIRFLNAGI-----FGKSQANA 113

Query: 166 LPLEVVRGAMVIRVNSLTRGHS AVRLV VLEALTNFLNHRITPIVPLRGSISASGDL SPLS 225
 LPL+ R A+++R N+L +G+S +R +L+ + LN ITP++PLRG+I+ASGDL PLS
 Sbjct: 114 LPLDAARA AVLVRTNTLMQGYSGIRWEILQTIEKLLNANITPLLPLRG TITASGDLVPLS 173

Query: 226 YIAGAITGHPDVKVHVLHEGTEKIMFAREAI SLFGLEAVV-LGPKEGLGLVNGTAVSASM 284
 Y+AG +TG P+ K V EG K++ EA+ + G+E L PKEGL +VNGTAV A +
 Sbjct: 174 YLAGVLTGRPNKA-VTAEG--KVVSGAEALKMVGVEKPFELQPKEGLAIVNGTAVGAGL 230

Query: 285 ATXXXXXXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQVEVARNIRTLTLLSG 344
 A+ E M G+ P H + + HPGQ+E A + LL G
 Sbjct: 231 ASMVCFDAHILALLSVVTSAMFCEVMQGKPEFTDPLTHRL-KHHPGQIEAAAAAMEYLLG 289

Query: 345 SSFAXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTDNPL 404
 S+ +QDRY LRTSPQ+LGP +E + A + E N+ DNP+
 Sbjct: 290 SALVKAASKLHGVDAKKP-KQDRYALRTSPQWLGPQIEVIRFATQLIQREINSVNDNPI 348

Query: 405 LDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCLA- 463
 +DV HGGNFQ + + +M+ RLALA IGKL F Q +EL+N N GLPS L+A
 Sbjct: 349 IDVSRDLALHGGNFQGTPIGTAMDNIRLALAAIGKLMFAQFSELVNDFYNNGLPSNLSAG 408

Query: 464 EDPSLNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVNSLALISARRTAEAND 523
 +PSL+Y KG +I +A+Y SEL +LANPVT VQ AE NQ VNSL LISAR+TAEA +
 Sbjct: 409 PNPSLDYGLKGGEIAMASYTSELEYLANPVTNHVQSAEQHNQDVNSLGLISARKTAEAVE 468

Query: 524 VLSLLASHLYCTLQAVDLRAMELDFKKQFDPLLPTLLQQHLGTGLDVNALALE-VKKAL 582
 VL L+ A++L QA+DLR +E + + ++ ++ L TG + LA +K L
 Sbjct: 469 VLKLMCATYLVGICQAIDLRHLEENLQAAVKQVVSQAACKTLTTGGNGVLLAARFCEKDL 528

Query: 583 NKRL--EQTTTYDLEP--RWHDAFSYATGTVVELLSSSPS-----ANVTLTAVNAWKVAS 633
 + + E TY +P + +VE +PS A +T + ++
 Sbjct: 529 LQVVDNEHVFTYADDPVSPGYPLMQRLRQVLVEHAIKNPSNERDEATSVMTRIPLFEDEL 588

Query: 634 AEKAISLTREVRNRFWQTPSSQAPAHAYLSRTRVLYSFVREELGVQARRGDVFGVQOE 693
 + + VR F A R+ LY FVR +LG Q + G + +
 Sbjct: 589 HSQPAELNVNRASF--DKGCPPIASKVEECRSFPLYQFVRAQLGTQ-----LLAGTRNQ 641

Query: 694 TIGSNVSRIYEAIKDGRINHVLVKML 719
 + G + +++AI DG + L++ L
 Sbjct: 642 SPGQDFEVVFDASDGLLMCPPLLQCL 667

☐ >gi|1483610|emb|CAA68036.1| phenylalanine ammonia-lyase [Triticum aestivum]
 gi|3024363|sp|Q43210|PALY_WHEAT Phenylalanine ammonia-lyase
 Length = 700

Score = 334 bits (857), Expect = 5e-90

Identities = 239/693 (34%), Positives = 348/693 (50%), Gaps = 36/693 (5%)

Query: 43 GHAAHQ---SQLEIVQELLSDPTDDVVELSGYSLTXXXXXXXXXXXXXXXXXQNDDEIRAR 99
 G AA + S LE V+ ++ + VV + G T + D+ R R
 Sbjct: 17 GKAAEELSGSHLEAVKRMVEEYRKPVVTMEG--ATTIAMVAAVAAGSDTRVELDESARGR 74

Query: 100 VDKSVDFLKAQLQNSV--YGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPTSVSSFS 157
 V +S D++ + N YGVTTGFG ++ RT++ +LQ+ LI G T
 Sbjct: 75 VKESSDWVMNSMMNGTDSYGVTTGFGATSHRRTKEGGALQRELIRFLNAGAFGTGTDG-- 132

Query: 158 VGRGLENLPLEVVVRGAMVIRVNSLTRGHSVRLVLEALTNFLNHRITPIVPLRGSISA 217
 + LP R AM++RVN+L +G+S +R +LE + LN +TP +PLRG+I+A
 Sbjct: 133 -----HVLPAATRAAMLVRVNTLLQGYSGIRFEILETIATLLNANVTPCLPLRGTTITA 186

Query: 218 SGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEA--VVLGPKEGLGLV 275
 SGDL PLSYIAG +TG P+ + +G++ + A EA + G++ L PKEGL +V
 Sbjct: 187 SGDLVPLSYIAGLVTGRPN-SMATAPDGSK--VNAAEAFKIAGIQHGFFELQPKEGLAMV 243

Query: 276 NGTAVSASMATXXXXXXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQVEVA 335
 NGTAV + +A+ E M G+ F + + HPGQ+E A
 Sbjct: 244 NGTAVGSGLASMVLFEANVLSLLAEVLSGVFCEVMNGKP-EFTDHLTHKLKHHPGQIEAA 302

Query: 336 RNIRTLGSSSFAXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLE 395
 + +L GSS+ +QDRY LRTSPQ+LGP +E + A ++ E
 Sbjct: 303 AIMEHILEGSSYMLAKKLGEIDPLMKP-KQDRYALRTSPQWLGPQIEVIRAATKSIERE 361

Query: 396 NNTTTDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNR 455
 N+ DNPL+DV + HGGNFQ + + +SM+ TRLA+A IGKL F Q +EL+N N
 Sbjct: 362 INSVDNPLIDVSRGKAIHGGNFQGTPIGVSMNTRLAIAAIGKLMFAQFSELVNDFFYN 421

Query: 456 GLPSCLA-AEDPSLNYHGKGLDIHIAAYASELGHLANPVTTTFVQPAEMGNQAVNSLALIS 514
 GLPS L+ +PSL+Y KG +I +A+Y SEL L NPVT VQ AE NQ VNSL LIS
 Sbjct: 422 GLPSNLGGRNPSSLDYGFKAIEAMASYCSELQFLGNPVTNHVQSAEQHNQDVNSLGLIS 481

Query: 515 ARRTAEANDVLSLLASHLYCTLQAVDLRAMELDFKKQFDPLLPTLLQQHLGT---GLDV 571
 +R+TAEA D+L L+ ++ L QA+DLR +E + K + T+ ++ L T G
 Sbjct: 482 SRKTAEADILKLMSSSTFLVALCQAIDLRHLEENVKNAVKSCVKTVARCTLSTDNNGHLH 541

Query: 572 NALALEVKKALNKRLEQTTTYDLEP--RWHDAFSYATGTVVE--LLSSSPSANVTLTAVN 627
 NA E L E Y +P + +VE L + A+V +
 Sbjct: 542 NARFCEKDLLLTIDREAVFAYADDPSCANYPLMQMRAVLVEHALANGEAEAHVETSVFA 601

Query: 628 AWKVASAEKAISLTREVR-NRFWQTPSSQAPAHAYLSPRTRVLYSFVREELGVQARRGDV 686
 + E L +EV R + A + R+ LY FVR+ELG +
 Sbjct: 602 KLAMFEQELRAVLPKEVEAARS AVENGTAQQNRIAECRSYPLYRFVRKELGT-----EY 656

Query: 687 FVGVOQETIGSNVSRIYEAIKDGRINHVLVKML 719
 G + + G V +++ A+ G+ L++ L
 Sbjct: 657 LTGEKTRSPGEEVDKVFVAMNQGHIDALLECL 689

☐ >gi|58618138|gb|AAW80635.1| phenylalanine ammonia lyase [Huperzia lucidula]
 Length = 668

Score = 334 bits (857), Expect = 5e-90

Identities = 233/673 (34%), Positives = 344/673 (51%), Gaps = 46/673 (6%)

Query: 66 VELSGYSLTXXXXXXXXXXXXXXXXXQNDDEIRARVDKSVDLKAQLQNSV--YGVTTGFG 123
 V + G LT + + RVD+S +++ + YGVTTGFG
 Sbjct: 14 VSIRGAELTVAQVAARIARREGVSVCLDASAAKKRVDSSNWVMQNMVMTGTDTYGVTTGFG 73

Query: 124 GSADTRTEDAVSLQKALIEHQLCGVTPPTSVSSFSVGRGLE---NTLPLEVVRGAMVIRVN 180
 ++ RT V LQ+ LI G+ +G G + N LP R AM++R N
 Sbjct: 74 ATSHRRTNQGVQLQELIRFLNAGI-----IGVGADAGGNVLPSWATRAAMLVRTN 124

Query: 181 SLTRGHSVRLVLEALTNFLNHRITPIVPLRGSIASGDLSPLSYIAGAITGHPDVKVH 240
 +L +G+S +R +LE L LN RITP VPLRG+I+ASGDL PLSYIAG ITG + +
 Sbjct: 125 TLMQGYSGIRWEILETLAKLLNARITPKVPLRGITASGDLVPLSYIAGLITGRKNARAV 184

Query: 241 VLHEGTEKIMFAEAI SLFGL-EAVVLGPKEGLGLVNGTAVSASMATXXXXXXXXXXXXX 299
 V G ++ + A EA+ + G+ +A VL PKEGL +VNGT+V A +A
 Sbjct: 185 V---GVDREVAEEAMKMVGVSQAFVLQPKGLAMVNGTSVGAGVAAIVCYDANVLAVFA 241

Query: 300 XXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQVEVARNIRTLGSSSFAXXXXXXXXXXXXX 359
 E M G+ P H + + HPGQ+E A + +L GSS+
 Sbjct: 242 VVASALFCEVMQKPEFSDPLTHKL-KHHPGQIEAAPAMEYILQGSSYMKAAAKMHETDP 300

Query: 360 XXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTDNPLLDVENKQTAHGGNFQ 419
 +QDRY LRTSPQ+LGP +E + A ++ E N+ DNPL+DV HGGNFQ
 Sbjct: 301 LKKP-KQDRYALRTSPQWLGPQIEVIRSATQSIQREINSVDNPLIDVSRDLALHGGNFQ 359

Query: 420 ASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCLA-AEDPSLNYHGKGLDIH 478
 + + +SM+ RLA+A IGKL F Q +EL+N N GLPS L+ +PSL+Y KG +I
 Sbjct: 360 GTPIGVSMNDLRLAIAAIGKLMFAQFSELVNDFYNNGLPSNLGGPNPSLDYGFKGAEIA 419

Query: 479 IAAYASELGHLANPVTTFVQPAEMGNQAVNSLALISARRTAEANDVLSLLLASHLYCTLQ 538
 +A+Y SEL LANPVT VQ AE NQ VNSL LISAR++AE+ ++L L+ +++L Q
 Sbjct: 420 MASYTSELQFLANPVTNHVQSAEQHNQDVNSLGLISARKSAESIEILKLMTSTYLVALCQ 479

Query: 539 AVDLRAMELDFKKQFDPLLPDLLQHLGTGLDVNALALEVKKALNKRLEQTTTYDLEPRW 598
 A+DLR +E + + ++ + ++ L TG D AL + K L + +
 Sbjct: 480 AIDLRHLEENMQAVVKQVSMVAKKTLATGADG---ALSPARFCEKDLLLLVDHQSFITY 536

Query: 599 HDAFSYATGTVVELL-----SSSPSANVTTLTAVNAWKVASAEKAIISLTREVRN 646
 D + AT +++ L + +P +T+ + + LTRE +
 Sbjct: 537 IDDPTSATYPLMQKLRQIMVEHALHDKADAPMIFNAITSFEDELKRHLQAEVLLTRENFD 596

Query: 647 RFWQTPSSQAPAHAYLSPRTRVLYSFVREELGVQARRGDVFGVQQTIGSNVSRIYEA 706
 + A + R+ LY FVR++L Q + +G + ++ G ++ AI
 Sbjct: 597 K-----GISAVRNRIQDCRSYPLYEFVRKDLDTQ-----MLIGTRIQSPGEVFETVFAAI 646

Query: 707 KDGRINHVLVKML 719
 +G++ L+K L
 Sbjct: 647 SEGKLVAPLLKCL 659

☐ >gi|5566388|gb|AAD45384.1| phenylalanine ammonia-lyase [Vigna unguiculata]
 Length = 655

Score = 333 bits (855), Expect = 9e-90

Identities = 223/632 (35%), Positives = 332/632 (52%), Gaps = 36/632 (5%)

Query: 95 EIRARVDKSVDFLKAQLQNSV--YGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPPTS 152
 E R V S D++ + YGVTTGFG ++ RT+ +LQ LI G+
 Sbjct: 24 ESRRGVKASSDWVIDSMSRGTD SYGVTTGFGATSHRRTKQGGALQNELIRFLNAGI---- 79

Query: 153 VSSFVSGRGLENTLPLEVVRGAMVIRVNSLTRGHSAVRLVLEALTNFLNHRITPIVPLR 212
 F G +TLP R AM++RVN+L +G+S +R ++EA+T FLNH ITP +PLR
 Sbjct: 80 ---FGNGTEASHTLPYSSTRAAMLVRVNTLLQGYSGIRFDIMEAITKFLNHNITPCLPLR 136

Query: 213 GSISASGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEA--VVLGPKE 270
 G+I+ASGDL PLSY+AG + G P+ K + G + + A++A L ++ L PKE
 Sbjct: 137 GTITASGDLVPLSYVAGLLIGRPNSK-SIGPNGED--LNAKDAFKLAEIDGGFFELQPKE 193

Query: 271 GLGLVNGTAVSASMATXXXXXXXXXXXXXXXXXXXXVEAMVGQQGSFAPFIHDVCRPHPG 330
 GL LVNGTAV + +A+ E M G+ F + + HPG
 Sbjct: 194 GLALVNGTAVGSLASIVLFEANLLVVLTEVLSAIFAEMVQGKP-EFTDHLTHKLKHHPG 252

Query: 331 QVEVARNIRTLLSGSSFAXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYS 390
 Q+E A + +L GSS+ +QDRY LRTSPQ+LGP +E + HA
 Sbjct: 253 QIEAAAIMEHILDGSSYIKEAQLHEIDPLQKP-KQDRYALRTSPQWLGPQIEVIRHATK 311

Query: 391 TLSLENNTTTDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLN 450
 + E N+ DNPL+DV + HGGNFQ + + +SM+ TRLA+A IGKL F Q +EL+N
 Sbjct: 312 MIEREINSVNDNPLIDVSRNKALHGGNFQGTPIGVSMNDNTRLAIASIGKLMFAQFSELVN 371

Query: 451 AAMNRGLPSCL-AAEDPSLNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVNS 509
 N GLPS L A +PSL+Y KG +I +A+Y SEL +LANPVT VQ AE NQ VNS
 Sbjct: 372 DFYNNGLPSNLTAGRNPSLDYGFKGAEIAMASYCSELQYLANPVTNHVQSAEQHNQDVNS 431

Query: 510 LALISARRTAEANDVLSLLLASHLYCTLQAVDLRAMELDFKKQFDPPLLPTLLQQHLGTGL 569
 L L+S+R+TAEA ++L L+ ++ L QA+DLR +E + K + + ++ L TG+
 Sbjct: 432 LGLVSSRKTAEEIILKLSSTFLVALCQAIDLRHLEENMKNAVKNVSVQAKRVLTGTI 491

Query: 570 DVNALALEVKKALNKRLEQTTTYDLEPRWHDASFYATGTVVELLS-----SPSA 619
 + L + K L + ++ + D T +++ L S A
 Sbjct: 492 NGE---LHPSRFCEKDLLKIVDHEYVFAYIDDPCSVTYPLMQKLRSVLVDHALQNGEKEA 548

Query: 620 NVTLTAVNAWKVASAEKAISLTREVRNRFWQTPSSQAPAHAYLSP-RTRVLYSFVREELG 678
 + + + + + E L +EV N + + + + R+ LY FVRE LG
 Sbjct: 549 SSSTSIFHKIRAFEEELITLLPKEVENARVEVENGNSSIPNRIKECRSYPLYKFVRESLG 608

Query: 679 VQARRGDVFGVQQETIGSNVSRIYEAIKDGR 710
 + G+ + ++ G +++ A+ +G+
 Sbjct: 609 TSLQYGE-----KVKSPGEECDKVFTALCEGK 635

☐ >gi|38103129|gb|EAA49872.1| ☒ hypothetical protein MG10036.4 [Magnaporthe grisea]
☒ gi|39966379|ref|XP_365191.1| ☒ hypothetical protein MG10036.4 [Magnaporthe grisea]
 Length = 626

Score = 333 bits (855), Expect = 9e-90

Identities = 200/476 (42%), Positives = 272/476 (57%), Gaps = 40/476 (8%)

Query: 115 VYGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPTS-----VSSFVGRGLEN----- 164
 +YGV TFGGSAD R++D +Q+ LI H CG+ + S S G N
 Sbjct: 79 IYGVNTGFGGSADARSDDLDRVQQILISHLTGCIISDAGNGGPKSDQSNQHAQNNGHSTQ 138

Query: 165 -----TLPLEVVRGAMVIRVNSLTRGHSVRLVLEALTNFLNHR 204
 +P R +M+IR+NSL G S +R+ + E+L N LN
 Sbjct: 139 SSEETKAIAPLPLTDALAATCMPESWARASMLIRLNSLAGGASGIRVELAESLVNLLNKD 198

Query: 205 ITPIVPLRGSISASGDLSPLSYIAGAITGHPDVKVHV-----LHEGTEKIMFAREAISLF 259
 + P +P+RGSISASGDLS L++IA + G + + ++ A A++
 Sbjct: 199 VVPRI PVRGSISASGDLSALAWIAALMQGKTSATAYSGPRDGQGKTARRVTRADVALADA 258

Query: 260 GLEAVVLGPKEGLGLVNGTAVSASMATXXXXXXXXXXXXXXXXXXXXVEAMVGQQGSFAP 319
 G+ + L KEGL +VNGTAVSA++A VEA+ G SF P
 Sbjct: 259 GISPITLHAKEGLAIVNGTAVSAVAALAAHESLHLAALSQVLTAMSVEALRGTDSEFDP 318

Query: 320 FIHDVCRPHPGQVEVARNIRTLLSGSSFAXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLG 379
 FI V R HPGQV+ ARNI+ ++GS LRQDRY +RT+ Q++G
 Sbjct: 319 FIGRV-RQHPGQVDSARNIKAFVAGSKLLKGPPTRGDGFT----LRQDRYSIRTASQWIG 373

Query: 380 PLVEDMMHAYSTLSLENNTTTDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGK 439
 P++ED AY L+ E N+ TDNPL+D + + HGGNFQA AV+ ++EK R L IG+
 Sbjct: 374 PVLEDFGLAYDQLTTELNSVTDNPLIDAASDRVLHGGNFQARAVTSAVEKLRQGLQSIGR 433

Query: 440 LNFTQCTELLNAAMNRGLPSCLAEDPSLNYHGKGLDIHIAAYASELGHLANPVTTTFVQP 499
 + FTQCTE++N A + GLP L ++DP+ ++ KGLD+ +AA SELG LANPV + VQ
 Sbjct: 434 MLFTQCTEMINPATSWGLPPNLCSDDPNDSFLFKGLDVVAALTSELGFLANPVGSHVQT 493

Query: 500 AEMGNQAVNSLALISARRTAEANDVLSLLLASHLYCTLQAVDLRAMELDFKKQFDP 555
 AEMGNQA+NSLAL+SAR T EA DVLS L A+HL QA+DLRA+E++ K+ P
 Sbjct: 494 AEMGNQAINSLALVSARYTLEAVDVLSQLAAHLLALCQALDLRAVEIEGKRVGSP 549

Score = 36.6 bits (83), Expect = 2.8

Identities = 33/115 (28%), Positives = 54/115 (46%), Gaps = 14/115 (12%)

Query: 618 SANVTLTAVNAWKVASAEKAI SLTREVRNRFWQTPSSQA---PAHAYLSPRTRVLYSFVR 674
SA TL AV+ +A ++L + + R + + A YL R +Y FVR

Sbjct: 508 SARYTLEAVDVLSQLAAAHLLALCQALDLRAVEIEGKRVGSPDATKYLGRAARMYRFVR 567

Query: 675 EELGVQARRGDVFGVQQETIGS---NVS-----RIYEAIKDGRINHVLVKML 719

+LG+ G+ + +G+ NVS R+YE+I+ GR+ V+V+ L

Sbjct: 568 HDLGIPFL-GERHLASSYGQVGATANVSPSMGLYNTRVYESIRSGRLYQVVVECL 621

☐ >gi|29367609|gb|AA072666.1| phenylalanine ammonia-lyase [Oryza sativa (japonica
cultivar-group)]
Length = 671

Score = 333 bits (855), Expect = 9e-90

Identities = 240/682 (35%), Positives = 366/682 (53%), Gaps = 41/682 (6%)

Query: 57 LLSDPD VVELSGYSLTXXXXXXXXXXXXXXXXXX--QNDDEIRARVDKSVDFLKAQLQNS 114
+++ + VV++ G SL + D+E R RV S +++ + +

Sbjct: 1 MVAQSREAVVKIEGSSLRVGQVA AVSAAKDASGVVVELDEEARPRVKASSEWILNCIAHG 60

Query: 115 --VYGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPTSVSSFSVGRGLE-NTLPLEVV 171
+YGVTTGFGG++ RT+D +LQ L+ H G+ G G + N+LP EV

Sbjct: 61 GDIYGVTTGFGGTSHRRTKDGQALQVELLRHLNAGI-----FGNGSDGNSLPSEVS 111

Query: 172 RGAMVIRVNSLTRGHSAVRLVLEALTNFLNHRITPIVPLRGSISASGDLSPLSYIAGAI 231
R AM++R+N+L +G+S +R +LEA+T +N ++P +PLRG+I+ASGDL PLSYIAG I

Sbjct: 112 RAAMLVRINTLLQGYSGIRFEILEAITKLINTGVSPCLPLRGITITASGDLVPLSYIAGLI 171

Query: 232 TGHPDVKVHVLHEGTEKIMFAREAI SLFGLEAVV--LGPKEGLGLVNGTAVSASMATXXX 289
TG P+ + V +G K + A EA + G++ L PKEGL +VNGT+V +++A

Sbjct: 172 TGRPNAQA-VTVDG--KKVDAAEFKIAGIQGGFFRLEPKEGLAIVNGTSVGSALAAMVL 228

Query: 290 XXXXXXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGSSFAX 349
E M G+ H + + HPG +E A + +L+GS+F

Sbjct: 229 YDANVLAVLSEVLSAVFCEVMNGKPEYTDHLTHKL-KHHPGSIEAAAIMEHILAGSAFMP 287

Query: 350 XXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTDNPLLDVEN 409
+QDRY LRTSPQ+LGP +E + A ++ E N+ DNP++DV

Sbjct: 288 HAQKVNEVDPLLKP-KQDRYALRTSPQWLGPQIEVIRAATKSIEREVNSVNDNPVIDVHR 346

Query: 410 KQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCLA-AEDPSL 468
+ HGGNFQ + + +SM+ TRLA+A IGKL F Q +EL+N N GL S LA + +PSL

Sbjct: 347 GKALHGGNFQGTPIGVSMDNTRLAIANIGKLMFAQFSELVNEFYNNGLTSNLAGSRNPSL 406

Query: 469 NYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVNSLALISARRTAEANDVLSLL 528
+Y KG +I +A+Y SEL LANPVT VQ AE NQ VNSL L+SAR+TAEA D+L L+

Sbjct: 407 DYGFKGTEIAMASYCSELQFLANPVTNHVQSAEQHNQDVNSLGLVSARKTAEAVDILKLM 466

Query: 529 LASHLYCTLQAVDLRAMELDFKKQFDPLLPTLLQQHLGTGLDVNAL--ALEVKKALNKRL 586
+++L QAVDLR +E + K + T+ ++ L TG L A +KAL +

Sbjct: 467 SSTYLVALCQAVDLRHLEENLKS AVKNCVTTVAKKVLTTG- PAGGLHSARFSEKALLTAI 525

Query: 587 EQTTTYDLEPRWHDFAFSYATGT-----VVELLSSSPSANVTLTAVNAWKVASAEKAI-- 638
++ Y A +Y T V L++ P+ ++V + K+ + E+ +

Sbjct: 526 DREAVYSYADDPCSA-NYPLMTKIRAVLVEHALANGPAEKDDGSSVFS-KITAFEEELRE 583

Query: 639 SLTREVRNRFWQTPSSQAP-AHAYLSPRTRVLYSFVREELGVQARRGDVFGVQQETIGS 697
 +L RE+ + AP + R+ LY FVREELG G + ++ G
 Sbjct: 584 ALPREMEAARVAFETGTAPITNRIKESRSFPLYRFVREELGCV-----YLTGEKCLKSPGE 638

Query: 698 NVSRIYEAIKDGRINHVLVKML 719
 +++++ AI + ++ +++ L
 Sbjct: 639 ECKNVFLAISERKLIDPMLLECL 660

☐ >gi|400726|sp|P31426|PAL2_SOLTU Phenylalanine ammonia-lyase 2
 Length = 590

Score = 333 bits (853), Expect = 1e-89
 Identities = 207/510 (40%), Positives = 290/510 (56%), Gaps = 20/510 (3%)

Query: 49 SQLEIVQELLSIPTDDVVELSGYSLTXXXXXXXXXXXXXXXXX---QNDDEIRARVDKSVD 105
 S+L+ V++++ + +V+L G +LT + + RA V S D
 Sbjct: 43 SKLDQVKKMVDEFKPIVKGGETLTVAQVASIANVDNKSNGVRVELSESARAGVKASSD 102

Query: 106 FLKAQLQNSV--YGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPTSVSSFSVGRGLE 163
 ++ + YGVTTGFG ++ RT++ +LQK LI GV F +G
 Sbjct: 103 WVMDSMSKGTDSYGVTTGFGATSHRRTKNGGTLQKNLIRFLNAGV-----FGIGTEST 155

Query: 164 NTLPLEVVRGAMVIRVNSLTRGHSVRLVLEALTNFLNHRITPIVPLRGSISASGDLSP 223
 +TLP R AM++R+N+L +G+S +R +LEA+T +N I+P +PLRG+++ASGDL P
 Sbjct: 156 HTLPHSATRAAMLVRINTLLQGYSGIRFEILEAITKLINSNISPCPLRGTVTASGDLVP 215

Query: 224 LSYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEA--VVLGPKEGLGLVNGTAVS 281
 LSYIAG +TG P+ K V G++ + A EA + G+ L PKEGL LVNGTAV
 Sbjct: 216 LSYIAGLLTGRPNKA-VGPTGSK--LDAAEAFRVAGVTGGFFELQPKEGLALVNGTAVG 272

Query: 282 ASMATXXXXXXXXXXXXXXXXXXXXXVEAMVGQQGSFAPFIHDVCRPHPGQVEVARNIRTL 341
 ++MA+ E M G+ F ++ + HPGQ+E A + +
 Sbjct: 273 SAMASIVLFESNILAVMFVLSAIFAEVMNGKP-EFTDYLTHKLKHHPGQIEAAIMEHI 331

Query: 342 LSGSSFAXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTD 401
 L GSS+ +QDRY LRTSPQ+LGP +E + A + E N+ D
 Sbjct: 332 LDGSSYVKAQKLHEMDPLQKP-KQDRYALRTSPQWLGPQIEVIRAATKMIEREINSVND 390

Query: 402 NPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCL 461
 NPL+DV + HGGNFQ + + +SM+ TRLALA IGKL F Q +EL+N N GLPS L
 Sbjct: 391 NPLIDVSRNKAIHGGNFQGTPIGVSMNTRLALASIGKLMFAQFSELVNDYYNNGLP SNL 450

Query: 462 -AAEDPSLNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVNSLALISARRTAE 520
 A +PSL+Y KG +I +A+Y SEL LANPVT VQ AE NQ VNSL LISAR+TAE
 Sbjct: 451 TAGRNPSLDYGFKAIEAMASYCSELQFLANPVTNHVQSAEQHNQDVNSLGLISARKTAE 510

Query: 521 ANDVLSLLLASHLYCTLQAVDLRAMELDFK 550
 A D+L L+ +++L QA+DLR +E + K
 Sbjct: 511 AVDILKLMSSSTYLVALCQAIDLRHLEENLK 540

☐ >gi|4808128|emb|CAB42794.1| phenylalanine-ammonia lyase [Citrus clementina x Cit
 Length = 718

Score = 333 bits (853), Expect = 1e-89

Identities = 237/685 (34%), Positives = 348/685 (50%), Gaps = 36/685 (5%)

Query: 49 SQLEIVQELLSDPTDDVVELSGYSLTXXXXXXXXXXXXXXXXXXXXQNDDEIRARVDKSVDFLK 108
S LE V+ ++++ VV L G +LT + + R V S D++
Sbjct: 45 SHLEEVKRMVAEYRKPVVNLGGETLTVAQVAAIATSSSTNV--ELSESAREGVKASSDWVM 102

Query: 109 AQLQNSV--YGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPTSVSSFSVGRGLENLTL 166
+ YGVTTGFG ++ T++ +LQK LI+ G+ F G +TL
Sbjct: 103 ESMNKGTDSDYGVTTGFGATSHRTTKNGGALQKELIKFLNAGI-----FGNGTKSSHTL 155

Query: 167 PLEVVRGAMVIRVNSLTRGHSAVRLVVLEALTNFLNHRITPIVPLRGSISASGDLSPLSY 226
P R AM++RVN+L +G+S +R +L+A+T LNH ITP +PLRG+I+ASGDL PLSY
Sbjct: 156 PHSATRAAMLVRVNTLLQGYSGIRFEILKAITKLLNHNITPCLPLRGTITASGDLVPLSY 215

Query: 227 IAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEAVVLGPKEGLGLVNGTAVSASMAT 286
IAG +TG P+ K +I+ +EA G L PKEGL LVNGTAV + +A+
Sbjct: 216 IAGLLTGRPNKAT---GPNGQIIDPQEASKPAGFGFFELQPKEGLALVNGTAVGSGLAS 272

Query: 287 XXXXXXXXXXXXXXXXXXXXXVEAMVGQQGSFAPFIHDVCRPHPGQVEARNIRTLLSGSS 346
E M G+ F + + HPGQ+E A + +L GSS
Sbjct: 273 MVLFEANNLALLSEILSAIFAEVMQGKP-EFTDHLTHKLKHPGQIEAAAIMEHILDGSS 331

Query: 347 FAXXXXXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTDNPLLD 406
+ +QDRY LRTSPQ+LGP +E + A ++ E N+ DNPL+D
Sbjct: 332 YVNVAKKLHEIDPLQKP-KQDRYALRTSPQWLGPQIEMIRFATKSIEREINSVNDNPLID 390

Query: 407 VENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRLPSCLA-AED 465
V + HGGNFQ + + +SM+ TRLA+A IGKL F Q +EL+N N GLPS L+ +
Sbjct: 391 VSRNKALHGGNFQGTPIGVSMDNTRLAIAAIGKLMFAQFSELVNDFYNNGLPSNLSGGRN 450

Query: 466 PSLNYHGKGLDIHIAAYASELGHLANPVTTFFVQPAEMGNQAVNSLALISARRTAEANDVL 525
PSL+Y KG +I +A+Y SEL LANPVT V AE NQ VNSL LIS+R+TAEA D+L
Sbjct: 451 PSLDYGFKGAEIAMASYCSELQFLANPVTNVHVSAAEQHNQDVNSLGLISSRKTAEAVIDIL 510

Query: 526 SLLLASHLYCTLQAVDLRAMELDFKKQFDPLLPTLLQQHLGTGLD-----VNALALEVKK 580
L+ ++ L QA+DLR +E + K + + ++ L G ++ K
Sbjct: 511 KLMSSTFLVALCQAIDLRHLEENLKHTVKNTVSQVAKKVLTVGASGELHPSRFCEKDLLK 570

Query: 581 ALNKRLEQTTTYDLEP--RWHDAFSYATGTVVELLSSSPSANVTLTAVNAWKVASAEKAI 638
A ++ E Y +P + +VE ++ T + K+A+ E+ +
Sbjct: 571 AADR--EHVFAYIDDPSCATYPLMQKLRQVLVEHALNNGENEKTANSSIFQKIAAFEEEL 628

Query: 639 S--LTREVRNRFWQTPSSQAPA--HAYLSPRTRVLYSFVREELGVQARRGDVFGVQOQET 694
L +EV N QT + +P + R+ LY VRE LG + G + +
Sbjct: 629 KTVLPKEVENA-RQTVENGSPPTIPNRIKECRSYPLYRLVREGLG-----SNFLTGEKVTS 682

Query: 695 IGSNVSRIYEAIKDGRINHLVKML 719
G +++ A+ G+I +++ L
Sbjct: 683 PGEEFDKVFTAMCQGKIIDPMLECL 707

☐ >gi|548454|sp|P35511|PAL1_LYCES Phenylalanine ammonia-lyase (PAL)
Length = 704

Score = 333 bits (853), Expect = 1e-89

Identities = 236/687 (34%), Positives = 354/687 (51%), Gaps = 33/687 (4%)

Query: 49 SQLEIVQELLSDPTDDVVELSGYSLTXXXXXXXXXXXXXXXXXXXX--QNDDEIRARVDKSVDFLK 105
S L+ V++++ + +V+L G +L+ + + RA V S D

Sbjct: 24 SHLDEVKKMVDEFKPIVKLGGETLSVAQVASIANVDDKSNGVKVELSESARAGVKASSD 83

Query: 106 FLKAQLQNSV--YGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPPTSVSFSVGRGLE 163
 ++ + YGVTT GFG ++ RT++ +LQK LI GV + SF

Sbjct: 84 WMDSMSKGTDSYGVVTAGFGATSHRRRTKNGGALQKELIRFLNAGVFGNGIESF----- 136

Query: 164 NTLPLEVVVRGAMVIRVNSLTRGHSVAVRLVVLEALTNFLNHRITPIVPLRGSISASGDLSP 223
 +TLP R AM++R+N+L +G+S +R +LEA+T +N ITP +PLRG+I+ASGDL P

Sbjct: 137 HTLPHSATRAAMLVRINTLLQGYSGIRFEILEAITKLINSNITPCLPLRGTTITASGDLVP 196

Query: 224 LSYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEA--VVLGPKEGLGLVNGTAVS 281
 LSYIAG +TG P+ K + EK+ A EA + G+ L PKEGL LVNGTAV

Sbjct: 197 LSYIAGLLTGRPNKA--VGPNGEKLN-AEEAFVAGISGGFFELQPKEGLALVNGTAVG 253

Query: 282 ASMATXXXXXXXXXXXXXXXXXXXXVEAMVGQQGSFAPFIHDVCRPHPGQVEVARNIRTL 341
 ++MA+ E M G+ F ++ + HPGQ+E A + +

Sbjct: 254 SAMASIVLFESNIFAVMSEVLSAIFTEVMNGKP-EFTDYLTHKLKHHPGQIEAAAIMEHI 312

Query: 342 LSGSSFAXXXXXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTDD 401
 L GSS+ +QDRY LRTSPQ+LGP +E + A + E N+ D

Sbjct: 313 LDGSSYVKVAQKLHEMDPLQKP-KQDRYALRTSPQWLGPQIEVIRAATKMIEREINSVND 371

Query: 402 NPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRLGPSCL 461
 NPL+DV + HGGNFQ + + +SM+ TRLALA IGKL F Q +EL+N N GLPS L

Sbjct: 372 NPLIDVSRNKALHGGNFQGTPIGVSMNTRLALASIGKLMFAQFSELVNDYNNGLPSNL 431

Query: 462 -AAEDPSLNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVNSLALISARRTAE 520
 A +PSL+Y KG +I +A+Y SEL LANPVT VQ AE NQ VNSL LISAR+TA+

Sbjct: 432 TAGRNPSLDYGFKAIEAMASYCSELQFLANPVTNHVQSAEQHNQDVNSLGLISARKTAK 491

Query: 521 ANDVLSLLLASHLYCTLQAVDLRAMELDFKKQFDPDLLPTLLQQHL--GTGLDVNALALEV 578
 A D+L ++ +++L QA+DLR +E + K + + ++ L G +++

Sbjct: 492 AVDILKIMSSTYLVALCQAIDLRHLEENLKSVVKNTVSQVAKRTLTMGANGELHPARFSE 551

Query: 579 KKALN-KRLEQTTTYDLEP--RWHDAFSYATGTVVELLSSSPSANVTLTAVNAWKVASAE 635
 K+ L E Y +P + +V+ + + + + K+ + E


Sbjct: 552 KELLRVVDREYLFAYADDPCCSSNYPLMQKLQVLVDQAMKNGESEKNVNSSIFQKIGAFE 611

Query: 636 KAI--SLTREVNR-RFWQTPSSQAPAHAYLSPRTRVLYSFVREELGVQARRGDVFGVQQ 692
 + L +EV + R + + R+ LY VREELG ++ G +

Sbjct: 612 DELIAVLPKEVESVRAVFESGNPLIRNRITECRSYPLYRLVREELGT-----ELLTGEKV 666

Query: 693 ETIGSNVSRIYEAIKDGRINHVLVKML 719
 + G + +++ AI +G+I L++ L

Sbjct: 667 RSPGEEIDKVFTAICNGQIIDPLECL 693

 >gi|2285893|dbj|BAA21643.1| phenylalanine ammonia-lyase [Populus kitakamiensis]
 Length = 715

Score = 333 bits (853), Expect = 1e-89

Identities = 248/740 (33%), Positives = 369/740 (49%), Gaps = 64/740 (8%)

Query: 8 LATTLANGFTNGSHAAPTKSAAGPTSALRRTP---GLDGHAHQSQLEIVQELLSDPTDD 64
 + T NG+ NGS + +R P G+ A S L+ V+ ++++

Sbjct: 1 METITKNQYQNGS-----SESICRQDPLSWGVAAEAMKGSLSHLDEVKRMVAEYRKP 51

Query: 65 VVELSGYSLTXXXXXXXXXXXXXXXXX-QNDDEIRARVDKSVDLKAQLQNSV--YGVTTG 121
 VV L+G +L + + R RV S D++ + YGVTTG

Sbjct: 52 VVNLAGQNLIIAQVASIAGHDASNVKVELSESARPRVKASSDWVMSMDKGTDSYGVTTG 111

Query: 122 FGGSADTRTEDAVSLQKALIEHQLCGVTPPTSVSSFSVGRGLENLPLEVVVRGAMVIRVNS 181
FG ++ RT+ +LQK LI G+ F G +TLP R AM++R+N+

Sbjct: 112 FGATSHRRTKQGGALQKELIRFLNAGI-----FGNGTETCHTLPHSATRAAMLVRINT 164

Query: 182 LTRGHSVRLVLEALTNFLNHRITPIVPLRGSISASGDLSPLSYIAGAITGHPDVKVHV 241
L +G+S +R +LEA+T LN+ ITP +PLRG+I+ASGDL PLSYIAG +TG P+ K

Sbjct: 165 LLQGYSGIRFEILEAITKLLNNNITPCLPLRGTTASGDLVPLSYIAGLLTGSPNSKAT- 223

Query: 242 LHEGTEKIMFAREAISLFGLEA--VVLGPKEGLLVNGTAVSASMATXXXXXXXXXXXXX 299
+++ A EA G+++ L PKEGL LVNGTAV + +A+

Sbjct: 224 --GPNGEVLDAVEAFKAAGIDSGFFELQPKGLLVNGTAVGSGLASMVLFTNLAVLS 281

Query: 300 XXXXXXVEAMVGQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGSSFAXXXXXXXXXXXXX 359
E M G+ F + + HPGQ+E A + +L GS++

Sbjct: 282 ELISAIFAEVMNGKP-EFTDHLTHKLKHHPGQIEAAIMEHILDGSAYMKAACKLHEMDP 340

Query: 360 XXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTNDPLLDVENKQTAHGGNFQ 419
+QDRY LRTSPQ+LGP +E + + + E N+ DNPL+DV + HGGNFQ

Sbjct: 341 LQKP-KQDRYALRTSPQWLGPQIEVIRFSTKSIEREINSVNDNPLIDVSRNKALHGGNFQ 399

Query: 420 ASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRLPSCL-AAEDPSLNYHGKGLDIH 478
+ + +SM+ RLA+A IGKL F Q +EL+N N GLPS L A+ +PSL+Y KG +I

Sbjct: 400 GTPIGVSMNVRLAIASIGKLLFAQFSELVNDFYNNGLPSNLTASRNPSLDYGFKGAIEA 459

Query: 479 IAAYASELGHLANPVTTFVQPAEMGNQAVNSLALISARRT-AEANDVLSLLLASHLYCTL 537
+A+Y SEL +LANPVT+ VQ AE NQ VNSL LIS+R+T +EA D+L L+ + L

Sbjct: 460 MASYCSELQYLANPVTSHVQSAEQHNQDVNSLGLISSRKTGSEAVDILKLMSTTFLVALC 519

Query: 538 QAVDLRAMELDFKKQFDPLLPTLLQQHLGTGLDVNALALEVKKALNKRLEQTTTYDLEPR 597
QAVDLR +E + + + + ++ L TG + L + K L + +

Sbjct: 520 QAVDLRHLEENLRSVKNVTVSHVSKRVLTTGANGE---LHPSRFCEKELLKVVDRE---- 572

Query: 598 WHDAFSYATG-----TVVELLSSSPSANVTLTAVNAWKVASAEKAIS--L 640
D F+YA V L++ + T+V K+A+ E + L

Sbjct: 573 --DVFAADDPCSATYPLMQKLRQVLVDHALANGENEKNASTSV-FQKIAAFEDELKALL 629

Query: 641 TREVRN-RFWQTPSSQAPAHAYLSPRTRVLYSFVREELGVQARRGDVFGVQQETIGSNV 699
+EV + R + A + R+ LY FVREELG + G + G

Sbjct: 630 PKEVESARAAYDSGNSAIENKIKECRSYPLYKFVREELGT-----GLLTGENVRSPGEEF 684

Query: 700 SRIYEAIKDGRINHVLVKML 719
+++ A+ G+I +++ L

Sbjct: 685 DKVFTAMCQGIIDPMLECL 704

☐ >gi|38569936|gb|AAR24505.1| phenylalanine ammonia-lyase [Bambusa oldhamii]
Length = 712

Score = 332 bits (852), Expect = 2e-89

Identities = 239/695 (34%), Positives = 360/695 (51%), Gaps = 37/695 (5%)

Query: 33 SALRRTPLDGHAAHQ---SQLEIVQELLSDPDDEVVELSGYSLTXXXXXXXXXXXXXXXXX 89
+A R P G AA + S L+ V+ ++++ VV++ G SL

Sbjct: 18 AAPRADPLNNGKAAEELMGSHLDEVKRMVAEYRQPVVKIEGASLRQAQVA AVAVAGDAKV 77

Query: 90 XQNDDEIRARVDKSVDFLKAQLQNSV--YGVTTGFGGSADTRTEDAVSLQKALIEHQLCG 147
+ D+ R RV S D++ + N YGVTTGFG ++ RT++ +LQ+ LI G

Sbjct: 78 -ELDESARERVKASSDWVMSMNGTDSYGVTTGFGATSHRRTKEGGALQRELIRFLNAG 136

Query: 148 VTPTSVSSFSVGRGLENLTPLLEVVRGAMVIRVNSLTRGHSAVRLVVLEALTNFLNHRITP 207
T + LP E R AM++R+N+L +G+S +R +LEA+T LN +TP

Sbjct: 137 AFGTGCDG-----HVLPAEATRAAMLVRINTLLQGYSIGIRFEILEAITKLLNANVTP 188

Query: 208 IVPLRGSISASGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEA--VV 265
+PLRG+++ASGDL PLSYIAG +TG + V V +G + + A EA + G++

Sbjct: 189 CLPLRGTVTASGDLVPLSYIAGLVTGREN-SVAVAPDGRK--VNAAEAFKIAGIQGGFFE 245

Query: 266 LGPKEGLGLVNGTAVSASMATXXXXXXXXXXXXXXXXXXXXVEAMVGQQGSFAPFIHDVC 325
L PKEGL +VNGTAV + +A+ E M G+ H +

Sbjct: 246 LQPKEGLAMVNGTAVGSGLASTVLFEANILAILAEVLSAVFCEVMNGKPEYTDHLTHKL- 304

Query: 326 RPHPGQVEVARNIRTLLSGSSFAXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDM 385
+ HPGQ+E A + +L GSS+ +QDRY LRTSPQ+LGP +E +

Sbjct: 305 KHHPGQIEAAAMEHILEGSSYMKLAKKLGDLDPLMKP-KQDRYALRTSPQWLGPQIEVI 363

Query: 386 MHAYSTLSLENNTTNDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQC 445
A ++ E N+ DNPL+DV + HGGNFQ + + +SM+ TRLA+A IGKL F Q

Sbjct: 364 RAATKSIEREINSVNDNPLIDVSRNKALHGGNFQGTPIGVSMDNTRLAIAAIGKLMFAQF 423

Query: 446 TELLNAAMNRGLPSCLA-AEDPSLNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGN 504
+EL+N N GLPS L+ +PSL+Y KG +I +A+Y SEL L NPVT VQ AE N

Sbjct: 424 SELVNDFYNNGLPSNLSSGRNPSLDYGFKGAEIAMASYCSELQFLGNPVTNHVQSAEQHN 483

Query: 505 QAVNSLALISARRTAEANDVLSLLASHLYCTLQAVDLRAMELDFKKQFDPPLLPTLLQQH 564
Q VNSL LIS+R+TAEA D+L ++ ++ L QA+DLR +E + K + T+ ++

Sbjct: 484 QDVNSLGLISSRKTAEAIDILKIMSSTFLVALCQAIDLRHIEENVKSAVKSCVMTVAKKT 543

Query: 565 LGTGLDVNA-LALEVKKALNKRLEQTTTY-----DLEPRWHDAFSYATGTVVELLSSSPS 618
T + +A +K L K +++ + P + + V L++ +

Sbjct: 544 PSTNSTGDLHVARFCEKDLLKEIDREAVFAYADDPSPNYPLMKKLRSVLVESALANGMA 603

Query: 619 ANVTLTAVNAWKVASAEKAI--SLTREVRNRFWQTPSSQAPAHAYLSP-RTRVLYSFVRE 675
T++ A +VA E+ + +L R V + A A ++ R+ LY FVRE

Sbjct: 604 EFNAETSIFA-RVALFEEELRAALPRAVEAARASVENGTAAAPNRITECRSYPLYRFVRE 662

Query: 676 ELGVQARRGDVFGVQQETIGSNVSRIYEAIKDG 710
ELG + G + + G +++ AI G+

Sbjct: 663 ELGT-----EYLTGEKTRSPGEELNKVLLAINQ GK 692

☐ >gi|58618152|gb|AAW80642.1| phenylalanine ammonia lyase [Ophioglossum reticulat
Length = 723

Score = 332 bits (852), Expect = 2e-89

Identities = 249/691 (36%), Positives = 362/691 (52%), Gaps = 45/691 (6%)

Query: 49 SQLEIVQELLSD--PTDDVVELSGYSLTXXXXXXXXXXXXXXXXXQNDDEIRARVDKSVDF 106
S E V++++ T+ VV + G SLT + ++RVD+S D+

Sbjct: 4 SHFEEVRQMIKQFYQTEKVV-IQSSSLTIGQVTAVTQKPLVKVELDAVVAKS RVDESFDW 62

Query: 107 LKAQLQNSV--YGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPTSVSSFSVGR-GLE 163
+ ++ YGVTTGFG ++ RT AV LQK LI GV +G+

Sbjct: 63 VSNNIRKGTDTYGVTTGFGATSHRRTNQAVELQKELIRFLNAGV-----IGKHDAL 113

Query: 164 NTLPLEVVRGAMVIRVNSLTRGHSAVRLVVLEALTNFLNHRITPIVPLRGSISASGDLSP 223
TLP V+ AM++R N+L +G+S +R +LEA+ +N + P +PLRG+I+ASGDL P

Sbjct: 114 TTLPPPFVKAAMLVRTNTLLQGYSGIRWEILEAMKKLMNANLLPRLPLRGTTITASGDLVP 173

Query: 224 LSYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGGL-EAVVLGPKEGLGLVNGTAVSA 282
 LSYIAG +TG P+ K + +G +++ + EA++L G+ E L PKEGL LVNGT+V A

Sbjct: 174 LSYIAGLLTGRPNKA-LAPDG--RLLTSTEALNLAGISEPFELQPKEGLALVNGTSVGA 230

Query: 283 SMATXXXXXXXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQVEVARNIRTLL 342
 ++A E M G+ P H + + HPGQ+E A + LL

Sbjct: 231 AVAANVCFDANILALLAEVLSALFCEVMQKGPEFADPLTHQL-KHHPGQIEAAAVMEFLL 289

Query: 343 SGSSFAXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTDN 402
 GSS+ +QDRY LRTSPQ+LGP +E + A ++ E N+ DN

Sbjct: 290 EGSSYMQAAAKLHETDPLSKP-KQDRYALRTSPQWLGPQIEVIRLATHSIEREINSVNDN 348

Query: 403 PLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRLPSCLA 462
 P++DV HGGNFQ + + +SM+ R+ALA IGKL F Q +EL+ N GLPS L+

Sbjct: 349 PIIDVSRDMALHGGNFQGTPIGVSMNMRIALAAIGKLLFAQFSELVCDYNYNCGLPNSLS 408

Query: 463 -AEDPSLNYHGKGLDIHIAAYASELGHLANPVTTTFVQPAEMGNQAVNSLALISARRTAEA 521
 DPSL+Y KG +I +AAY SEL +LANPVTT VQ AE NQ VNSL LI+AR+TAEA

Sbjct: 409 GGPDPPLDYGFKGAEIAMAAYCSELQYLANPVTTTHVQSAEQHNQDVNSLGLIAARKTAEA 468

Query: 522 NDVLSLLLASHLYCTLQAVDLRAMELDFKKQFDPLLPTLLQQHLGTGLDVNALALEVKKA 581
 ++L L+ A++L QA+DLR +E + + ++ + ++ L T N + L +

Sbjct: 469 VEILKLMFATYLVALCQAIDLRHLEENMQAVVKHVLEVAKKTLYT--SENGILLP-SRF 525

Query: 582 LNKRLQTTTTYDLEPRWHDFAFS---YA-----TGTVVELLSSSP--SANVTLTAVNAWKV 631
 K L Q + + DA S YA +V+ ++P + + V

Sbjct: 526 SEKELLQIVDHQPVFSYIDAPSNPCYALMVQLREVLVDQTLNTPEEESKDSPPMFRTIPV 585

Query: 632 ASAEKAISLTREV---RNRFWQTPSSQAPAHAYLSRTRVLYSFVREELGVQARRGDV FV 688
 E SL EV R RF A + + RT LY FVR ELG +G V

Sbjct: 586 FEEELKKSLEEVVKARQRF--DNGDYAVPNRIKNCRTYPLYKFVRSELGTCLLQGTV-- 641

Query: 689 GVQQETIGSNVSRIYEAIKDGRINHVLVKML 719
 + G ++ ++++AI +G++ L+K L

Sbjct: 642 ---PRSPGEDIEKVFDAILLEGKLVLP LLKCL 669

☐ >gi|14326459|gb|AAK60275.1| phenylalanine ammonia-lyase 2 [Manihot esculenta]
 Length = 712

Score = 332 bits (852), Expect = 2e-89

Identities = 243/720 (33%), Positives = 362/720 (50%), Gaps = 43/720 (5%)

Query: 8 LATTLANGFTNGSHAAPTKSAAGPTSALRRTPGLDGHAHQSQLEIVQELLSDPD VVE 67
 +AT NG NGS + +A P + GL + S L+ V+++++ +V+

Sbjct: 1 MATISQNGHQNGSLDSLCTARDPLNW-----GLAAESMSGSHLDEVKKMVAEFRKPLVK 54

Query: 68 LSGYSLTXXXXXXXXXXXXXXXXXQNDDEIRARVDKSVDLKAQLQNSV--YGVTTGFGGS 125
 L G +LT + + RA V S D++ + YGVTTGFG +

Sbjct: 55 LGGETLTVAQVAIARESGLQV-ELAESARAGVKASSDWMDSMSKGTDSYGVTTGFGAT 113

Query: 126 ADTRTEDAVSLQKALIEHQLCGVTPTSVSSFSVGRGLENLPLEVVRGAMVIRVNSLTRG 185
 + RT+ +LQ+ LI G+ S +TL R AM++R+N+L +G

Sbjct: 114 SHRRTKQGGALQRELIRFLNAGIFGNKTESC-----HTLSHSATRAAMLVRINTLLQG 166

Query: 186 HSAVRLVVLEALTNFLNHRITPIVPLRGSISASGDLSPLSYIAGAITGHPDVKVHVLHEG 245
 +S +R +LEA+T LNH ITP +PLRG+I+ASGDL PLSYIAG +TG P+ K V G

Sbjct: 167 YSGIRFEILEAITKLLNHNITPCLPLRGTTITASGDLVPLSYIAGLLTGRPNSKA-VGPNG 225

Query: 246 TEKIMFAREAISLFGLEA--VVLGPKEGLGLVNGTAVSASMATXXXXXXXXXXXXXXXXXXXX 303
+ A++A G+++ L PKEGL LVNGTAV + +A+

Sbjct: 226 ES--LDAQQAFHSAGIDSGFFELQPK EGLALVNGTAVGSGGLASMLFEANVLAVLSEVLS 283

Query: 304 XXXVEAMVGQQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGSSFAXXXXXXXXXXXXXXXXXXGI 363
E M G+ F + + HPGQ+E A + +L GSS+

Sbjct: 284 AIFAEVMNGKP-EFTDHLTHKLKHHPGQIEAAAIMEHILDGSSYIKAAKKLHEIDPLQKP 342

Query: 364 LRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTNDNPLLDVENKQTAHGGNFQASAV 423
+QDRY LRTSPQ+LGP +E + + ++ E N+ DNPL+DV + HGGNFQ + +

Sbjct: 343 -KQDRYALRTSPQWLGPQIEVIRFSTKSIEREINSVNDNPLIDVSRNKALHGGNFQGTPI 401

Query: 424 SISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCL-AAEDPSLNYHGKGLDIHIAAY 482
+SM+ RLA+A IGKL F Q +EL+N N GLPS L A+ +PSL+Y KG +I +A+Y

Sbjct: 402 GVSMDNARLAIASIGKLMFAQFSELVNDFYNNGLPSNLTASRNPSLDYGFKGAEIAMASY 461

Query: 483 ASELGHLANPVTTFVQPAEMGNQAVNSLALISARRTAEANDVLSLLLASHLYCTLQAVDL 542
SEL +LANPVT+ VQ AE NQ VNSL LIS+R+T EA D+L L+ + L QA+DL

Sbjct: 462 CSELQYLANPVTSHVQSAEQHNQDVNSLGLISSRKTEEAVDILKLMSTTFLVALCQAIDL 521

Query: 543 RAMELDFKKQFDPLLPTLLQQHLGTGLDVNALALEVKKALNKRLEQTTTYDLEPRWHDFAF 602
R +E + K + + ++ L TG L + K L + + + D

Sbjct: 522 RHLEENLKHAVKNTVSQVAKRILTTGASGE---LHPSRFCEKDLLKVVDREQVFSYVDDA 578

Query: 603 SYATGTVVE-----LLSSSPSANVTLTAVNAWKVASAEKAISLTREVRN-RFWQT 651
AT +++ L + N + + + E L +EV + R

Sbjct: 579 CSATYPLMQKLRQVLVDHALANGESEKNASTSIFQKIRAFEELKALLPKEVESAREAYE 638

Query: 652 PSSQAPAHAYLSPRTRVLVSFVREELGVQARRGDVFGVQVQETIGSNVSRIYEAIKDGRI 711
+ A A+ R+ LY FVREE+G + G + + G +++ A+ G+I

Sbjct: 639 NGNPAIANKIKECRSYPLYKFVREEIGT-----GLLTGEKIRSPGEEFDKVFMTAMCQGKI 693

☐ >gi|56966621|pdb|1w27|B **S** Chain B, Phenylalanine Ammonia-Lyase (Pal) From *Petroselinum*

gi|56966620|pdb|1w27|A **S** Chain A, Phenylalanine Ammonia-Lyase (Pal) From *Petroselinum*
Length = 714

Score = 332 bits (851), Expect = 3e-89

Identities = 241/697 (34%), Positives = 352/697 (50%), Gaps = 41/697 (5%)

Query: 40 GLDGHAHQSQLEIVQELLSDPTDDVVELSGYSLTXXXXXXXXXXXXXXXXXXXX-QNDDEIRA 98
G+ A S L+ V+++++ VV+L G +LT + + RA

Sbjct: 31 GIAAEAMTGSHLDEVKKMVAEYRKPVVKLGGETLTISQVAAISARDGSGVTVELSEAARA 90

Query: 99 RVDKSVDFLKAQLQNSV--YGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPTSVSSF 156
V S D++ + YGVTTGFG ++ RT+ +LQK LI G+

Sbjct: 91 GVKASSDWVMDSMNKGTD SYGVTTGFGATSHRRTKQGGALQKELIRFLNAGI----- 142

Query: 157 SVGRGLENLPLEVVRGAMVIRVNSLTRGHSVRLVVLEALTNFLNHRITPIVPLRGSIS 216
G G +NTLP R AM++R+N+L +G+S +R +LEA+T FLN ITP +PLRG+I+

Sbjct: 143 -FGNGSDNTLPHSATRAAMLVRINTLLQGYSGIRFEILEAITKFLNQNITPCLPLRGTTIT 201

Query: 217 ASGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEA--VVLGPKEGLGL 274
DL PLSYIAG +TG P+ K T I+ EA L G+E L PKEGL L

Sbjct: 202 X--DLVPLSYIAGLLTGRPNKAV---GPTGVILSPEEAFKLAGVEGGFFELQPKEGLAL 256

Query: 275 VNGTAVSASMATXXXXXXXXXXXXXXXXXXVEAMVGQQGSFAPFIHDVCRPHPGQVEV 334
VNGTAV + MA+ E M G+ F + + HPGQ+E

Sbjct: 257 VNGTAVSGMASMVLFEANILAVLAEVMSAIFAEMQKQP-EFTDHLTHKLKHHPGQIEA 315

Query: 335 ARNIRTLGSSSFAXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSL 394
A + +L GS++ +QDRY LRTSPQ+LGP +E + + +

Sbjct: 316 AAIMEHILDGSAYVKAQAQKLHEMDPLQKP-KQDRYALRTSPQWLGPQIEVIRSSTKMIER 374

Query: 395 ENNTTTDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMN 454
E N+ DNPL+DV + HGGNFQ + + +SM+ TRLA+A IGKL F Q +EL+N N

Sbjct: 375 EINSVNDNPLIDVSRNKAIHGGNFQGTPIGVSMNTRLAIAAIGKLMFAQFSELVNDNFYN 434

Query: 455 RGLPSCLA-AEDPSLNHYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVNSLALI 513
GLPS L+ +PSL+Y KG +I +A+Y SEL LANPVT VQ AE NQ VNSL LI

Sbjct: 435 NGLPSNLSSGRNPGLDYGFKGAEIAMASYCSELQFLANPVTNHVQSAEQHNQDVNSLGLI 494

Query: 514 SARRTAEANDVLSLLLASHLYCTLQAVDLRAMELDFKKQFDPLLPDLLQHLGTGLDVNA 573
S+R+T+EA ++L L+ + L QA+DLR +E + K + ++ ++ L G++

Sbjct: 495 SSRKTSEAVEILKLMSTTFLVGLCQAIDLRHLEENLKSTVKNTVSSVAKRVLTMGVNGE- 553

Query: 574 LALEVKKALNKRLEQTTTYDLEPRWHDAFSYAT-----GTVVELLSSSPSANVTLTA 625
L + K L + + + D AT T+VE + L+

Sbjct: 554 --LHPSRFCEKDLLRVVDREYIFAYIDDPSCATYPLMQKLRQTLVEHALKNGDNERNLST 611

Query: 626 VNAWKVASAEKAIS--LTREVRN-RFWQTPSSQAPAHAYLSPRTRVLYSFVREELGVQAR 682
K+A+ E + L +EV + R + A + R+ LY FVR+ELG

Sbjct: 612 SIFQKIATFEDELKALLPKEVESARAALESNGPAIPNRIEECRSYPLYKFVRKELGT--- 668

Query: 683 RGDVFGVGQQETIGSNVSRIYEAIKDGRINHLVKML 719
+ G + + G +++ A+ G I L++ L

Sbjct: 669 --EYLTGEKVTSPGEEFEKVFIAMSKGEIIDPILLECL 703

☐ >gi|23451809|gb|AAN32866.1| phenylalanine ammonia-lyase 1 [Coffea canephora]
Length = 717

Score = 332 bits (850), Expect = 3e-89

Identities = 252/730 (34%), Positives = 368/730 (50%), Gaps = 50/730 (6%)

Query: 13 ANGFTNGSHAAPT--KSAAGPTSALRRTPGLDGHAAHQSG---QLEIVQELLSDPDTPDDVV 66
ANG NG+ A T AGP L+ +AA +S L+ V+ ++ + +V

Sbjct: 4 ANG--NGNDLAETFTCTQRAGPAP-----DPLNWNAAAESLKGSHLDEVKRMVDEFRRPLV 56

Query: 67 ELSGYSLTXXXXXXXXXXXXXXXXXQNDDE-IRARVDKSVDFLKAQLQNSV--YGVTTGFG 123
L G +LT E RA V S D++ ++ YG+TTGFG

Sbjct: 57 RLGGETLTIAQVAAVAASSDAAVKVELSEGARAGVKASSDWVMESMRKGTDSYGITTTGFG 116

Query: 124 GSADTRTEDAVSLQKALIEHQLCGVTPPTSVSSFSVGRGLENTLPLEVVRGAMVIRVNSLT 183
++ RT+ +LQ+ LI G+ F G +TLP R +M++R+N+L

Sbjct: 117 ATSHRRTKQGGALQEELIRFLNAGI-----FGNGTETCTLPHSATRASMLVRINTLL 169

Query: 184 RGHSAVRLVVLEALTNFLNHRITPIVPLRGSISASGDLSPLSYIAGAITGHPDVKVHVLH 243
+G+S +R +LEA+T LN+ ITP +PLRG+I+ASGDL PLSYI G +TG P+ K V

Sbjct: 170 QGYSGIRFEILEAITKLLNNNITPCLPLRGTTITASGDLVPLSYIVGLLTGRPNKA-VGP 228

Query: 244 EGTEKIMFAEAIISLFGLEA--VVLGPKEGLGLVNGTAVSASMATXXXXXXXXXXXXXXXXX 301
+G K + A EA SL G++ L KEGL LVNGTAV +++A+

Sbjct: 229 DG--K FVNATEAFSLAGIDTGFFELQAKEGLALVNGTAVGSALASMLFEANILAVLAEV 286

Query: 302 XXXXXVEAMVGQQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGSSFAXXXXXXXXXXXXXX 361
E M G+ F + + HPGQ+E A + +L GSSF

Sbjct: 287 LSGIFAEVMHGKP-EFTDHLTHKLKHHPGQIEAAAIMEHILDGSSSFVKEAQRVHEFDPLQ 345

Query: 362 GILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTNDNPLLDVENKQTAHGGNFQAS 421
+QDRY LRTSPQ+LGPL+E + + ++ E N+ DNPL+DV + HGGNFQ +

Sbjct: 346 KP-KQDRYALRTSPQWLGPLIEVIRASTKSIEREINSVNDNPLIDVSRNKALHGGNFQGT 404

Query: 422 AVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCLA-AEDPSLNYHGKGLDIHIA 480
+ +SM+ TRLA+A IGKL F Q +EL+N N GLPS L+ +PSL+Y KG +I +A

Sbjct: 405 PIGVSMDNTRLAIASIGKLMFAQFSELVNDFFYNNGLP SNLSGGRNPSLDYGFGKGAETAMA 464

Query: 481 AYASELGHLANPVTTFVQPAEMGNQAVNSLALISARRTAEANDVLSLLASHLYCTLQAV 540
AY SEL LANPVT VQ AE NQ VNSL LIS+R+TAEA D+L L+ +++L QA+

Sbjct: 465 AYCSELQFLANPVTNHVQSAEQHNQDVNSLGLISSRKTAEAVDILKLMSSTYLVALCQAI 524

Query: 541 DLRAMELDFKKQFDPLLP TLLQQLHGTGLDVNALALEVKKALNKRL-----EQTTTYDL 594
DLR +E + K + + ++ L G + L + K L E Y

Sbjct: 525 DLRHLEENLKASVKNTVSLVAKKVLTMGYNGE---LHPSRFCEKDLLKVVDREHVFAYID 581

Query: 595 EP--RWHDAFSYATGTVVELLSSSPSANVTLTAVNAWKVASAEKAIS--LTREVRNRFWQ 650
+P + +VE ++ T K+ + E + L +EV + +

Sbjct: 582 DPCSGTYPLMQKLRQVLVEHSLANGDKEKDATT SIFQKIGAFEDLKALLPKEVESARCE 641

Query: 651 TPSSQ-APAHAYLSPRTRVLYSFVREELGVQARRGDVFGVQVQETIGSNVSRIYEAIKDG 709
+ + A+ R+ LY FVR ELG + G + + G +++ AI +G

Sbjct: 642 LENGKPGIANRIKDCRSYSLYKFVRGELGT-----NFLTGEKVRSPGEEFDKVF TAICEG 696

Query: 710 RINHVLVKML 719
++ L+ L

Sbjct: 697 KLIDPLLDCL 706

☐ >gi|871494|emb|CAA61198.1| phenylalanine ammonia-lyase [Oryza sativa (indica cul
gi|2130081|pir|S66313 phenylalanine ammonia-lyase (EC 4.3.1.5) - rice
gi|1709563|sp|P53443|PAL2_ORYSA Phenylalanine ammonia-lyase
Length = 710

Score = 331 bits (849), Expect = 4e-89

Identities = 240/713 (33%), Positives = 352/713 (49%), Gaps = 53/713 (7%)

Query: 18 NGSHAAPT KSAAGPTSALRRTPGLDGHAHQSQLEIVQELLS DPTDDVVELSGYSLTXXX 77
NG + A P + + T + G SQ++ V+ + ++ +V++ G SL

Sbjct: 11 NGMSGLCVRPRADPLNWGKATEEMTG-----SQVDEVKRIGAEYRQPLVKIEGASLRIAQ 65

Query: 78 XXXXXXXXXXXXXQNDDEIRARVDKSVDFLKAQLQNSV--YGVTTGFGGSADTRTEDAVS 135
+ D+ R RV S D++ + N YGVTTGFG ++ RT++ +

Sbjct: 66 VAAVAAAGEARV-ELDESARERVKASSDWMNSMMNGTDSYGVTTGFGATSHRRTKEGGA 124

Query: 136 LQKALIEHQLCGVTP TSVSSFSVGRGLENTLPLEVVIRGAMVIRVNSLTRGHSAVRLVVLE 195
LQ+ LI G T + LP E R AM++R+N+L +G+S +R +LE

Sbjct: 125 LQRELIRFLNAGAFGTGTG-----HVLPAEATRAAMLVRINTLLQGYSGIRFEILE 176

Query: 196 ALTNFLNHRITPIVPLRGSISASGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIMFAREA 255
A+ LN +TP +PLRG+I+ASGDL PLSYIAG +TG + L K+ A E

Sbjct: 177 AIAKLLNANVTPCLPLRGTTITASGDLVPLSYIAGLVTGRENA--WALPPDGSKVN-AAEG 233

Query: 256 ISLFGLEA--VVLGPKEGLGLVNGTAVSASMATXXXXXXXXXXXXXXXXXXXXVEAMVGQ 313
 + + G++ L PKEGL +VNGTAV + +A+ E M G+

Sbjct: 234 LKIAGIQGGFFELQPKEGLAMVNGTAVGSGLASTVLFLEANILAILAEVLSAVFCEVMNGK 293

Query: 314 QGSFAPFIHDVCRPHPGQVEVARNIRTLLSGSSFAXXXXXXXXXXXXXXGILRQDRYPLRT 373
 H + + HPGQ+E A ++ +L GSS+ +QDRY LRT

Sbjct: 294 PEYTDHLTHKL-KHHPGQIEAAAIMKHILEGSSYMKHAKKLGEPLMKP-KQDRYALRT 351

Query: 374 SPQFLGPLVEDMMHAYSTLSLENNTTTDNPLLDVENKQTAHGGNFQASAVSISMEKTRLA 433
 SPQ+LGP +E + A ++ E N+ DNPL+DV + HGGNFQ + + +SM+ TRLA

Sbjct: 352 SPQWLGPQIEVIRAAATKSIEREINSVNDNPLIDVSRGKALHGGNFQGTPIGLSMDNTRLA 411

Query: 434 LALIGKLNFTQCTELLNAAMNRGLPSCLA-AEDPSLNYHGKGLDIHIAAYASELGHLANP 492
 +A IGKL F Q +EL+N N GLPS L+ +PSL+Y KG +I +A+Y SEL L NP

Sbjct: 412 IAAIGKLMFAQFSELVNDFYNNGLPSNLSSGRNPISLDYGFKGAEIAMASYCSELQFLGNP 471

Query: 493 VTTFVQPAEMGNQAVNSLALISARRTAEANDVLSLLASHLYCTLQAVDLRAMELDFKKQ 552
 VT VQ AE NQ VNLS LIS+R+TAEA D+L L+ ++ L QAVDLR +E + K

Sbjct: 472 VTNHVQSAEQHNQDVNSLGLISSRKTAEAIDILKMSSTFLIALCQAVDLRHIEENVKSA 531

Query: 553 FDPLLPTLLQQHLGTGLDVNA-LALEVKKALNKRL--EQTTTYDLEPRWHDASFYATGTV 609
 + T+ ++ L T + +A +K L K + E Y +P H+

Sbjct: 532 VKSCVMTVAKKTLSTNSTGDLHVARFCEKDLLKEIDREGVFAYGDDPCSHN----- 582

Query: 610 VELLSSSPSANVTLTAVNAWKVASAEKASISLTREVRNRFWQTPSSQAPAHAYLSP----- 664
 L+ + V NA +V + R VR T A +

Sbjct: 583 YPLMKKLNRNVLVERALANAGRVQRRHLGVRQGRAVRGGLRATLPGAIDGRAAVENGTAI 642

Query: 665 -----RTRVLYSFVREELGVQARRGDVFGVQVQETIGSNVSRIYEAIK DGR 710
 R+ LY FVREELG + G + + G ++++ AI +G+

Sbjct: 643 PSRITECRSYPLYRFVREELGTK-----YLTGEKTRSPGEELNKVLVAINEGK 690

☐ >gi|51594297|gb|AAU08174.1| phenylalanine ammonia-lyase [Camellia sinensis]
 Length = 714

Score = 331 bits (849), Expect = 4e-89

Identities = 238/698 (34%), Positives = 348/698 (49%), Gaps = 40/698 (5%)

Query: 40 GLDGHAHQSQLEIVQELLSDPTDDVVELSGYSLTXXXXXXXXXXXXXXXXXQNDDEIRAR 99
 G+ A S L+ V+ ++ + VV L G +LT + + R

Sbjct: 28 GVAAEAMKGSHLKEVKGMVEEFRKPVVRLGGETLTISQVAAIAVRGSEVAVELSESAREG 87

Query: 100 VDKSVDFLKAQLQNSV--YGVTTFGGGSADTRTEDAVSLQKALIEHQLCGVTPTSVSSFS 157
 V S D++ + YGVTTFGG ++ RT++ +LQK LI G+

Sbjct: 88 VKASSDWVMESMNKGTDSYGVTTFGGATSHRRTKEGGALQKELIRFLNAGI----- 138

Query: 158 VGRGLEN--TLPLEVVRGAMVIRVNSLTRGHSVRLVVLEALTNFLNHRITPIVPLRGS 215
 G G E+ TLP R AM++R+N+L +G+S +R +LE ++ FLN+ ITP +PL G+I

Sbjct: 139 FNGGTESCHTL PQSATRAAMLVRINTLLQGYSGIRFQILETISKFLNNNITPCLPLPGTI 198

Query: 216 SASGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEAVV--LGPKEGLG 273
 +ASGDL PLSYIAG +TG P K T K +EA L E L PKEGL

Sbjct: 199 TASGDLIPLSYIAGLLTGPPHSKAV---GPTGKTFPPKEAFPLTWNEGGFFDLQPKEGLA 255

Query: 274 LVNGTAVSASMATXXXXXXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQVE 333
 LVNGTAV + +A+ E M G+ F + + HPGQ+E

Sbjct: 256 LVNGTAVGSLASMLFEANILAVLSEVLSAIFAEMQKGP-EFTDHLTHKLKHHPGQIE 314

Query: 334 VARNIRTLTSGSSFAXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLS 393
 A + +L GSS+ +QDRY LRTSPQ+LGPL+E + + ++
 Sbjct: 315 AAAIMEHILDGSSYVKAQKLHEMDPLQKP-KQDRYALRTSPQWLGPLIEVIRSSTKSIE 373

Query: 394 LENNTTTDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAM 453
 E N+ DNPL++V + HGGNFQ + + +SM+ TRLA+A IGKL F Q +EL+N
 Sbjct: 374 REINSVNDNPLINVSRLKALHGGNFQGTPIGVSMNTRLAVASIGKLMFAQFSELVNDFY 433

Query: 454 NRGLPSCLA-AEDPSLNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVNSLAL 512
 N GLPS L+ +PSL+Y KG +I +AAV SEL LANPVT VQ AE NQ VNSL L
 Sbjct: 434 NNGLPSNLSGGRNP SLDYGFKAETIAAAYCSELQFLANPVTNHVQSAEQHNQDVNSLGL 493

Query: 513 ISARRTAEANDVLSLLLASHLYCTLQAVDLRAMELDFKKQFDPLLPTLLQQHLGTGLDVN 572
 IS+R+TAEA D+L L+ +++L QAVDLR E + + + + ++ L G++
 Sbjct: 494 ISSRKTAEAVDILKLMSSSTYLVALCQAVDLRHFEENLRNTVKSTVSQVAKRVLTMGVNGE 553

Query: 573 ALALEVKKALNKRLEQTTTYDLEPRWHDAFSYATGTVE-----LLSSSPSANVT 622
 L + K L + + + D AT +++ L + N++
 Sbjct: 554 ---LHPSRFCEKDLLRVVDREYIFAYIDDPSCATYPLMQKLRQVLVEHALKNGESEKNLS 610

Query: 623 LTAVNAWKVASAEKAISLTREVRN-RFWQTPSSQAPAHAYLSPRTRVLYSFVREELGVQA 681
 + + E L +EV + R + A + R+ LY FVREELG
 Sbjct: 611 TSIFQKIRAFEEEEIKTLLPKEVESTRAAIENGNSAIPNRIKECRSYPLYKFVREELGT-- 668

Query: 682 RRGDVFGVGVQQTIGSNVSRIYEAIKDGRINHVLVKML 719
 ++ G + + G +++ A+ G + L+ L
 Sbjct: 669 ---ELLTGEKVRSPGEEFDKVF TALCKGEMIDPLMDCL 703

☐ >gi|58618150|gb|AAW80641.1| phenylalanine ammonia lyase [Botrychium virginianum]
 Length = 680

Score = 331 bits (849), Expect = 4e-89

Identities = 230/638 (36%), Positives = 341/638 (53%), Gaps = 35/638 (5%)

Query: 97 RARVDKSVDFLKAQLQNSV--YGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPTSVS 154
 + RVD+S +++ + YGVTTGFG ++ RT+ + LQK LI G+
 Sbjct: 11 KERVDSESEWMNHVMKGTDTYGVTTGFGATSHRRTKQGIELQKELIRFLNAGILSGDKE 70

Query: 155 SFSVGRGLENTLPLEVVRGAMVIRVNSLTRGHSAVRLVVLEALTNFLNHRITPIVPLRGS 214
 S TL + VR AM++R N+L +G+S +R +LEA+ LN++ITP +PLRGS
 Sbjct: 71 ECS-----TLSSAVRAAMLVRTNTLMQGYSGIRWEILEAMGKLLNNQITPRLPLRGS 123

Query: 215 ISASGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGL-EAVVLGPKEGLG 273
 I+ASGDL PLSYIAG +T P+ V EG E + +EA+ L G+ E L PKEGL
 Sbjct: 124 ITASGDLVPLSYIAGVLTARPN-SAAVTAEGKE--VTGKEALELAGVAEPFELKPKEGLA 180

Query: 274 LVNGTAVSASMATXXXXXXXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQVE 333
 LVNGTAV + +A+ E M G+ F + + HPGQ+E
 Sbjct: 181 LVNGTAVGSLASLVICYDANILALLAEVLSALFCEVMQGKP-EFTDHLTHRLKHHPGQIE 239

Query: 334 VARNIRTLTSGSSFAXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLS 393
 A + LL GSS+ +QDRY LRTSPQ+LGP VE + A +
 Sbjct: 240 AAAIMEWLLDGSSYVQTAACKLHEADPLKKP-KQDRYALRTSPQWLGPQVEVIRLATHAIQ 298

Query: 394 LENNTTTDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAM 453
 E N+ DNPL+DV + HGGNFQ + + +SM+ RLA+A IG+L F Q +EL+N
 Sbjct: 299 REINSVNDNPLIDVARDKALHGGNFQGTPIGVSMNRLAIAAIGRLMFAQFSELVNDFY 358

Query: 454 NRGLPSCLA-AEDPSLNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVNSLAL 512
 N GLPS L+ +PSL+Y KG +I +A+Y SEL +LANPVT T VQ AE NQ VNSL L
 Sbjct: 359 NNGLPSNLSGGPNPSLDYGFKGAEIAMASYTSELQYLANPVTTHVQSAEQHNQDVNSLGL 418

Query: 513 ISARRTAEANDVLSLLLASHLYCTLQAVDLRLAMELDFKKQFDPLLPTLLQQHLGTGLDVN 572
 ISAR+T E D+L ++ ++ + QAVDLR +E + ++ + ++ L + D N
 Sbjct: 419 ISARKTKETVDILKMMSSTFMVALCQAVDLRHLEENMTAVVKHVVCQVARRTLYS--DQN 476

Query: 573 ALALEVKKALNKRLEQTTTYYDLEPRWHDFAFSYATGTVVELL-----SSSPSANVTTLTA 625
 L L + K L Q ++ + D S T T+++ L + A L +
 Sbjct: 477 GLLLP-SRFCEKELLQVVEHEPIFSYIDHASADTSTLMQKLRQVLVDHALKNVAKEKLD 535

Query: 626 VNAW-KVASAEKAISLTREVR-NRFWQT--PSSQAPAHAYLSPRTRVLYSFVREELGVQA 681
 N ++ S E+ + + ++ R W++ A + + RT LY VR+ L Q
 Sbjct: 536 ANVLNRIISFEELLKIRLQIEIPRAWESFDKGQCAVLNRIQNCRTYPLYKLVRDLLDTQ- 594

Query: 682 RRGDVFGVQQETIGSNVSRIYEAIKGRINHVLVKML 719
 + G +++ G + +++EAI +G++ L++ +
 Sbjct: 595 ----ILSGAKKQCPGQDFQKVFEAISEGKLAAPLLECM 628

☐ >gi|2570156|dbj|BAA22963.1| phenylalanine ammonia-lyase [Nicotiana tabacum]
 gi|3123241|sp|P35513|PAL2_TOBAC Phenylalanine ammonia-lyase
 gi|2564055|dbj|BAA22947.1| phenylalanine ammonia-lyase [Nicotiana tabacum]
 Length = 712

Score = 331 bits (849), Expect = 4e-89

Identities = 240/691 (34%), Positives = 350/691 (50%), Gaps = 42/691 (6%)

Query: 49 SQLEIVQELLSDPTDDVVELSGYSLTXXXXXXXXXXXXXXXXXQND--DEIRARVDKSVDF 106
 S L+ V+++++ VV+L G +LT + + + RA V S D+
 Sbjct: 33 SHLDEVKKMVAEFRKPVVKLGGETLTVAQVAAIAAKDNVKTVKVELSEGARAGVKASSDW 92

Query: 107 LKAQLQNSV--YGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPTSVSSFSVGRGLEN 164
 + + YGVTTGFG ++ RT++ +LQK LI GV G G E+
 Sbjct: 93 VMDSMGKGTDSYGVTTGFGATSHRRTKNGGALQKELIRFLNAGV-----FGNGTES 143

Query: 165 --TLPLEVVRGAMVIRVNSLTRGHSARLVVLEALTNFLNHRITPIVPLRGSISASGDL 222
 TLP R AM++R+N+L +G+S +R +LEA+T LNH +TP +PLRG+I+ASGDL
 Sbjct: 144 CHTLPQSGTRAAMLVRINTLLQGYSGIRFEILEAITKLLNHNVTPLPLRGITITASGDLV 203

Query: 223 PLSYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEA--VVLGPKEGLGVNGTAV 280
 PLSYIAG +TG P+ K + T + A EA + G+ L PKEGL LVNGTAV
 Sbjct: 204 PLSYIAGLLTGRPNKAVGPNGET---LNAAEAFRVAGVNGGFFELQPKEGLALVNGTAV 260

Query: 281 SASMATXXXXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQVEVARNIRT 340
 + +A+ E M G+ F + + HPGQ+E A +
 Sbjct: 261 GSGGLASMLFDANVLAVFSEVLSAIFAEVMNGKP-EFTDHLTHKLKHHPGQIEAAAIM 319

Query: 341 LLSGSSFAXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTT 400
 +L GSS+ +QDRY LRTSPQ+LGP +E + A + E N+
 Sbjct: 320 ILDGSSYVKAQKLHETDPLQKP-QDRYALRTSPQWLGPQIEVIRSATKMIEREINSVN 378

Query: 401 DNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRLPSC 460
 DNPL+DV + HGGNFQ + + +SM+ RLALA IGKL F Q +EL+N N GLPS
 Sbjct: 379 DNPLIDVSRNKALHGGNFQGTPIGVSMDNARLALASIGKLMFGQFSELVNDYYNGLPSN 438

Query: 461 L-AAEDPSLNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVNSLALISARRTA 519
 L A +PSL+Y KG +I +A+Y SEL LANPVT VQ AE NQ VNSL LISAR+TA

Sbjct: 439 LTAGRNPSLDYGFKGSEIAMASYCSELQFLANPVTNHVQSAEQHNQDVNSLDLISARKTA 498

Query: 520 EANDVLSLLLASHLYCTLQAVDLRAMELDFKKQFDPLLPTLLQQHLGTGLDVNALALEVK 579
EA D+L L+ +++L QA+DLR +E + + + + ++ L G + L

Sbjct: 499 EAVDILKLMSSSTYLVALCQAIIDLRLHLEENLRNAVKNVTSQVAKRTLTMGTNGE---LHPS 555

Query: 580 KALNKRLEQTTTYDLEPRWHDFAFSYATGTVVE-----LLSSSPSANVTLTAVNAW 629
+ K L + + + D A +++ L + N +

Sbjct: 556 RFCEKDLLRVVDREYVFAYADDACSANYPLMQKLRQVLVDHALQNGENEKNANSSIFQKI 615

Query: 630 KVASAEKAISLTREVRN-RFQWTPSSQAPAHAYLSPRTRVLYSFVREELGVQARRGDVVF 688
E L +EV + R + A A+ R+ LY FVR ELG ++

Sbjct: 616 LAFEDELKAVLPKEVESARAALESNGPAIANRIKECRSYPLYRFVRGELG-----AELLT 670

Query: 689 GVQQETIGSNVSRIYEAIKDGRINHLVKML 719
G + + G +++ A+ +G+I L++ L

Sbjct: 671 GEKVRSPGEECDKVFTAMCNGQIIDSLECL 701

☐ >gi|82496|pir|S06475 phenylalanine ammonia-lyase (EC 4.3.1.5) - rice
Length = 701

Score = 331 bits (849), Expect = 4e-89

Identities = 237/690 (34%), Positives = 358/690 (51%), Gaps = 59/690 (8%)

Query: 49 SQLEIVQELLSDPTDDVVELSGYSLTXXXXXXXXXXXXXXXXXX--XXQNDDEIRARVDKSVDF 106
S L+ V+ +++ + +V++ G +L + D+E R RV S ++

Sbjct: 25 SHLDEVKRMVAQFREPLVKIQGATLRVGQVAAVAQAKDAARVAVELDEEARPRVKASSEW 84

Query: 107 LKAQLQNS--VYGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPTSVSSFSVGRGLEN 164
+ + + +YGVTTGFGG++ RT+D +LQ L+ H G+ T +

Sbjct: 85 ILTCIAHGDIYGVTTGFGGTSRRRTKDGPAQVELLRHLNAGIFGTGSDG-----H 136

Query: 165 TLPLEVVRGAMVIRVNSLTRGHSVRLVLEALTNFLNHRITPIVPLRGSISASGDLSP 224
TLP E VR AM++R+N+L +G+S +R +LEA+T LN +TP +PLRG+I+ASGDL PL

Sbjct: 137 TLPSETVRAAMLVRINTLLQGYSGIRFEILEAITKLLNTGVTPCLPLRGTITASGDLVPL 196

Query: 225 SYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEA--VVLGPKEGLGLVNGTAVSA 282
SYIAG ITG P+ + + +G+ + + A EA L G+E L PKEGL +VNGT+V +

Sbjct: 197 SYIAGLITGRPNAQA-ISPDRK--VDAAEAFKLAGIEGGFFTLNPKEGLAIVNGTSVGS 253

Query: 283 SMATXXXXXXXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQVEVARNIRTL 342
++A E M G+ H + + HPG ++ A + +L

Sbjct: 254 ALAATVMFDANILAVLSEVL SAVFCEVMNGKPEYTDHLTHKL-KHHPGSIDAAAIMEHIL 312

Query: 343 SGSSFAXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTDN 402
+GSSF +QDRY LRTSPQ+LGP ++ + A ++ E N+ DN

Sbjct: 313 AGSSFM SHAKKVNEMDPLLKP-KQDRYALRTSPQWLGPQIQVIRAATKSIEREVNSVNDN 371

Query: 403 PLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELNNAAMNRLPSCLA 462
P++DV + HGGNFQ + + +SM+ RLA+A IGKL F Q +EL+N N GL S LA

Sbjct: 372 PVIDVHRGKALHGGNFQGTPIGVSM DNARLAIANIGKLMFAQFSELVNEFYNNGLTSNLA 431

Query: 463 -AEDPSLNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVNSLALISARRTAEA 521
+ +PSL+Y KG +I +A+Y+SEL +LANP+T VQ AE NQ VNSL L+SAR+T EA

Sbjct: 432 GSRNPSLDYGFKGTEIAMASYSELQYLANPITNHVQSAEQHNQDVNSLGLVSARKTLEA 491

Query: 522 NDVLSLLLASHLYCTLQAVDLRAMELDFKKQFDPLLPTLLQQHL---GTGLDVNALALEV 578
D+L L+ ++++ QAVDLR +E + K + + ++ L TG D+++

Sbjct: 492 VDILKLMSTYIIVALCQAVDLRHLEENIKSSSVKNCVTQVAKKVLTMNPTG-DLSSARFSE 550

Query: 579 KKALNKRLEQTTTYDLEPRWHDAFSYATG-----TVVELLSSSPSANVTL 623
 K L T D E FSYA V L+S L

Sbjct: 551 KNLL-----TAIDREA----VFSYADDPCSANYPLMQKLRAVLVEHALTSGDRRARGL 599

Query: 624 TAVNAWKVASAEKAISLTREVRNRFWQTPSSQAP-AHAYLSPRTRVLYSFVREELGVQAR 682
 + +V + + R R + AP A+ + R+ LY FVREELG

Sbjct: 600 RVLQDHQVRGGAPLCAAPGD-RGRPRRRRQRTAPVANRIVESRSFPLYRFVREELGC--- 655

Query: 683 RGDVFFV-GVQQETIGSNVSRIYEAIKDGRI 711
 VF+ G + ++ G +++++ I G++

Sbjct: 656 ---VFLTGEKLGKSPGEECNKVFLGISQKGL 682

☐ >gi|17467274|gb|AAL40137.1| phenylalanine ammonia-lyase [Zea mays]
 Length = 703

Score = 331 bits (848), Expect = 6e-89
 Identities = 239/696 (34%), Positives = 350/696 (50%), Gaps = 64/696 (9%)

Query: 49 SQLEIVQELLSDPDDEVELSGYSLTXXXXXXXXXXXXXXXXXX--XXQNDDEIRARVDKSVDF 106
 S L+ V+ +++ VV++ G +L + D+E R RV S ++

Sbjct: 25 SHLDEVKRMVAQARQPVVKIEGSTLRVGQVAASAKDASGVAVELDEEARPRVKASSEW 84

Query: 107 LKAQLQNS--VYGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPTSVSSFSVGRGLEN 164
 + + + +YGVTTGFGG++ RT+D +LQ L+ H G+ T +

Sbjct: 85 ILDCIAHGGDIYGVTTGFGGTSHRRTKDGPAQVELLRHLNAGIFGTGSDG-----H 136

Query: 165 TLPLEVVRGAMVIRVNSLTRGHSVRLVLEALTNFLNHRITPIVPLRGSISASGDLSP 224
 TLP EV R AM++R+N+L +G+S +R +LEA+T LN ++P +PLRG+I+ASGDL PL

Sbjct: 137 TLPSEVTRAAMLVRINTLLQGYSGIRFEILEAITKLLNTGVSPCLPLRGITITASGDLVPL 196

Query: 225 SYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEA--VVLGPKEGLGLVNGTAVSA 282
 SYIAG ITG P+ + V +G + + A EA + G+E L PKEGL +VNGT+V +

Sbjct: 197 SYIAGLITGRPNAQA-VTVDRGR--VDAAEAFKIAGIEGGFFKLNPKGLAIVNGTSVGS 253

Query: 283 SMATXXXXXXXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQVEVARNIRTL 342
 ++A E M G+ H + + HPG +E A + +L

Sbjct: 254 ALAATVMYDANVLAVLSEVL SAVFCEVMNGKPEYTDHLTHKL-KHHPGSIEAAAIMEHIL 312

Query: 343 SGSSFAXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTDN 402
 GSSF +QDRY LRTSPQ+LGP +E + A ++ E N+ DN

Sbjct: 313 DGSSFMKQAKKVNELDLLKP-KQDRYALRTSPQWLGPQIEVIRAATKSIEREVNSVNDN 371

Query: 403 PLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCLA 462
 P++DV + HGGNFQ + + +SM+ RLA+A IGKL F Q +EL+N N GL S LA

Sbjct: 372 PVIDVHRGKALHGGNFQGTPIGVSMNDARLAIANIGKLMFAQFSELVNEFYNNGLTSNLA 431

Query: 463 -AEDPSLNHYHGKGLDIHIAAYASELGHLANPVTTTFVQPAEMGNQAVNSLALISARRTAEA 521
 + +PSL+Y KG +I +A+Y SEL +L NP+T VQ A+ NQ VNSL L+SAR+TAEA

Sbjct: 432 GSRNPSTDYGFKGTEIAMASYCSELQYLGNPITNHVQSADEHNQDVNSLGLVSARKTAEA 491

Query: 522 NDVLSLLLASHLYCTLQAVDLRAMELDFKKQFDPLLPTLLQQHLGTGLDVNALALEVKKA 581
 D+L L+ +++++ QAVDLR +E + K + + Q L +N E+ A

Sbjct: 492 IDILKLMSTYIIVALCQAVDLRHLEENIKAS----VKNTVTQVAKKVLTMNPSG-ELSSA 546

Query: 582 LNKRLQETTTTYDLEPRWHDAFSYATGTVVELLSSSPSANVTLT--AVNAWKVASAEKAIS 639
 E + D E F+YA L L A+++ + + +

Sbjct: 547 RFSEKELISAIDREA-----VFTYAEDAASASLPLMQKLRAVLVDHALSSGERGAGALRVL 602

Query: 640 LTREVRNRFWQTPSSQAP-----AHAYLSPRTRVLYSFVREELGVQARR 683
 +VR P AP A+ R+ LY FVREELG

Sbjct: 603 QDHQVRG---GAPRGAAPGGGGRPRGVAEGTAPVANRIADSRSFPLYRFVREELGCVFLT 659

Query: 684 GD-----VFVGVQQETIGSNVSRIYEAIKD 708
 G+ VFVG+ Q G V + E +K+

Sbjct: 660 GERLKSPGEECNKVFGISQ---GKLVDPMLECLKE 692

☐ >gi|48869195|gb|AAT47186.1| phenylalanine aminomutase [Taxus canadensis]
 Length = 698

Score = 331 bits (848), Expect = 6e-89

Identities = 241/641 (37%), Positives = 336/641 (52%), Gaps = 38/641 (5%)

Query: 94 DEIRARVDKSVDFLKAQLQNS--VYGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPPT 151
 ++ RARV+ +++ + ++ +YGVTTGFG + RT LQ++LI L GV

Sbjct: 56 EQCRARVETCSSWVQRKAEDGADIYGVTTGFGACSSRRTNQLSELQESLIRCLLAGVFTK 115

Query: 152 SVSSFSVGRGLENLTPLEVVRGAMVIRVNSLTRGHSVAVRLVVLEALTNFLNHRITPIVPL 211
 +S SV + LP R AM++R+NS T G S +R V+EAL LN ++P VPL

Sbjct: 116 GCAS-SV-----DELPATATRSAMLRLNSFTYGCSGIRWEVMEALEKLLNSNVSPKVPL 169

Query: 212 RGSISASGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEAVVLGPKEG 271
 RGS+SASGDL PL+YIAG + G P V + G + + A EA+S GL L KEG

Sbjct: 170 RGSVSASGDLIPLAYIAGLLIGKPSVARI---GDDVEVPAPPEALSRVGLRPFKLQAKEG 226

Query: 272 LGLVNGTAVSASMATXXXXXXXXXXXXXXXXXXVEAMVGQQGSFAPFIHDVCRPHPGQ 331
 L LVNGT+ + ++A+ E + G++ P IH V +PHPGQ

Sbjct: 227 LALVNGTSFATALASTVMYDANVLLLLVETLCGMFCEVIFGREEFAHPLIHKV-KPHPGQ 285

Query: 332 VEARNIRTLTSGSSFAXXXXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYST 391
 +E A + LL S F +QDRY LR+SPQ+L PLV+ + A +T

Sbjct: 286 IESAELEWLLRSPFQDLSREYYSIDKLKKP-KQDRYALRSSPQWLAPLVQTIRDATTT 344

Query: 392 LSLENNTTTDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNA 451
 + E N+ DNP++D N + HG NFQ SAV M+ R+A+A +GKL F Q TEL+

Sbjct: 345 VETEVNSANDNPIIDHANDRALHGANFQGSAGVFYMDYVRIAVAGLGKLLFAQFTELMIE 404

Query: 452 AMNRGLPSCLA-AEDPSLNYHGKGLDIHIAAYASELGHLANPVTTTFVQPAEMGNQAVNSL 510
 + GLP L+ D S++Y KGLDI +AAY+SEL +LANPVTT V AE NQ +NSL

Sbjct: 405 YYSNGLPGNLSLGPDLSDYGLKGLDIAMAAYSSELQYLANPVTTTHVHSAEQHNQDINS 464

Query: 511 ALISARRTAEANDVLSLLASHLYCTLQAVDLRAMELDFKKQFDPLLPTLLQQHLGTGLD 570
 ALISAR+T EA D+L L++ASHL QAVDLR +E K + ++ TL + G D

Sbjct: 465 ALISARKTEEALDILKLMIAASHLTAMCQAVDLRQLEEALVKVVENVVSTLADE-CGLPND 523

Query: 571 VNALALEVKKALNKRLEQTTTYD-LEPRWHDASFYATGTVVVELLSSSPSANVTLTAVNAW 629
 A L V KA+ + D P G+++ L TL

Sbjct: 524 TKARLLYVAKAVPVYTYLESPCDPTLPLLLGLEQSCFGSILALHKKDGIETDTLVD---- 579

Query: 630 KVASAEKAIS--LTREV-----RNRFWQTPSSQAPAHAYLSPRTRVLYSFVREEL--G 678
 ++A EK +S L E+ + +T + R Y FVREEL G

Sbjct: 580 RLAEFEKRLSDRLENEMTAVRVLYEKKGHKTADNNDALVRIQGSRFLPFYRFVREELDTG 639

Query: 679 VQARRGDVFGVGVQQETIGSNVSRIYEAIKDGRINHVLVKML 719
 V + R +++T +V ++++AI DGRI L+ L

Sbjct: 640 VMSAR-----REQTPQEDVQKVFDAIADGRITVPLLHCL 673

☐ >gi|58618144|gb|AAW80638.1| phenylalanine ammonia lyase [Selaginella kraussiana]
Length = 723

Score = 331 bits (848), Expect = 6e-89

Identities = 246/739 (33%), Positives = 367/739 (49%), Gaps = 64/739 (8%)

Query: 13 ANGFTNGS-HAAPTksAAGPTSALRRTPGLDGHAHQSQLEIVQELLSDPTDDVVELSGY 71
ANG T + P +A P R + +H ++ + E + + + G
Sbjct: 8 ANGSTGLCIKSTPVVAAPLPDPLNWRKAAAEMEGSHLDEVAMVETVYGGDQVSISIEGT 67

Query: 72 SLTXXXXXXXXXXXXXXXXXQNDDEIRARVDKSVDFL--KAQLQNSVYGVTTGFGGSADT 128
LT + D R RVD+S ++ A YGVTTGFG ++
Sbjct: 68 RLTVAQVAAIALRGADATVELDAVAARGVRDRSSRWLDNAMKGTDTYGVTTGFGATSHR 127

Query: 129 RTEDAVSLQKALIEHQLCGVTPTSVSSFSVGRGLENL-LPLEVVRGAMVIRVNSLTRGHS 187
RT V LQ+ LI G+ F+ G G T LP V R +++R N+L +G+S
Sbjct: 128 RTNQGVLELQRELIRFLNAGI-----FAAGSGAATTVLPPAVARASVLVRTNTLMQGY 180

Query: 188 AVRLVVLEALTNFLNHRITPIVPLRGSISASGDLSPLSYIAGAITGHPDVKVHVLHEGTE 247
+R +L+A+ +N ITP +PLRGS+SASGDL PLSY+AG +TG P+ K + +GT
Sbjct: 181 GIRWDILDAMAKLVNAGITPRIPLRGSVSASGDLVPLSYVAGLLTGRPNAKAYG-PDGT 239

Query: 248 KIMFAREAISLFGLEAVV-LGPKEGLGLVNGTAVSASMATXXXXXXXXXXXXXXXXXXXX 306
++ EA+ + G+ A L PKEGL +VNGTAV A++A+
Sbjct: 240 -LLNGDEALKMAGIAAPFELQPKGLAIVNGTAVGAASIASCFDANVLALLAEVISALF 298

Query: 307 VEAAMVGQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGSSFAXXXXXXXXXXXXXXGILRQ 366
EAM G+ P H + + HPGQ+E A + +L SS+ +Q
Sbjct: 299 CEAMQKGPEYTDPLTHKL-KHHPGQIEAAVMEHVLLNSSYMKAAAKLHEADPLKKP-KQ 356

Query: 367 DRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTDNPLLDVENKQTAHGGNFQASAVSIS 426
DRY LRTSPQ+LGP +E + A +++ E N+ DNP++DV+ + HGGNFQ + V +S
Sbjct: 357 DRYALRTSPQWLGPQIEVIRAATHSIAREINSVNDNPIIDVDRDKALHGGNFQGTTPGV 416

Query: 427 MEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCLAED-PSLNYHGKGLDIHIAAYASE 485
M+ RLA+A IGKL F Q +EL+N N GLPS L+ D PSL+Y KG +I +A+Y SE
Sbjct: 417 MDNVRLAIAAIGKLMFAQFSELVNDYNNGLPSNLSSGDNPSLDYGFKAIEIAMASYTSE 476

Query: 486 LGHLANPVTTFVQPAEMGNQAVNSLALISARRTAEANDVLSLLLASHLYCTLQAVDLRAM 545
L +LANPVT VQ AE NQ VNSL L+SAR+TAEA ++L L+ ++ L QA+DLR +
Sbjct: 477 LQYLANPVTNHVQSAEQHNQDVNSLGLVSARKTAEAEILKLMSSTFLVALCQAIDLRHL 536

Query: 546 ELDFKKQFDPLLPDLLQHLGTGLDVNALALEVKKALNKRLEQ-----TT 590
E + ++ T+ ++ L T + AL+ + K L Q +
Sbjct: 537 EENLTSVVKNVVSTVAKKTLTTS---SGGALQASRFAEKDLLQVVDHTPVFTYADDP 593

Query: 591 TYDLEPRWHDFAFSYATGTVVELLSSSSPSANV-----TLTAVNAWKVASAEKAISL- 640
+Y L + + +E S SA++ L A +VA+A +A
Sbjct: 594 SYPLMQKLRQVLVEHSLKNLEHEDESRSASIFSKIGVFEEELKAKLPVEVAAARRAFEEG 653

Query: 641 TREVRNRWFQTPSSQAPAHAYLSPRTRVLYSFRVREELGVQARRGDVFGVQVQETIGSNVS 700
+ NR + S+ LY FVR + + +G + T G + S
Sbjct: 654 NAAIPNRIFDCASAP-----LYEFVR-----KVGESSILMGTKSGTPGEDFS 695

Query: 701 RIYEAIKDGRINHVLVKML 719
+I++AI G++ L+K +

Sbjct: 696 KIFDAICQGKMVAPLLKCM 714

☐ >gi|58618146|gb|AAW80639.1| phenylalanine ammonia lyase [Equisetum arvense]
Length = 778

Score = 330 bits (847), Expect = 7e-89

Identities = 241/695 (34%), Positives = 349/695 (50%), Gaps = 38/695 (5%)

Query: 45 AAHQSQLLEIVQELLSD--PTDDVVELSGYSLTXXXXXXXXXXXXXXXXXQNDDEIRARVDK 102
A S E ++ ++ T+ VV L G SLT ++ +ARVD+

Sbjct: 50 ALQSSHYEEIRRMIRQFLETEKVV-LQGSSSLTVGQVTAVTQRSEVAVELDEATAKARVDE 108

Query: 103 SVDFLKAQLQNSV--YGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPTS SVSSFSVGR 160
S +++ + YGVTTGFG ++ RT A LQ+ LI GV + G+

Sbjct: 109 SSNWVLNNILKGTDTYGVTTGFGATSHRRTTQAHDLQRELIRFLNAGV-----ITAGK 161

Query: 161 GLENTLPLEVVRGAMVIRVNSLTRGHSVRLVLEALTNFLNHRITPIVPLRGSISASGD 220
G TLPL + AM++R N+L +G+S +R +L +N I P +PLRG+I+ASGD

Sbjct: 162 GANCTLPLPYAKAAMLVRTNTLMQGYSGIRWAILNGFEKLMNGNIIPKMPLRGITITASGD 221

Query: 221 LSPLSYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEA-VVLGPKEGLGLVNGTA 279
L PLSYIAG IT P+ + + G E + A EA+ L G+E VL PKEGL +VNGT+

Sbjct: 222 LVPLSYIAGLITARPNSRA-ITPSGEE--IPAAEALKLVGIEEPFVLQPKEGLAIVNGTS 278

Query: 280 VSASMATXXXXXXXXXXXXXXXXXXXXVEAMVGQQGSFAPFIHDVCRPHPGQVEVARNIR 339
V A++A E M G+ P H + + HPGQ+E A +

Sbjct: 279 VGAAVAANVCFDANVLVLLAEVISALFCEVMQKPEFTDPLTHQL-KHHPGQIEAAAVME 337

Query: 340 TLLSGSSFAXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTT 399
LL GSS+ +QDRY LRTSPQ+LGP E + A + E N+

Sbjct: 338 YLLEGSSYMQAAAKLHETDPLSKP-KQDRYALRTSPQWLGPQAEVIRAATHCIEREINSV 396

Query: 400 TDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPS 459
DNPL+DV HGGNFQ + + +SM+ R+ALA IGKL F Q +EL+ N GLPS

Sbjct: 397 NDNPLIDVSRDMALHGGNFQGTPIGVSMNDMRIAALAAIGKLMFAQFSELVCDHYNSGLPS 456

Query: 460 CLA-AEDPSLNYHGKGLDIHIAAYASELGHLANPVTTTFVQPAEMGNQAVNSLALISARRT 518
L+ +PSL+Y KG +I +AAY SEL +LANPVTT VQ AE NQ VNSL LISAR+T

Sbjct: 457 NLSGGPNPSLDYGFKAIEIAMAAYCSELQYLANPVTHVQSAEQHNQDVNSLGLISARKT 516

Query: 519 AEANDVLSLLASHLYCTLQAVDLRAMELDFKKQFDPLLPTLLQQHL-----GTG 568
AEA ++L L+ AS+L QA+DLR +E + + ++ ++++ L G

Sbjct: 517 AEAIEILKLMSASYLVALCQAIDLRHLEENMQAIVKHVVKKVIKKSLYNVEGESLLPWAG 576

Query: 569 LDVNALALEVKKALNKRLEQTTT--YDLEPRWHDFAFSYATGTVVELLSSSPSANVTLTAV 626
+ L++ + + ++ + Y L + T V AN + +

Sbjct: 577 AEKELLSIIDHQPVFSYIDNASNPDYALMLQLRQILVEQTFKVPADSEDESGANSQMPVL 636

Query: 627 -NAWKVASAEKAISLTREV-RNRFWQTPSSQAPAHAYLSPRTRVLYSFVREELGVQARRG 684
NA V +L +E+ + R A + + RT LY FVR ELG R

Sbjct: 637 FNAIPVFEQALKEALDKEIPKARESYDSGDFAVPNRINNCRITYPLYKFVRSELGTNLLR- 695

Query: 685 DVFVGQQETIGSNVSRIYEAIKDGRINHVLVKML 719

G + G ++ +++ I +G++ L++ L

Sbjct: 696 ----GTAPRSPGEDIEKVFNGIMEGKLAIPLLRCL 726

☐ >gi|38385686|gb|AAR19393.1| phenylalanine ammonia-lyase [Stellaria longipes]
Length = 699

Score = 330 bits (845), Expect = 1e-88

Identities = 241/689 (34%), Positives = 353/689 (51%), Gaps = 42/689 (6%)

Query: 49 SQLEIVQELLSDPTDDVVELSGYSLTXXXXXXXXXXXXXXXXXQNDDEIRARVDKSVDFLK 108
S LE V+++++ + V+L G +LT N R RV S D++
Sbjct: 24 SHLEEVKKMVAEYRNKDVKLVGETLTVAQVAAVARSQVTVELCN--AARDRVKASSDWVM 81

Query: 109 AQLQNSV--YGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPTSVSSFSVGRGLEN-- 164
+ YGVTTGFG ++ RT +LQK LI GV G G EN
Sbjct: 82 DMSKGTDSYGVTTGFGATSHRRTSKGGALQKELIRFLNAGV-----FGNGTENS 132

Query: 165 TLPLEVVRGAMVIRVNSLTRGHSVRLVLEALTNFLNHRITPIVPLRGSISASGDLSP 224
TLP R AM++R+N+L +G+S +R +LEA+T LN +TP +PLRG+I+ASGDL PL
Sbjct: 133 TLPHTASRAAMLVRINTLLQGYSGIRWEILEAITKLNSDVTPLPLRGTITASGDLVPL 192

Query: 225 SYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEAVV--LGPKEGLGLVNGTAVSA 282
SYIAG +TG P+ K V G +++ A +A +++ L PKEGL +VNGTAV +
Sbjct: 193 SYIAGLLTGRPNAKA-VGPNG--EVLTAEQAFKAIDSPPFELQPKGLAMVNGTAVGS 249

Query: 283 SMATXXXXXXXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQVEVARNIRTL 342
MA+ E M G+ F + + HPGQ+E A + +L
Sbjct: 250 GMASIVLFEANILAVLAEVISAVFAEVMNGKP-EFTDHLTHKLKHHPGQIEAAAIMEHIL 308

Query: 343 SGSSFAXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTT 402
GSS+ RQ RY LR SPQ+LGP + + A ++ E N+ DN
Sbjct: 309 DGSSYMKAALHDMPLQRP-RQARYALRASQWLGPQIGVIRWATKSIEREINSVNDN 367

Query: 403 PLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRLPSCL- 461
PL+DV + HGGNFQ + + +SM+ TRLA+A IGKL F Q +EL+N N GLPS L
Sbjct: 368 PLIDVSRNKAIHGGNFQGTPIGVSMDNTRLAIAAIGKLMFAQFSELVNDYYNGLPSNLT 427

Query: 462 AAEDPSLNYHGKGLDIHIAAYASELGHLANPVTTTFVQPAEMGNQAVNSLALISARRTAEA 521
A+ +PSL+Y KG +I +A+Y SEL LANPVT VQ AE NQ VNSL LISAR+TAEA
Sbjct: 428 ASREPSLDYGFKAIEIAMASYCSELQFLANPVTNHVQSAEQHNQDVNSLGLISARKTAEA 487

Query: 522 NDVLSLLLASHLYCTLQAVDLRAMELDFKKQFDPLLPTLLQQHLGTGLDVNALALEVKA 581
D+L L+ +S L QAVDLR +E + + + + ++ L TG++ L +
Sbjct: 488 VDILKLMSSSFLVAICQAVDLRHIEENLQSAVKNSVSQVCRRVLITGVNGE---LHPGRF 544

Query: 582 LNKRLQTTTTYDLEPRWHDASFYATGTVVE-----LLSSSPSANVTLTAVNAWKV 631
+ L + + + D +T +++ L + NVT +
Sbjct: 545 CEEDLIRVVEREHVFAYADDPSSSTYPLLQKLRLQVLIDQALANGDSEKNVTTTIFQKIGA 604

Query: 632 ASAEKAISLTREVRN-RFWQTPSSQAPAHAYLSRTRVLYSFVREELGVQARRGDVFGV 690
E L++++ R S+A + R+ LY FVRE+L + G+ GV
Sbjct: 605 FEEELKARLSKDIEAVRSAIENRSEAIENRIKECRSYPLYKFVREQLKTELLTGE---GV 661

Query: 691 QQETIGSNVSRIYEAIKDGRINHLVKML 719
G + +++ A+ +G+I+ L++ L
Sbjct: 662 TSP--GEEIDKVFTALNEGKISDPLLECL 688

☐ >gi|50910715|ref|XP_466846.1| ☒ putative phenylalanine ammonia-lyase [Oryza sativa
cultivar-group]

gi|48716549|dbj|BAD23152.1| ☒ putative phenylalanine ammonia-lyase [Oryza sativa]

cultivar-group]]
Length = 713

Score = 330 bits (845), Expect = 1e-88

Identities = 236/700 (33%), Positives = 352/700 (50%), Gaps = 47/700 (6%)

Query: 33 SALRRTPGLDGHAHQ---SQLEIVQELLSDPTDDVVELSGYSLTXXXXXXXXXXXXXXXXX 89
+A R P G AA + S L+ V+ ++++ +V++ G SL

Sbjct: 19 AAPRADPLNWGKAAEEMSGSHLDEVKRMVAEYRQPLVKIEGASLRQAQVAAVAAAGEARV 78

Query: 90 XQNDDEIRARVDKSVDFLKAQLQNSV--YGVTTGFGGSADTRTEDAVSLQKALIEHQLCG 147
+ D+ R RV S D++ + N YGVTTGFG ++ RT++ +LQ+ LI G

Sbjct: 79 -ELDESARERVKASSDWVMNSMNGTDSYGVTTGFGATSHRRTKEGGALQRELIRFLNAG 137

Query: 148 VTPTSVSSFSVGRGLENLPLEVVRGAMVIRVNSLTRGHSVRLVLEALTNFLNHRITP 207
T + L E R AM++R+N+L +G+S +R +LEA+T LN +TP

Sbjct: 138 AFGTGTG-----HVLSAEATRAAMLVRINTLLQGYSGIRFEILEAITKLLNANVTP 189

Query: 208 IVPLRGSISASGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIMFAEAISLFGLEA--VV 265
+PLRG+++ASGDL PLSYIAG +TG + V V +G++ + A EA + G++

Sbjct: 190 CLPLRGTVTASGDLVPLSYIAGLVTGREN-SVAVAPDGSK--VNAAEAFKIAGIQGGFFE 246

Query: 266 LGPKEGLGLVNGTAVSASMATXXXXXXXXXXXXXXXXXXXXVEAMVGQQGSFAPFIHDVC 325
L PKEGL +VNGTAV + +A+ E M G+ H +

Sbjct: 247 LQPKEGLAMVNGTAVGSGLASTVLFANILAVLAEVLSAVFCEVMNGKPEYTDHLTHKL- 305

Query: 326 RHPGQVEVARNIRTLLSGSSFAXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDM 385
+ HPGQ+E A + +L GSS+ +QDRY LRTSPQ+LGP +E +

Sbjct: 306 KHHPGQIEAAIMEHILEGSSYMKLAKKLGEIDPLMKP-KQDRYALRTSPQWLGPQIEVI 364

Query: 386 MHAYSTLSLENNTTTNDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQC 445
A ++ E N+ DNPL+DV + HGGNFQ + + +SM+ TRLA+A IGKL F Q

Sbjct: 365 RAATKSIEREINSVNDNPLIDVSRDKALHGGNFQGTPIGVSMNDNTRLAIAAIGKLMFAQF 424

Query: 446 TELLNAAMNRGLPSCLA-AEDPSLNYHGKGLDIHIAAYASELGHLANPVTTTFVQPAEMGN 504
+EL+N N GLPS L+ +PSL+Y KG +I +A+Y SEL L NPVT VQ AE N

Sbjct: 425 SELVNDYYNGLPSNLSGGRNPISLDYGFKAETAMASYCSELQFLGNPVTNHVQSAEQHN 484

Query: 505 QAVNSLALISARRTAEANDVLSLLLASHLYCTLQAVDLRAMELDFKKQFDPLLPTLLQQH 564
Q VNSL LIS+R+TAEA ++L L+ ++ L QA+DLR +E + K + T+ ++

Sbjct: 485 QDVNSLGLISSRKTAEAIVEILKMSSTFLVALCQAIDLRQIEENVKSAVKSCVMTVARKT 544

Query: 565 LGTGLDVNALALE-VKKALNKRLEQTTTY----DLEPRWHDAFSYATGTVVVELLSSSPSA 619
L T A +K L + +++ + D + +VE ++ +A

Sbjct: 545 LSTSATGGLHAARFCEKDLLQEIDREAVFAYADDPCSANYPLMKKLRNVLVERALANGAA 604

Query: 620 NVTLTAVNAWKVASAEK-----AISLTREVRNRFWQTPSSQAPAHAYLSPRTRVLY 670
KVA E+ ++ V N TP+ +Y LY

Sbjct: 605 EFNAETSVFAKVAQFEEELRAALPAVLAARAAVENGTAATPNRITECRSY-----PLY 658

Query: 671 SFVREELGVQARRGDVFGVQQETIGSNVSRIYEAIKDGR 710
FVREELG G + + G ++++ AI G+

Sbjct: 659 RFVREELGTA-----YLTGEKTRSPGEELNKVLVAINQGK 693

☐ >gi|51341137|gb|AAU01183.1| phenylalanine aminomutase [Taxus chinensis]
Length = 687

Score = 330 bits (845), Expect = 1e-88

Identities = 240/650 (36%), Positives = 335/650 (51%), Gaps = 56/650 (8%)

Query: 94 DEIRARVDKSVDFLKAQLQNS--VYGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPPT 151
 ++ RARV+ +++ + ++ +YGVTTGFG + RT LQ++LI L GV

Sbjct: 56 EQCRARVETCSSWVQRKAEDGADIYGVTTGFGACSSRRTNQLSELQESLIRCLLAGVFTK 115

Query: 152 SVSSFSVGRGLENLPLEVVRGAMVIRVNSLTRGHSVAVRLVLEALTNFLNHRITPIVPL 211
 +S SV + LP R AM++R+NS T G S +R V+EAL LN ++P VPL

Sbjct: 116 GCAS-SV-----DELPATATRSAMLLRLNSFTYGC SGIRWEVMEALEKLLNSNVSPKVPL 169

Query: 212 RGSISASGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEAVVLGPKKEG 271
 RGS+SASGDL PL+YIAG + G P V + G + + A EA+S GL L KEG

Sbjct: 170 RGSVSASGDLIPLAYIAGLLIGKPSVIARI---GDDVEVPAPPEALSRVGLRPFKLQAKEG 226

Query: 272 LGLVNGTAVSASMATXXXXXXXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQ 331
 L LVNGT+ + ++A+ E + G++ P IH V +PHPGQ

Sbjct: 227 LALVNGTSFATAVASTVMYDANVLLLLVETLCGMFCEVIFGREEFAHPLIHKV-KPHPGQ 285

Query: 332 VEARNIRTLTSGSSFAXXXXXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYST 391
 +E A + LL S F +QDRY LR+SPQ+L PLV+ + A +T

Sbjct: 286 IESAELEWLLRSSPFQELSREYYSIDKLKKP-KQDRYALRSSPQWLAPLVQTIRDATTT 344

Query: 392 LSLENNTTTNDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNA 451
 + E N+ DNP++D N + HG NFQ SAV M+ R+A+A +GKL F Q TEL+

Sbjct: 345 VETEVNSANDNPIIDHANDRALHGANFQGSVAGFYMDYVRIAVAGLGKLLFAQFTELMIE 404

Query: 452 AMNRGLPSCLA-AEDPSLNYHGKGLDIHIAAYASELGHLANPVTTTFVQPAEMGNQAVNSL 510
 + GLP L+ D S++Y KGLDI +AAY+SEL +LANPVTT V AE NQ +NSL

Sbjct: 405 YYSNGLPGNLSLGPDLSDYGLKGLDIAMAAYSSELQYLANPVTTTHVHSAEQHNQDINS 464

Query: 511 ALISARRTAEANDVLSLLLASHLYCTLQAVDLRAMELDFKKQFDPLLPTLLQQHLGTGLD 570
 ALISAR+T EA D+L L++ASHL QAVDLR +E K + ++ TL + G D

Sbjct: 465 ALISARKTEEALDILKLMIAASHLTAMCQAVDLRQLEEALVKVVENNVSTLADE-CGLPND 523

Query: 571 VNALALEVKKALNKRLEQTTTYDLEPRWHDFAFSYATGTVVVELLSSSPSANVTLTAVNAWK 630
 A L V KA+ P + S T+ LL S T+ A++


Sbjct: 524 TKARLLYVAKV-----PVYTYLESPCDPTLPLLLGLKQSCFDTILALHKKD 570


Query: 631 VASAEKAISLTREVRNRFWQTPSSQAPAHAYLSPR-----TRV-----LYS 671
 + + E R ++ A L + R+ Y


Sbjct: 571 GIETDTLVDRLAEFKRLSDRLENEMTAVRVLYEKKGHKTADNNDALVRIQGSKFLPFYR 630

Query: 672 FVREEL--GVQARRGDVFGVGVQQETIGSNVSRIYEAIKDGRINHVLVKML 719
 FVREEL GV + R +++T +V ++++AI DGRI L+ L

Sbjct: 631 FVREELDTGVMSAR-----REQTPQEDVQKVFDAIADGRITVPLLHCL 673

☐ >gi|50931453|ref|XP_475254.1|  putative phenylalanine ammonia-lyase (EC 4.3.1.5) (japonica cultivar-group)]

gi|53981741|gb|AAV25018.1|  putative phenylalanine ammonia-lyase [Oryza sativa (cultivar-group)]

gi|46391133|gb|AAS90660.1|  putative phenylalanine ammonia-lyase (EC 4.3.1.5) [O (japonica cultivar-group)]

Length = 716

Score = 329 bits (844), Expect = 2e-88

Identities = 240/689 (34%), Positives = 348/689 (50%), Gaps = 42/689 (6%)

Query: 43 GHAAHQ---SQLEIVQELLSDPTDDVVELSGYSLTXXXXXXXXXXXXXXXXXX--QNDDEIR 97
 G AA + S L+ V+ ++++ VV + G SL + D+ R
 Sbjct: 29 GKAAEEMAGSHLDEVKRMVAEYRQPVVRIEGASLRQAQVAAVAGAGDGEAMVELDESAR 88

Query: 98 ARVDKSVDFLKAQLQNSV--YGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPPTS SVSS 155
 RV S D++ + N YGVTTGFG ++ RT++ +LQ+ LI G T
 Sbjct: 89 ERVKASSDWVMNSMANGTDSYGVTTGFGATSHRRTKEGGALQRELIRFLNAGAFGTGADG 148

Query: 156 FSVGRGLENLTPLEVVVRGAMVIRVNSLTRGHSVRLVLEALTNFLNHRITPIVPLRGS I 215
 + LP R AM++R+N+L +G+S +R +LEA+ LN +TP +PLRG+I
 Sbjct: 149 -----HVLPA GATRAAMLVRINTLLQGYS GIRFEILEAVAKLLNANVTPLPLRGTI 200

Query: 216 SASGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEA--VVLGPKEGLG 273
 +ASGDL PLSYIAG +TG + V V +G + + A EA + G++ L PKEGL
 Sbjct: 201 TASGDLVPLSYIAGLVTGREN-SVAVAPDGRK--VNAAEAFKIAGIQGGFFELQPKEGLA 257

Query: 274 LVNGTAVSASMATXXXXXXXXXXXXXXXXXXXXXVEAMVGQQGSFAPFIHDVCRPHPGQVE 333
 +VNGTAV + +A+ E M G+ H + + HPGQ+E
 Sbjct: 258 MVNGTAVGSGLASTVLFEANVLAILAEVLSAVFCEVMNGKPEYTDHLTHKL-KHHPGQIE 316

Query: 334 VARNIRTLLSGSSFAXXXXXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLS 393
 A + +L GSS+ +QDRY LRTSPQ+LGP +E + A ++
 Sbjct: 317 AAAIMEHILEGSSYMKEAKRLGELDPLMKP-KQDRYALRTSPQWLGPQIEVIRAATKSIE 375

Query: 394 LENNTTTDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAM 453
 E N+ DNPL+DV + HGGNFQ + + +SM+ TRLA+A IGKL F Q +EL+N
 Sbjct: 376 REINSVNDNPLIDVSRGKALHGGNFQGTPIGVSMNTRLAIAAIGKLMFAQFSELVNDFY 435

Query: 454 NRGLPSCLA-AEDPSLNYHGKGLDIHIAAYASELGHLANPVTTTFVQPAEMGNQAVNSLAL 512
 N GLPS L+ +PSL+Y KG +I +A+Y SEL L NPVT VQ AE NQ VNSL L
 Sbjct: 436 NNGLPSNLSGGRNP SLDYGFKGA EIAMASYCSELQFLGNPVTNHVQSAEQHNQDVNSLGL 495

Query: 513 ISARRTAEANDVLSLLLASHLYCTLQAVDLRAMELDFKKQFDPLLPTLLQQHLGTGLDVN 572
 IS+R+TAEA D+L L+ ++ L QA+DLR +E + K + T+ ++ L T +
 Sbjct: 496 ISSRKTAEAIDILKMSSTFLVALCQAIDLRHIEENVKGAVKTCVMTVAKKTLSTN---S 552

Query: 573 ALALEVKKALNKRL-----EQTTTYDLEP--RWHDAFSYATGTVVVELLSSSPSANVTLT 624
 L V + K L E Y + P + +VE ++ +A
 Sbjct: 553 TGGLHVARFCEKDLLSEIDREAVFAYADDP CSANYPLMKKLRSVLVERALANGAAEFDAE 612

Query: 625 AVNAWKVASAEKAI--SLTREVRNRFWQTPSSQAPAHAYLSP-RTRVLYSFVREELGVQA 681
 KVA E+ + +L R V S A A ++ R+ LY FVREELG
 Sbjct: 613 TSVLAKVARFEEELRAALPRAVEAARA AVESGTAAAPNRIAECRSYPLYRFVREELGTA- 671

Query: 682 RRGDVFGVGVQQETIGSNVSRIYEAIKDGR 710
 G + + G ++++ AI G+
 Sbjct: 672 ----YLTGEKTRSPGEELNKVLVAINQ GK 696

☐ >gi|58618142|gb|AAW80637.1| phenylalanine ammonia lyase [Isoetes lacustris]
 Length = 718

Score = 329 bits (844), Expect = 2e-88

Identities = 241/709 (33%), Positives = 358/709 (50%), Gaps = 44/709 (6%)

Query: 31 PTSALRRTPGLD----GHAAHQSQLEIVQELLSDP-TDDVVELSGYSLTXXXXXXXXXXXX 85
 P +A++++ L+ G A +S LE V+E++ + V + G LT
 Sbjct: 21 PPAAMKKSDPLNWGKAGEALQRSHLEEVKEMIKTVYSSKKVSI EGTKLTIAQVAAIARRA 80

Query: 86 XXXXXQNDDEIRARVDKSVDFLKAQLQNSV-----YGVTTGFGGSADTRTEDAVSLQKAL 140
 + + + RV++S +++ LQN++ YGVTTGFG ++ RT+ V LQK L

Sbjct: 81 EVEVHLDAEAAKKRVEESSNWV---LQNAKGTDTYGVTTGFGATSHRRTDQGVLELQKEL 137

Query: 141 IEHQLCGVTPTSVSSFSVGRGLENLPLEVVRGAMVIRVNSLTRGHSAVRLVVLEALTNF 200
 I G+ F G +N LP R AM++R N+L +G+S +R +L +

Sbjct: 138 IRFLNAGI-----FHSPEGCDNVLPSSSTARAAMLVRTNTLMQGYSGIRWEILATMEKL 190

Query: 201 LNHRTPIVPLRGSISASGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIMFAREAIISLFG 260
 LN ITP +PLRG+I+ASGDL PLSYIAG +TG P+ + V +G KI+ EA+++ G

Sbjct: 191 LNaNITPKLPLRGTTITASGDLVPLSYIAGLLTGRPNRA-VTCDG--KIITGAELAMVG 247

Query: 261 LEAVV-LGPKEGLGLVNGTAVSASMATXXXXXXXXXXXXXXXXXXXXVEAMVGQGSFAP 319
 +E L PKEGL LVNGTAV + +A+ E M G+ P

Sbjct: 248 VEKPFELQPKLEGLLVNGTAVGSGLASIVCFEANVLAVLAEILSAFFCEVMQGAFTDP 307

Query: 320 FIHDVCRPHPGQVEVARNIRTLLSGSSFAXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLG 379
 H + + HPGQ+E A + +L GS++ +QDRY LRTSPQ+LG

Sbjct: 308 LTHKL-KHHPGQIEAAAVMEYVLEGSAYMKAACKLHETDSLKKP-KQDRYALRTSPQWL 365

Query: 380 PLVEDMMHAYSTLSLENNTTNDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGK 439
 P +E + A ++ E N+ DNP++DV + HGGNFQ + + +SM+ RL++A IGK

Sbjct: 366 PQIEVIRMASHSIEREINSVNDNPIIDVSRDKALHGGNFQGTPIGVSMNVRLSIAAIGK 425

Query: 440 LNFTQCTELLNAAMNRLPSCLA-AEDPSLNYHGKGLDIHIAAYASELGHLANPVTTFVQ 498
 L F Q +EL+ N GLPS L+ +PSL+Y KG +I +A+Y SEL LANPVT VQ

Sbjct: 426 LMFAQFSELVCDFYNNGLPSNLGGPNPSLDYGFKGAEIAMASYCSELQFLANPVTNHVQ 485

Query: 499 PAEMGNQAVNSLALISARRTAEANDVLSLLLASHLYCTLQAVDLRAMELDFKKQFDPLLP 558
 AE NQ VNSL LISAR+TAEA ++L L+ S L QAVDLR +E + ++

Sbjct: 486 SAEQHNQDVNSLGLISARKTAEAVEILKLMSTSFLVALCQAVDLRHLEEIMQSTVKS SVS 545

Query: 559 TLLQQHLGTGLDVNALALEVKKALNKRLEQTTTYDLEPRWHDFAFSYATGTVVLELSSSPS 618
 ++ L TGL + L + + L+ + D S A + +L

Sbjct: 546 HAAKKTLLTGL--GGVLLPSRFCEKELLQVVDNVHVFYVDDPASAAAYPLMQKLRQVLVE 603

Query: 619 ANVTLTAVNAWKVASAEKAIISLTREVRNRWFQTPSSQAP-----AHAYLSPRTRV 668
 ++ + S K I+L E + T A A+ R+

Sbjct: 604 HSLKNIHEEGDESTSVFKKITLFEEELKKQLVTEVPLARDAYDKGQFSIANKIQECSRYP 663

Query: 669 LYSFVREELGVQARRGDVFGVQQETIGSNVSRIYEAIKDGRINHVLVK 717
 LY FVR+E G + G + + G + ++Y A+ G++ L+K

Sbjct: 664 LYEFVRKEAGT-----TLLSGTRVLSPGEDFDKVYAAMSAGKLVTPLLK 707

☐ >gi|51341139|gb|AAU01184.1| phenylalanine aminomutase [Taxus x media]
 Length = 687

Score = 329 bits (843), Expect = 2e-88

Identities = 239/650 (36%), Positives = 337/650 (51%), Gaps = 56/650 (8%)

Query: 94 DEIRARVDKSVDFLKAQLQNS--YGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPT 151
 ++ RARV+ +++ + ++ +YGVTTGFG + RT LQ++LI L GV

Sbjct: 56 EQCRARVETCSSWVQRKAEDGADIYGVTTGFGACSSRRTNQLSELQESLIRCLLAGVFTK 115

Query: 152 SVSSFSVGRGLENLPLEVVRGAMVIRVNSLTRGHSAVRLVVLEALTNFLNHRTPIVPL 211
 +S SV + LP V R AM++R+NS T G S +R V+EAL LN ++P VPL

Sbjct: 116 GCAS-SV-----DELPATVTRSAMLLRLNSFTYGC SGIRWEVMEALEKLLNSNVS PKVPL 169

Query: 212 RGSISASGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEAVVLGPKEG 271
 RGS+SASGDL PL+YIAG + G P V + G + + A EA+S GL L KEG
 Sbjct: 170 RGSVSASGDLIPLAYIAGLLIGKPSVIARI---GDDVEVPAPPEALSRVGLRPFKLQAKEG 226

Query: 272 LGLVNGTAVSASMATXXXXXXXXXXXXXXXXXXXXXVEAMVGQQGSFAPFIHVDVCRPHPGQ 331
 L LVNGT+ + ++A+ E + G++ P IH V +PHPGQ
 Sbjct: 227 LALVNGTSFATALASTVMYDANVLLLLLVETLCGMFCEVIFGREEFAHPLIHKV-KPHPGQ 285

Query: 332 VEVARNIRTLLSGSSFAXXXXXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYST 391
 +E A + LL S F +QDRY LR+SPQ+L PLV+ + A +T
 Sbjct: 286 IESAELEWLLRSSPFQELSREYYSIDKLKKP-KQDRYALRSSPQWLAPLVQTIRDATTT 344

Query: 392 LSLENNTTTDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNA 451
 + E N+ DNP++D N + HG NFQ SAV M+ R+A+A +GKL F Q TEL+
 Sbjct: 345 VETEVNSANDNPIIDHANDRALHGANFQGSVAVGYMDYVRIAVAGLGKLLFAQFTELMIE 404

Query: 452 AMNRGLPSCLA-AEDPSLNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVNSL 510
 + GLP L+ D S++Y KGLDI +AAY+SEL +LANPVT V AE NQ +NSL
 Sbjct: 405 YYSNGLPGNLSLGPDLSDVDYGLKGLDIAMAAYSSELQYLANPVTTHVHSAEQHNQDINS 464

Query: 511 ALISARRTAEANDVLSLLLASHLYCTLQAVDLRAMELDFKKQFDPLLPTLLQQHLGTGLD 570
 ALISAR+T EA D+L L++ASHL QAVDLR +E K + ++ TL + G D
 Sbjct: 465 ALISARKTDEALDILKLMIAASHLTAMCQAVDLRQLEEALVKVVENVVSTLADE-CGLPND 523

Query: 571 VNALALEVKKALNKRLEQTTTYDLEPRWHDFAFSYATGTVVVELLS SSPSANVTLTAVNAWK 630
 A L V KA+ P + S + T+ LL S ++ A++
 Sbjct: 524 TKARLLYVAKAV-----PVYTYLESPSDPTLPLLLGLKQSCFDSILALHKKD 570

Query: 631 VASAEKAISLTREVRNRFWQTPSSQAPAHAYLSPR-----TRV-----LYS 671
 + + E R ++ A L + R+ Y
 Sbjct: 571 GIETDTLVDRLAEFKRLSDRLENEMTAVRVLYEKKGHKTADNNDALVRIQGSKFLPFYR 630

Query: 672 FVREEL--GVQARRGDVFGVQVQETIGSNVSRIYEAIKDGRINHVLVKML 719
 FVR+EL GV + R +++T +V ++++AI DGRI L+ L
 Sbjct: 631 FVRDELDTGVMSAR-----REQTPQEDVQKVFDAIADGRITVPLLHCL 673

☐ >gi|2052094|emb|CAA89007.1| phenylalanine ammonia-lyase [*Hordeum vulgare* subsp.
 gi|7437114|pir||T05970 phenylalanine ammonia-lyase (EC 4.3.1.5) - barley (fragmen
 Length = 549

Score = 329 bits (843), Expect = 2e-88

Identities = 211/556 (37%), Positives = 298/556 (53%), Gaps = 22/556 (3%)

Query: 20 SHAAPTKSAAGPTSALRRTPGLDGHAHQ---SQLEIVQELLS DPTDDVVELSGYSLTXX 76
 +H A R P G AA + S L+ V+ ++ + VV + G SLT
 Sbjct: 6 AHVAANGDGLCVAQPARADPLNWGKAAEELSGSHLDAVKRMVEEYRKPVVTMEGASLTIA 65

Query: 77 XXXXXXXXXXXXXXXQNDDEIRARVDKSVDFLKAQLQNSV--YGVTTGFGGSADTRTEDAV 134
 + D+ R RV +S D++ + N YGVTTGFG ++ RT++
 Sbjct: 66 MVAAVAAGNDTRV-ELDESARGRVKESSDWMNSMMNGTDSYGVTTGFGATSHRRTKEGG 124

Query: 135 SLQKALIEHQLCGVTPTSVSSFSVGRGLENLPLEVVRGAMVIRVNSLTRGHSVAVRLVVL 194
 +LQ+ LI G T + LP R AM++RVN+L +G+S +R +L
 Sbjct: 125 ALQRELIRFLNAGAFGTGTDG-----HVLPAATTRAAMLVRVNTLLQGYSGIRFEIL 176

Query: 195 EALTNFLNHRITPIVPLRGSISASGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIMFARE 254
 E + LN +TP +PLRG+I+ASGDL PLSYIAG +TG P+ V +GT+ + A E
 Sbjct: 177 ETIATLLNANVTPLPLRGITASGDLVPLSYIAGLVTGRPN-SVATAPDGTK--VNAAE 233

Query: 255 AISLFGLEA--VVLGPKEGLGLVNGTAVSASMATXXXXXXXXXXXXXXXXXXXXXVEAMVG 312
 A + G++ L PKEGL +VNGTAV + +A+ E M G
 Sbjct: 234 AFKIAGIQHGFFELQPKEGLAMVNGTAVGSGGLASMVLFEANVLSLLAEVLSAVFCEVMNG 293

Query: 313 QQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGSSFAXXXXXXXXXXXXXXXXXXGILRQDRYPLR 372
 + H + + HPGQ+E A + +L GSS+ +QDRY LR
 Sbjct: 294 KPEYTDHLTHKL-KHHPGQIEAAAIMEHILEGSSYMLAKKLGEPLMKP-KQDRYALR 351

Query: 373 TSPQFLGPLVEDMMHAYSTLSLENNTTTNDNPLLDVENKQTAHGGNFQASAVSISMEKTRL 432
 TSPQ+LGP +E + A ++ E N+ DNPL+DV + HGGNFQ + + +SM+ TRL
 Sbjct: 352 TSPQWLGPQIEVIRAATKSIEREINSVNDNPLIDVSRGKAIHGGNFQGTPIGVSMNDTRL 411

Query: 433 ALALIGKLNFTQCTELLNAAMNRLPSCLA-AEDPSLNYHGKGLDIHIAAYASELGHLAN 491
 A+A IGKL F Q +EL+N N GLPS L+ +PSL+Y KG +I +A+Y SEL L N
 Sbjct: 412 AIAAIGKLMFAQFSELVNDNFYNNGLPSNLSSGRNPSLDYGFKAIEAMASYCSELQFLGN 471

Query: 492 PVTTFVQPAEMGNQAVNSLALISARRTAEANDVLSLLASHLYCTLQAVDLRAMELDFKK 551
 PVT VQ AE NQ VNSL LIS+R+TAEA D+L L+ ++ L QA+DLR +E + K
 Sbjct: 472 PVTNHVQSAEQHNQDVNSLGLISSRKTAEAIDILKLSSTFLVALCQAIDLRHLEENVKN 531

Query: 552 QFDPLLPTLLQQHLGT 567
 + T+ ++ L T
 Sbjct: 532 AVKSCVKTVARKTLST 547

☐ >gi|295824|emb|CAA34226.1| phenylalanine ammonia-lyase [Oryza sativa (japonica
 cultivar-group)]
 gi|129591|sp|P14717|PAL1_ORYSA Phenylalanine ammonia-lyase
 Length = 701

Score = 329 bits (843), Expect = 2e-88

Identities = 236/690 (34%), Positives = 358/690 (51%), Gaps = 59/690 (8%)

Query: 49 SQLEIVQELSDPTDDVVELSGYSLTXXXXXXXXXXXXXXXXXX--XXQNDDEIRARVDKSVDF 106
 S L+ V+ +++ + +V++ G +L + D+E R RV S ++
 Sbjct: 25 SHLDEVKRMVAQFREPLVKIQGATLRVGQVAAVAQAKDAARVAVELDEEARPRVKASSEW 84

Query: 107 LKAQLQNS--VYGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPTSVSSFSVGRGLEN 164
 + + + +YGVTTGFGG++ RT+D +LQ L+ + G+ T +
 Sbjct: 85 ILTCIAHGDDIYGVTTGFGGTSHRRTKDGPALQVELLRYLNAGIFGTGSDG-----H 136

Query: 165 TLPLEVVRGAMVIRVNSLTRGHSVRLVLEALTNFLNHRITPIVPLRGSISASGDLSP 224
 TLP E VR AM++R+N+L +G+S +R +LEA+T LN +TP +PLRG+I+ASGDL PL
 Sbjct: 137 TLPSETVRAAMLVRINTLLQGYSGIRFEILEAITKLLNTGVTPLPLRGITITASGDLVPL 196

Query: 225 SYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEA--VVLGPKEGLGLVNGTAVSA 282
 SYIAG ITG P+ + + +G + + A EA L G+E L PKEGL +VNGT+V +
 Sbjct: 197 SYIAGLITGRPNAQA-ISPDRK--VDAAEAFKLAGIEGGFTLNPKEGLAIVNGTSVGS 253

Query: 283 SMATXXXXXXXXXXXXXXXXXXXXXVEAMVGQQGSFAPFIHDVCRPHPGQVEVARNIRTLL 342
 ++A E M G+ H + + HPG ++ A + +L
 Sbjct: 254 ALAATVMFDANILAVLSEVLSAVFCEVMNGKPEYTDHLTHKL-KHHPGSIDAAAIMEHIL 312

Query: 343 SGSSFAXXXXXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTND 402
 +GSSF +QDRY LRTSPQ+LGP ++ + A ++ E N+ DN
 Sbjct: 313 AGSSFMASHAKKVNEMDPLLKP-KQDRYALRTSPQWLGPQIQVIRAATKSIEREVNSVNDN 371

Query: 403 PLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRLPSCLA 462

P++DV + HGGNFQ + + +SM+ RLA+A IGKL F Q +EL+N N GL S LA
 Sbjct: 372 PVIDVHRGKALHGGNFQGTPIGVSMNARLAIANIGKLMFAQFSELVNEFYNNGLTSNLA 431

Query: 463 -AEDPSLNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVNSLALISARRTAEA 521
 + +PSL+Y KG +I +A+Y+SEL +LANP+T VQ AE NQ VNSL L+SAR+T EA
 Sbjct: 432 GSRNPSLDYGFKGTEIAMASYSELQYLANPITNHVQSAEQHNQDVNSLGLVSARKTLEA 491

Query: 522 NDVLSLLLASHLYCTLQAVDLRAMELDFKKQFDPLLPTLLQQHL---GTGLDVNALALEV 578
 D+L L+ +++++ QAVDLR +E + K + + ++ L TG D+++
 Sbjct: 492 VDILKLMTSTYIVALCQAVDLRHLEENIKSSVKNCVTQVAKKVLTMNPTG-DLSSARFSE 550

Query: 579 KKALNKRLEQTTTYDLEPRWHDAFSYATG-----TVVELLSSSPSANVTL 623
 K L T D E FSYA V L+S L
 Sbjct: 551 KNLL-----TAIDREA----VFSYADDPCSANYPLMQKLRAVLVEHALTSGDRRARGL 599

Query: 624 TAVNAWKVASAEKAI SLTREVRNRFWQTPSSQAP-AHAYLSPRTRVLYSFVREELGVQAR 682
 + +V + + R R + AP A+ + R+ LY FVREELG
 Sbjct: 600 RVLQDHQVRGGAPLCAAPGD-RGRPRRRRQRTAPVANRIVESRSFPLYRFVREELGC--- 655

Query: 683 RGDVFFV-GVQQETIGSNVSRIYEAIKDGR I 711
 VF+ G + ++ G +++++ I G++
 Sbjct: 656 ---VFLTGEKLGKSPGEECNKVF LGISQGL 682

☐ >gi|42529530|gb|AAS18574.1| phenylalanine ammonia-lyase [Arabidopsis thaliana]
 Length = 694

Score = 329 bits (843), Expect = 2e-88

Identities = 236/676 (34%), Positives = 341/676 (50%), Gaps = 24/676 (3%)

Query: 49 SQLEIVQELLSIPTDDVVELSGYSLTXXXXXXXXXXXXXXXXXQNDDEIRARVDKSVDFLK 108
 S LE V++++ D V+L G +LT + +E R V S D++
 Sbjct: 27 SHLEEVKKMKDYRKGT VQLGGETLTIGQVA AVASGGPTV--ELSEEARGGVKASSDWVM 84

Query: 109 AQLQNSV--YGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPTSVSSFSVGRGLENL 166
 + YG+TTGFG S+ RT+ +LQK LI + G+ T + NTL
 Sbjct: 85 ESMNRD TD TYGIT TGF GSSRRRTDQGAALQKELIRYLNAGIFATG---NEDDDRNTL 140

Query: 167 PLEVVRGAMVIRVNSLTRGHSVRLVLEALTNFLNHRITPIVPLRGSISASGDLSPLSY 226
 P R AM+IRVN+L +G+S +R +LEA+T LN +ITP++PLRG+I+ASGDL PLSY
 Sbjct: 141 PRPATRAAMLIRVNTLLQGYSGIRFEILEAITLLNCKITPLLPLRGITITASGDLVPLSY 200

Query: 227 IAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEAVV-LGPKEGLGLVNGTAVSASMA 285
 IAG + G P+ + V G +I+ A EA L G+ + L PKEGL LVNGTAV +++A
 Sbjct: 201 IAGFLIGRPNSR-SVGPSG--EILTALEAFKLAGVSSFFELRPKEGLALVNGTAVGSALA 257

Query: 286 TXXXXXXXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGS 345
 + E M G+ F + + HPGQ+E A + +L GS
 Sbjct: 258 STVLYDANILVVFSEVASAMFAEVMQGKP-EFTDHLTHKLKHHPGQIEAAIMEHILDGS 316

Query: 346 SFAXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTDNPLL 405
 S+ +QDRY LRTSPQ+LGP +E + A + E N+ DNPL+
 Sbjct: 317 SYVKEALHLHKIDPLQKP-KQDRYALRTSPQWLGPQIEVIRAATKMIEREINSVNDNPLI 375

Query: 406 DVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCLA-AE 464
 DV + HGGNFQ + + ++M+ TR LALA IGKL F Q TEL+N N GLPS L+
 Sbjct: 376 DVSRNKAIHGGNFQGTPIGVAMDNTRLALASIGKLMFAQFTELVDNFYNNGLPSNLSGGR 435

Query: 465 DPSLNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVNSLALISARRTAEANDV 524

+PSL+Y KG ++ +A+Y SEL LANPVT V+ A NQ VNLS LIS+R TAEA +
 Sbjct: 436 NPSLDYGLKGAEVAMASYCSELQFLANPVTNHVESASQHNQDVNSLGLISSRTTAEAVVI 495

Query: 525 LLLLLASHLYCTLQAVDLRAMELDFKKQFDPLLPDLLQQHLGTGLDVNALALEVKKALNK 584
 L L+ ++L QA DLR +E KK + ++ + L ++ ++ +N+
 Sbjct: 496 LKLMSTTYLVALCQAFDLRHLEELKKAVNEVVSHSTAKSVL--AIEPFRKHDDILGVVNR 553

Query: 585 RLEQTTTYDLEPRWHDFAFSYATGTVVELLSSSPSANVTLTAVNAWKVASAEKAI SLTREV 644
 + D + + + P T T AE L +EV
 Sbjct: 554 EYVFSYVDDPSSLTNPLMQKLRHVLFDKALAEPEGE-TDTVFRKIGAFEALKFLLPKEV 612

Query: 645 -RNRFWQTPSSQAPAHAYLSPRTRVLYSFVREELGVQARRGDVFGVQQETIGSNVSRIY 703
 R R + A+ R+ LY FVR EL + + G + G + +++
 Sbjct: 613 ERVRTEYENGTFNVANRIKKCRSYPLRYFVRNELETR-----LLTGEDVRSPGEDFDKVF 667

Query: 704 EAIKDGRINHVLVKML 719
 AI G++ L + L
 Sbjct: 668 RAISQGLIDPLFECL 683

☐ >gi|1076371|pir||S52992 phenylalanine ammonia-lyase (EC 4.3.1.5) 3 - Arabidopsis
 gi|507948|gb|AAA69905.1| PAL3 gene product
 Length = 695

Score = 329 bits (843), Expect = 2e-88
 Identities = 236/676 (34%), Positives = 341/676 (50%), Gaps = 23/676 (3%)

Query: 49 SQLEIVQELSDPTDDVVELSGYSLTXXXXXXXXXXXXXXXXXQNDDEIRARVDKSVDFLK 108
 S LE V++++ D V+L G +LT + +E R V S D++
 Sbjct: 27 SHLEEVKKMKDYRKGTQVQLGGETLTIGQVAVASGGGPTV-ELSEEARGGVKASSDWM 85

Query: 109 AQLQNSV--YGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPTSVSSFSVGRGLENL 166
 + YG+TTGFG S+ RT+ +LQK LI + G+ T + NTL
 Sbjct: 86 ESMNRDSTDYGITTTGFGSSRRRTDQGAALQKELIRYLNAGIFATG----NEDDDRNTL 141

Query: 167 PLEVVRGAMVIRVNSLTRGHSAVRLVLEALTNFLNHRITPIVPLRGSISASGDLSPLSY 226
 P R AM+IRVN+L +G+S +R +LEA+T LN +ITP++PLRG+I+ASGDL PLSY
 Sbjct: 142 PRPATRAAMLIRVNTLLQGYSGIRFEILEAITTLLNCKITPLLPLRGITITASGDLVPLSY 201

Query: 227 IAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEAVV-LGPKEGLLVNGTAVSASMA 285
 IAG + G P+ + V G +I+ A EA L G+ + L PKEGL LVNGTAV +++A
 Sbjct: 202 IAGFLIGRPNSR-SVGPSG--EILTALEAFKLAGVSSFFELRPKEGLALVNGTAVGSALA 258

Query: 286 TXXXXXXXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGS 345
 + E M G+ F + + HPGQ+E A + +L GS
 Sbjct: 259 STVLYDANILVVFSEVASAMFAEVMQGKP-EFTDHLTHKLKHHPGQIEAAAIMEHILDGS 317

Query: 346 SFAXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTNDNPLL 405
 S+ +QDRY LRTSPQ+LGP +E + A + E N+ DNPL+
 Sbjct: 318 SYVKEALHLHKIDPLQKP-KQDRYALRTSPQWLGPQIEVIRAATKMIEREINSVNDNPLI 376

Query: 406 DVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCLA-AE 464
 DV + HGGNFQ + + ++M+ TRALA IGKL F Q TEL+N N GLPS L+
 Sbjct: 377 DVSRNKAIHGGNFQGTPIGVAMDNTRLALASIGKLMFAQFTELVDNFYNNGLPSNLSGGR 436

Query: 465 DPSLNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVNSLALISARRTAEANDV 524
 +PSL+Y KG ++ +A+Y SEL LANPVT V+ A NQ VNLS LIS+R TAEA +
 Sbjct: 437 NPSLDYGLKGAEVAMASYCSELQFLANPVTNHVESASQHNQDVNSLGLISSRTTAEAVVI 496

Query: 525 LSLLLASHLYCTLQAVDLRAMELDFKKQFDPLLPTLLQQHLGTGLDVNALALEVKKALNK 584
 L L+ ++L QA DLR +E KK + ++ + L ++ ++ +N+
 Sbjct: 497 LKLMSTTYLVALCQAFDLRHLEELKKAVNEVVSHAKSVL--AIEPFRKHDDILGVVNR 554

Query: 585 RLEQTTTYDLEPRWHDFAFSYATGTVVELLSSSPSANVTLTAVNAWKVASAEKAISLTREV 644
 + D + + + P T T AE L +EV
 Sbjct: 555 EYVFSYVDDPSSLTNPLMQKLRHVLFDKALAEPEGE-TDTVFRKIGAFEAEKFLLPKEV 613

Query: 645 -RNRFWQTPSSQAPAHAYLSPRTRVLYSFVREELGVQARRGDVFGVQQETIGSNVSRIY 703
 R R + A+ R+ LY FVR EL + + G + G + +++
 Sbjct: 614 ERVRTEYENGTFNVANRIKKCRSYPLYRFVRNELETR-----LLTGEDVRSPGEDFDKVF 668

Query: 704 EAIKDGRIHVLVKML 719
 AI G++ L + L
 Sbjct: 669 RAISQGLIXPLFECL 684

☐ >gi|14195674|sp|P45725|PAL3_ARATH Phenylalanine ammonia-lyase 3
 Length = 695

Score = 329 bits (843), Expect = 2e-88

Identities = 236/676 (34%), Positives = 341/676 (50%), Gaps = 23/676 (3%)

Query: 49 SQLEIVQELLSDPDDEVELSGYSLTXXXXXXXXXXXXXXXXXQNDDEIRARVDKSVDFLK 108
 S LE V++++ D V+L G +LT + +E R V S D++
 Sbjct: 27 SHLEEVKKMKDYRKGTVQLGGETLTIGQVAASGGGPTV-ELSEEARGGVKASSDWVM 85

Query: 109 AQLQNSV--YGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPTSVSSFSVGRGLENLTL 166
 + YG+TTGFG S+ RT+ +LQK LI + G+ T + NTL
 Sbjct: 86 ESMNRD TDYGITGFGSSRRRTDQGAALQKELIRYLNAGIFATG----NEDDDRNTL 141

Query: 167 PLEVVRGAMVIRVNSLTRGHSVRLVLEALTNFLNHRITPIVPLRGSISASGDLSPLSY 226
 P R AM+IRVN+L +G+S +R +LEA+T LN +ITP++PLRG+I+ASGDL PLSY
 Sbjct: 142 PRPATRAAMLIRVNTLLQGYSGIRFEILEAITTLLNCKITPLLPLRGTTITASGDLVPLSY 201

Query: 227 IAGAITGHPDVKVHVLHEGTEKIMFAREAI SLFGLEAVV-LGPKEGLGLVNGTAVSASMA 285
 IAG + G P+ + V G +I+ A EA L G+ + L PKEGL LVNGTAV +++A
 Sbjct: 202 IAGFLIGRPNSR-SVGPSG--EILTALEAFKLAGVSSFFELRPKEGLALVNGTAVGSALA 258

Query: 286 TXXXXXXXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGS 345
 + E M G+ F + + HPGQ+E A + +L GS
 Sbjct: 259 STVLYDANILVVFSEVASAMFAEVMQGP-EFTDHLTHKLKHHPGQIEAAAIMEHILDGS 317

Query: 346 SFAXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTDNPLL 405
 S+ +QDRY LRTSPQ+LGP +E + A + E N+ DNPL+
 Sbjct: 318 SYVKEALHLHKIDPLQKP-KQDRYALRTSPQWLGPQIEVIRAATKMIEREINSVNDNPLI 376

Query: 406 DVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCLA-AE 464
 DV + HGGNFQ + + ++M+ TRALA IGKL F Q TEL+N N GLPS L+
 Sbjct: 377 DVSRNKAIHGGNFQGTPIGVAMDNTRLALASIGKLMFAQFTELVNDFYNNGLPSNLSSGR 436

Query: 465 DPSLNYHGKGLDIHIAAYASELGHLANPVTTTFVQPAEMGNQAVNSLALISARRTAEANDV 524
 +PSL+Y KG ++ +A+Y SEL LANPVT V+ A NQ VNSL LIS+R TAEA +
 Sbjct: 437 NPSLDYGLKGAEVAMASYCSELQFLANPVTNHVESASQHNQDVNSLGLISSRTTAEAVVI 496

Query: 525 LSLLLASHLYCTLQAVDLRAMELDFKKQFDPLLPTLLQQHLGTGLDVNALALEVKKALNK 584
 L L+ ++L QA DLR +E KK + ++ + L ++ ++ +N+
 Sbjct: 497 LKLMSTTYLVALCQAFDLRHLEELKKAVNEVVSHAKSVL--AIEPFRKHDDILGVVNR 554

Query: 585 RLEQTTTYDLEPRWHDFAFSYATGTVVELLSSSSPSANVTLTAVNAWKVASAEKAISLTREV 644
 + D + + + P T T AE L +EV
 Sbjct: 555 EYVFSYVDDPSSLTNPLMQKLRHVLFDKALAEPEGE-TDTVFRKIGAFEAEKFLLPKEV 613

Query: 645 -RNRFWQTPSSQAPAHAYLSPRTRVLYSFVREELGVQARRGDVFGVGVQQTIGSNVSRIY 703
 R R + A+ R+ LY FVR EL + + G + G + +++
 Sbjct: 614 ERVRTEYENGTFNVANRIKKCRSYPLYRFVRNELETR-----LLTGEDVRSPGEDFDKVF 668

Query: 704 EAIKDGRINHVLVKML 719
 AI G++ L + L
 Sbjct: 669 RAISQGLIDPLFECL 684

☐ >gi|51341141|gb|AAU01185.1| phenylalanine aminomutase [Taxus canadensis]
 Length = 687

Score = 328 bits (842), Expect = 3e-88
 Identities = 241/651 (37%), Positives = 334/651 (51%), Gaps = 58/651 (8%)

Query: 94 DEIRARVDKSVDFLKAQLQNS--VYGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPPT 151
 ++ RARV+ +++ + ++ +YGVTTGFG + RT LQ++LI L GV
 Sbjct: 56 EQCRARVETCSSWVQRKAEDGADIYGVTTGFGACSSRRTNQLSELQESLIRCLLAGVFTK 115

Query: 152 SVSSFSVGRGLENLPLEVVRGAMVIRVNSLTRGHSVRLVLEALTNFLNHRITPIVPL 211
 +S SV + LP V R AM++R+NS T G S +R V+EAL LN ++P VPL
 Sbjct: 116 GCAS-SV-----DELPATVTRSAMLRLNSFTYGC SGIRWEVMEALEKLLNSNVSPKVPL 169

Query: 212 RGSISASGDLSPSYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEAVVLGPKEG 271
 RGS+SASGDL PL+YIAG + G P V + G + + A EA+S GL L KEG
 Sbjct: 170 RGSVSASGDLIPLAYIAGLLIGKPSVIARI---GDDVEVPAPPEALSRVGLRPFKLQAKEG 226

Query: 272 LGLVNGTAVSASMATXXXXXXXXXXXXXXXXXXVEAMVGQQGSFAPFIHDVCRPHPGQ 331
 L LVNGT+ + ++A+ E + G++ P IH V +PHPGQ
 Sbjct: 227 LALVNGTSFATALASTVMYDANVLLLLVETLCGMFCEVIFGREEFAHPLIHKV-KPHPGQ 285

Query: 332 VEVARNIRTLLSGSSFAXXXXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYST 391
 +E A + LL S F +QDRY LR+SPQ+L PLV+ + A +T
 Sbjct: 286 IESAELEWLLRSPFQDLSREYYSIDKLKKP-KQDRYALRSSPQWLAPLVQTIRDATTT 344

Query: 392 LSLENNTTTDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNA 451
 + E N+ DNP++D N + HG NFQ SAV M+ R+A+A +GKL F Q TEL+
 Sbjct: 345 VETEVNSANDNPIIDHANDRALHGANFQGSAGVFYMDYVRIAVAGLGKLLFAQFTELMIE 404

Query: 452 AMNRGLPSCLA-AEDPSLNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVNSL 510
 + GLP L+ D S++Y KGLDI +AAY+SEL +LANPVT V AE NQ +NSL
 Sbjct: 405 YYSNGLPGNLSLGPDLSDYGLKGLDIAMAAYSSELQYLANPVTTHVHSAEQHNQDINS 464

Query: 511 ALISARRTAEANDVLSLLASHLYCTLAVDLRAMELDFKKQFDPLLP TLLQQHLGTGLD 570
 ALISAR+T EA D+L L++ASHL QAVDLR +E K + ++ TL + G D
 Sbjct: 465 ALISARKTDEALDILKLMIAASHLTAMCQAVDLRQLEEALVKVVENVVSTLADE-CGLPND 523

Query: 571 VNALALEVKA-----LNKRLEQT-----TTYDLEPRWHDFAFSYATGTVVELLSS 615
 A L V KA L + T + +D H T T+V+ L+
 Sbjct: 524 TKARLLYVAKAVPVYTYLES PCDPTLPLLLGLKQSCFDSILALHKKDGIETDTLVDR LAE 583

Query: 616 -----SPSANVTLTAVNAWKVASAEKAISLTREVRNRFWQTPSSQAPAHAYLSPRTRVLY 670
 S +TAV K T + + Y
 Sbjct: 584 FEKRLSDRLENEMTAVRVLYEKKGHK-----TADNNDALVRIQGSKFLPFY 629

Query: 671 SFVREEL--GVQARRGDVFGVGVQQTIGSNVSRIYEAIKDRINHVLVKML 719
 FVR+EL GV + R +++T +V ++++AI DGRI L+ L
 Sbjct: 630 RFVRDELDTGVMSAR-----REQTPQEDVQKVFDAIADGRITVPLLHCL 673

☐ >gi|3334284|sp|O04058|PALY_HELAN Phenylalanine ammonia-lyase
 gi|2887304|emb|CAA73065.1| phenylalanine ammonia lyase [Helianthus annuus]
 Length = 667

Score = 328 bits (841), Expect = 4e-88
 Identities = 238/658 (36%), Positives = 344/658 (52%), Gaps = 35/658 (5%)

Query: 40 GLDGHAHQSQLEIVQELLSDPTDDVVELSGYSLTXXXXXXXXXXXXXXXXXQND--DEIR 97
 G+ A S L+ V++++ + VV+L G +LT + + + R
 Sbjct: 23 GVAAEALTGSHLDEVKKMVGEFRKPVVKLGGETLTVSQVAGISAAGDGNMVKVELSEAR 82

Query: 98 ARVDKSVDFLKAQLQNSV--YGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPPTSVSS 155
 A V S D++ + YGVTTGFG ++ RT++ +LQK LI G+
 Sbjct: 83 AGVKASSDWVMESEMNKGTDSYGVTTGFGATSHRRTKNGGALQKELIRFLNAGI----- 135

Query: 156 FSVGRGLENLTPLEVVVRGAMVIRVNSLTRGHSVRLVLEALTNFLNHRITPIVPLRGTI 215
 F G +TLP R AM++R+N+L +G+S +R +LEA+T FLN+ ITP +PLRG+I
 Sbjct: 136 FGNGTESSHTLPHSATRAAMLVRINTLLQGYSGIRFEILEAITKFLNNNITPCPLRGTI 195

Query: 216 SASGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIMFAREAI SLFGLEA--VVLGPKEGLG 273
 +ASGDL PLSYIAG +TG P+ K V G +++ A A + G+E L PKEGL
 Sbjct: 196 TASGDLVPLSYIAGLLTGRPNKA-VGPAG--EVLNAESAFAQAGVEGGFFELQPKEGLA 252

Query: 274 LVNGTAVSASMATXXXXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQVE 333
 LVNGTAV + MA+ E M G+ F + + HPGQ+E
 Sbjct: 253 LVNGTAVSGMASMVLFEANVLALLSEVLSAIFAEVMQGKP-EFTDHLTHKLKHHPGQIE 311

Query: 334 VARNIRTLTSGSSFAXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLS 393
 A + +L GS + +QDRY LRTSPQ+LGP +E + A +
 Sbjct: 312 AAAIMEYILDGSDYVKAQKVHEMDPLQKP-KQDRYALRTSPQWLGPQIEVIRSATKMIE 370

Query: 394 LENNTTTDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAM 453
 E N+ DNPL+DV + HGGNFQ + + +SM+ TRLA+A IGK+ Q +EL+N
 Sbjct: 371 REINSVNDNPLIDVSRNKALHGGNFQGTPIGVSMDNTRLAIAAIGKVIAQFSELVNDFY 430

Query: 454 NRGLPSCLA-AEDPSLNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVNSLAL 512
 N GLPS L+ +PSL+ KG +I +A+Y SEL LANPVT VQ AE NQ VNSL L
 Sbjct: 431 NNGLPSHLSGGRNP SLDSGFKGGEIAMASYCSELQLANPVTNHVQSAEQHNQDVNSLGL 490

Query: 513 ISARRTAEANDVLSLLASHLYCTLQAVDLRAMELDFKKQFDPLLPTLLQQHLGTGLDVN 572
 ISAR+TAEA D+L L+ +++L Q++DLR +E + K + + ++ L G++
 Sbjct: 491 ISARKTAEAVDILKLSSTYLVALCQSIDLRHLEENMKSTVKNTVSQVAKKVLTMGVNGE 550

Query: 573 ALALEVKKALKNRLEQTTTYDLEPRWHDFAFSYATGTVVVELLSS---SPSANVTLTAVNA- 628
 L + K L + + + D T +++ L + N T NA
 Sbjct: 551 ---LHPSRFCEKDLLRVVDREYVFAYADDPCLTTYPLMQKLRQVLVDHALNNGETEKAN 607

Query: 629 ----WKVASAE---KAISLTREVRN-RFWQTPSSQAPAHAYLSPRTRVLYSFVREELG 678
 K+A+ E KAI L +EV + R + + + + R+ LY FVREELG
 Sbjct: 608 TSIFQKIATFEDELKAI-LPKEVESVRVAFENGMSIPNRIKACRSYPLYRFVREELG 664

☐ >gi|1491619|emb|CAA68256.1| phenylalanine ammonia-lyase [Bromheadia finlaysoniar
gi|3024359|sp|Q42609|PALY_BROFI Phenylalanine ammonia-lyase
Length = 703

Score = 328 bits (840), Expect = 5e-88

Identities = 205/527 (38%), Positives = 289/527 (54%), Gaps = 19/527 (3%)

Query: 49 SQLEIVQELLSDPTDDVVELSGYSLTXXXXXXXXXXXXXXXXXQNDDEIRARVDKSVDFLK 108
S L+ V++++ + VV+L G L + + RA V S D++
Sbjct: 29 SHLDEVKKMVVEEFRPVVKLEGVKLKISQVAAVAFGGGASAVELAESARAGVKASSDWVL 88

Query: 109 AQLQNSV--YGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPTSVSSFSVGRGLENLTL 166
+ YGVTTGFG ++ RT+ +LQK LI+ G+ G G NTL
Sbjct: 89 ESVDKGTDSYGVTTGFGATSHRRTKQGGALQKELIKFLNAGI-----FGSGNSNTL 139

Query: 167 PLEVVRGAMVIRVNSLTRGHSVRLVLEALTNFLNHRITPIVPLRGSISASGDLSPLSY 226
P R AM++R+N+L +G+S +R +L+A+ LN ITP +PLRG+I+ASGDL PLSY
Sbjct: 140 PSAATRAAMLVRINTLLQGYSGIRFEILKAIATLLNKNITPCLPLRGTITASGDLVPLSY 199

Query: 227 IAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEAVV--LGPKEGLGLVNGTAVSASM 284
+AG +TG P+ K + T + A A L G+ + L PKEGL LVNGTAV + +
Sbjct: 200 LAGILTRPNSKARTPNGST---VDATTAFLRAGISSGFFDLQPEGLALVNGTAVGSGV 256

Query: 285 ATXXXXXXXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQVEVARNIRTLTSLG 344
A+ E M G+ F + + HPGQ+E A + +L G
Sbjct: 257 ASIVLFETNILAVMAELLSALFCEVMQGKP-EFTDHLTHKLKHHPGQIEAAAVMEHILEG 315

Query: 345 SSFAXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTDNPL 404
SS+ +QDRY LRTSPQ+LGP +E + A ++ E N+ DNPL
Sbjct: 316 SSYMKMAKKLHEMDPLQKP-KQDRYALRTSPQWLGPQIEVIRAATKSIEREINSVNDNPL 374

Query: 405 LDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCLA- 463
+DV + HGGNFQ + + +SM+ TRLA+A IGKL F Q +EL+N N GLPS L++
Sbjct: 375 IDVSRNKALHGGNFQGTPIGVSMDNTRLAIAAIGKLMFAQFSELVNDFYNGLPSNLSSG 434

Query: 464 EDPSLNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVNSLALISARRTAEAND 523
+PSL+Y KG +I +A+Y SEL LANPVT VQ AE NQ VNSL LIS+R+TAEA D
Sbjct: 435 RNPSLDYGFKAIEIAMASYCSELQALANPVTNHVQSAEQHNQDVNSLGLISSRKTAEAVD 494

Query: 524 VLSLLLASHLYCTLQAVDLRAMELDFKKQFDPLLPDLLQHLGTGLD 570
+L L+ + L QAVDLR +E + K + + ++ L G++
Sbjct: 495 ILKLMSTTFLVGLCQAVDLRHLEENLKNVKNNTVSQVAKRVLTMGVN 541

☐ >gi|7208614|gb|AAF40223.1| phenylalanine ammonia-lyase 1 [Rubus idaeus]
gi|14195012|sp|Q9M568|PAL1_RUBID Phenylalanine ammonia-lyase 1 (RiPAL1)
Length = 710

Score = 328 bits (840), Expect = 5e-88

Identities = 238/691 (34%), Positives = 355/691 (51%), Gaps = 44/691 (6%)

Query: 49 SQLEIVQELLSDPTDDVVELSGYSLTXXXXXXXXXXXXXXXXXQNDDEIRARVDKSVDFLK 108
S ++ ++ ++SD VV+L G +LT + +E RA V S D++
Sbjct: 33 SHVDELKRMVSDYRKPVVKLGGETLTIGQVAAIASHDGGVRVELSEEKRAVKASSDWVM 92

Query: 109 AQLQNSV--YGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPTSVSSFSVGRGLENLTL 166
+ YGVTTGFG ++ RT++ +LQ+ LI G+ +S+ S + L
Sbjct: 93 DSMGKGTDSYGVTTGFGATSHRRTKNGGALQRELIRFLNAGIFGSSLDS-----THKL 145

Query: 167 PLEVVRGAMVIRVNSLTRGHSAVRLVVLEALTNFLNHRITPIVPLRGSISASGDLSPLSY 226
P R AM++R N+L +G+S +R +LEA+T FLN ITP +PLRG+I+ASGDL PLSY
Sbjct: 146 PHTATRAAMLVRFNTLLQGYSGIRFEILEAITKFLNGNITPCLPLRGTITASGDLVPLSY 205

Query: 227 IAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEA--VVLGPKEGLGLVNGTAVSASM 284
IAG + G P+ K V +G + + E L G++ L PKEGL LVNGTAV + M
Sbjct: 206 IAGLLIGRPNSK-SVGPKG--ETLSPAEGFKLAGIDGGFFELQPKEGLALVNGTAVGSGM 262

Query: 285 ATXXXXXXXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQVEVARNIRTLLSG 344
A+ E M G+ F + + HPGQ+E A + +L G
Sbjct: 263 ASMVLFDANTLAVLSEVMSAIFAEMVQKQP-EFTDHLTHKLKHHPGQIEAAIMEHILEG 321

Query: 345 SSFAXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTDNPL 404
SS+ +QDRY LRTSPQ+LGP +E + A + E N+ DNPL
Sbjct: 322 SSVYKEAKKVHEMDPLQKP-KQDRYALRTSPQWLGPQIEVIRAATKMIEREINSVNDNPL 380

Query: 405 LDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCS-AA 463
+DV + HGGNFQ + ++M+ TRLA+A IGKL F Q +EL+N N GLPS L +
Sbjct: 381 IDVSRNKALHGGNFQELPIGVAMDNTRLAIASIGKLIFAQFSELVNDYYNGLPSILTGS 440

Query: 464 EDPSLNYHGKGLDIHIAAYASELGHLANPVTTTFVQPAEMGNQAVNSLALISARRTAEAND 523
+PSL+Y KG +I +A+Y SEL LANPVT VQ AE NQ VNSL LIS+R+T+EA D
Sbjct: 441 SNPSLDYGFKGAEIAMASYCSELQFLANPVTNHVQSAEQHNQDVNSLGLISSRKTSEAVD 500

Query: 524 VLSLLLASHLYCTLQAVDLRAMELDFKKQFDPDLLPTLLQQHLGTGLDVNALALEVKKALN 583
+L L+ ++ L QA+DLR +E + K + + ++ L + L +
Sbjct: 501 ILKLMSSTFLVALCQAIDLRHLEENLKIVVKTTVSNVAKRTLTVSPNGE---LHPSRFSE 557

Query: 584 KRLEQTTTYDLEPRWHDAFSYATGTVVELLS-----SPSANVTLTAVNAWKV 631
K L + + D AT +++ L + SAN ++ K+
Sbjct: 558 KDLLTVVDREYLFYSYIDDPCLATYPLMQKLRAELVEHALKNGERERSANTSI----FHKI 613

Query: 632 ASAEKAIS--LTREVRNRFWQTPSSQAPAHAYLSP-RTRVLYSFVREELGVQARRGDVVF 688
A+ E+ + L +EV N + + ++ + R+ LY FVREELG +
Sbjct: 614 AAFEEELKTILPKEVDNARIEIENGKSEIPNRIKECRSYPLYRFVREELGT-----SLLT 668

Query: 689 GVQOETIGSNVSRIYEAIKDGRINHLVKML 719
G + ++ G +++ AI G++ L++ L
Sbjct: 669 GEKIKSPGEECYKFVNAICAGKLVDPLECL 699

☐ >gi|30721857|gb|AAP34199.1| phenylalanine ammonia-lyase [Phalaenopsis x Doritaer
cultivar]
Length = 703

Score = 328 bits (840), Expect = 5e-88
Identities = 205/530 (38%), Positives = 287/530 (54%), Gaps = 25/530 (4%)

Query: 49 SQLEIVQELLSIPTDDVVELSGYSLTXXXXXXXXXXXXXXXXXQNDDEIRARVDKSVDFLK 108
S L+ V++++ + VV+L G L + + RA V S D++
Sbjct: 29 SHLDEVKKMVEEFRPVPVQLEGAKLKISQVAAVAIGGGASVELAESARAGVKASSDWVL 88

Query: 109 AQLQNSV--YGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPPTSVSFSVGRGLENL 166
+ YGVTTGFG ++ RT+ +LQK LI G+ G G NTL
Sbjct: 89 ESVDKGTDSYGVTTGFGATSHRRTKQGGALQKELIRFLNAGI-----FGSGNSNTL 139

Query: 167 PLEVVRGAMVIRVNSLTRGHSAVRLVVLEALTNFLNHRITPIVPLRGSISASGDLSPLSY 226
P R AM++R+N+L +G+S +R +LEA+ LN ITP +PLRG+I+ASGDL PLSY

Sbjct: 140 PSSATRAAMLVRINTLLQGYSGIRFEILEAIATLLNTNITPCLPLRGTTITASGDLIPLSY 199

Query: 227 IAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEAVVLG-----PKEGLLVNGTAVS 281
IAG +TG P+ K + T +A++ F L + G PKEGL LVNGTAV

Sbjct: 200 IAGILTGRPNKALTSNGSTV-----DAVTAFRLAGISTGFFELQPKEGLLVNGTAVG 253

Query: 282 ASMATXXXXXXXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQVEVARNIRTL 341
+ +A+ E M G+ H + + HPGQ+E A + +

Sbjct: 254 SGLASLVLFETNILAIMAEVLSALFCEVMQKPEYTDHLTHKL-KHHPGQIEAAAIMEHI 312

Query: 342 LSGSSFAXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTDD 401
L GSS+ +QDRY LRTSPQ+LGP +E + A ++ E N+ D

Sbjct: 313 LEGSSYMKVAKKLHEMDPLQKP-KQDRYALRTSPQWLGPQIEVIRAATKSIEREINSVND 371

Query: 402 NPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCL 461
NPL+DV + HGGNFQ + + +SM+ TRLA+A IGKL F Q +EL+N N GLPS L

Sbjct: 372 NPLIDVSRNKALHGGNFQGTPIGVSMONTRLAIAAIGKLMFAQFSELVNDFYNNGLPSNL 431

Query: 462 -AAEDPSLNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVNSLALISARRTAE 520
+ +PSL+Y KG +I +A+Y SEL LANPVT VQ AE NQ VNSL LIS+R+TAE

Sbjct: 432 TSGRNPSTDYGFKGAEIAMASYCSELQALANPVTNHVQSAEQHNQDVNSLGLISSRK'TAE 491

Query: 521 ANDVLSLLLASHLYCTLQAVDLRAMELDFKKQFDPLLPTLLQQHLGTGLD 570
+ D+L L+ + L QAVDLR +E + K + + ++ L G++

Sbjct: 492 SVDILKLMTTTTFLVGLCQAVDLRHLEENLKNVKNVTSQVAKRTLTMGVN 541

☐ >gi|51341135|gb|AAU01182.1| phenylalanine aminomutase [Taxus chinensis]
Length = 687

Score = 327 bits (839), Expect = 6e-88

Identities = 240/650 (36%), Positives = 335/650 (51%), Gaps = 56/650 (8%)

Query: 94 DEIRARVDKSVDFLKAQLQNS--VYGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPPT 151
++ RARV+ +++ + ++ +YGVTTGFG + RT LQ++LI L GV T

Sbjct: 56 EQCRARVETCSSWVQRKAEDGADIYGVTTGFGACSSRRTNRLSELQESLIRCLLAGVF-T 114

Query: 152 SVSSFSVGRGLENLPLEVVRGAMVIRVNSLTRGHSVAVRLVVLEALTNFLNHRITPIVPL 211
+ SV + LP R AM++R+NS T G S +R V+EAL LN ++P VPL

Sbjct: 115 KGCAPSV-----DELPATATRSAMLLRLNSFTYGC SGIRWEVMEALEKLNSNVSPKVPL 169

Query: 212 RGSISASGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEAVVLGPKEG 271
RGS+SASGDL PL+YIAG + G P V + G + + A EA+S GL L KEG

Sbjct: 170 RGSVSASGDLIPLAYIAGLLIGKPSVIARI---GDDVEVPAPPEALS RVGLRPFKLQAKEG 226

Query: 272 LGLVNGTAVSASMATXXXXXXXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQ 331
L LVNGT+ + ++A+ E + G++ P IH V +PHPGQ

Sbjct: 227 LALVNGTSFATAVASTVMYDANVLLLLVETLCGMFCEVIFGREEFAHPLIHKV-KPHPGQ 285

Query: 332 VEARNIRTTLLSGSSFAXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYST 391
+E A + LL S F +QDRY LR+SPQ+L PLV+ + A +T

Sbjct: 286 IESAELEWLLRSSPFQELSREYYSIDKLKKP-KQDRYALRSSPQWLAPLVQTIRDATTT 344

Query: 392 LSLENNTTDDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNA 451
+ E N+ DNP++D N + HG NFQ SAV M+ R+A+A +GKL F Q TEL+

Sbjct: 345 VETEVNSANDNPIIDHANDRALHGANFQGSAGFYMDYVRIAVAGLGKLLFAQFTELMIE 404

Query: 452 AMNRGLPSCLA-AEDPSLNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVNSL 510
+ GLP L+ D S++Y KGLDI +AAY+SEL +LANPVT T V AE NQ +NSL

Sbjct: 405 YYSNGLPGNLSLGPDLSDVDYGLKGLDIAMAAYSSELQYLANPVTTHVHSAEQHNQDINSL 464

Query: 511 ALISARRTAEANDVLSLLLASHLYCTLQAVDLRAMELDFKKQFDPLLPTLLQQHLGTGLD 570
 ALISAR+T EA D+L L++ASHL QAVDLR +E K + ++ TL + G D

Sbjct: 465 ALISARKTEEALDILKLMIAASHLTAMCQAVDLRQLEEALVKVVENNVSTLADE-CGLPND 523

Query: 571 VNALALEVKKALNKRLEQTTTYDLEPRWHDAFSYATGTVVELLSSSPSANVTLTAVNAWK 630
 A L V KA+ P + S T+ LL S T+ A++

Sbjct: 524 TKARLLYVAKAV-----PVYTYLESPCDPTLPLLLGLKQSCFDITILALHKKD 570

Query: 631 VASAEKAISLTREVRNRFWQTPSSQAPAHAYLSPR-----TRV-----LYS 671
 + + E R ++ A L + R+ Y

Sbjct: 571 GIETDTLVDRLAEFKRLSDRLENEMTAVRVLYEKKGHKTADNNDALVRIQGSKFLPFYR 630

Query: 672 FVREEL--GVQARRGDVFGVGVQETIGSNVSRIYEAIKDGRINHVLVKML 719
 FVREEL GV + R +++T +V ++++AI DGRI L+ L

Sbjct: 631 FVREELDTGVMSAR-----REQTPQEDVQKVFDAIADGRITVPLLHCL 673

☐ >gi|23451811|gb|AAN32867.1| phenylalanine ammonia-lyase 2 [Coffea canephora]
 Length = 619

Score = 326 bits (835), Expect = 2e-87

Identities = 225/618 (36%), Positives = 326/618 (52%), Gaps = 34/618 (5%)

Query: 116 YGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPPTSVSFSVGRGLENTLPLEVVRGAM 175
 YG+TTGFG ++ RT+ +LQ+ LI G+ F G +TLP R +M

Sbjct: 11 YGITTGFGATSHRRTKQGGALQEELIRFLNAGI-----FGNGTETSHTLPHSATRASM 63

Query: 176 VIRVNSLTRGHSVRLVVLEALTNFLNHRITPIVPLRGSISASGDLSPLSYIAGAITGHP 235
 ++R+N+L +G+S +R +LEA+T LN+ ITP +PLRG+I+ASGDL PLSYI G +TG P

Sbjct: 64 LVRINTLLQGYSGIRFEILEAITKLLNNNITPCLPLRGTTITASGDLVPLSYIVGLLTGRP 123

Query: 236 DVKVHVLHEGTEKIMFAEAIISLFGLEA--VVLGPKEGLGLVNGTAVSASMATXXXXXXX 293
 + K V +G K + A EA SL G++ L KEGL LVNGTAV +++A+

Sbjct: 124 NSKA-VGPDG--KFVNATEAFSLAGIDTGFFELQAKEGLALVNGTAVGSALASMLFEAN 180

Query: 294 XXXXXXXXXXXXXVEAMVGQQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGSSFAXXXXX 353
 E M G+ F + + HPGQ+E A + +L GSSF

Sbjct: 181 ILAVLAEVLSGIFAEVMHGKP-EFTDHLTHKLKHHPGQIEAAAIMEHILDGSSFVKEAQR 239

Query: 354 XXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTNDNPLLDVENKQTA 413
 +QDRY LRTSPQ+LGPL+E + + ++ E N+ DNPL+DV +

Sbjct: 240 VHEFDPLQKP-KQDRYALRTSPQWLGPLIEVIRASTKSIEREINSVNDNPLIDVSRNKAL 298

Query: 414 HGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCLA-AEDPSLNYHG 472
 HGGNFQ + + +SM+ TRLA+A IGKL F Q +EL+N N GLPS L+ +PSL+Y

Sbjct: 299 HGGNFQGTPIGVSMNDTRLAIASIGKLMFAQFSELVNDFYNNGLPSNLSSGRNPPLDYGF 358

Query: 473 KGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVNSLALISARRTAEANDVLSLLLASH 532
 KG +I +AAY SEL LANPVT VQ AE NQ VNSL LIS+R+TAEA D+L L+ +++

Sbjct: 359 KGAEIAMAAYCSELQFLANPVTNHVQSAEQHNQDVNSLGLISSRKTAEAVDILKLMSSSTY 418

Query: 533 LYCTLQAVDLRAMELDFKKQFDPLLPTLLQQHLGTGLDVNALALEVKKALNKR----- 586
 L QA+DLR +E + K + + ++ L G + L + K L

Sbjct: 419 LVALCQAIDLRHLEENLKASVKNTVSLVAKKVLTMGYNGE---LHPSRFCEKDLLKVVD 475

Query: 587 EQTTTYDLEP--RWHDAFSYATGTVVELLSSSPSANVTLTAVNAWKVASAEKAIS--LTR 642
 E Y +P + +VE ++ T K+ + E + L +

Sbjct: 476 EHVFAIDDPCSGTYPLMQKLRQVLVEHSLANGDKEKDATTTSIFQKIGAFEDELKALLPK 535

Query: 643 EVNRNRFWQTPSSQ-APAHAYLSPRTRVLYSFVREELGVQARRGDVFGVGVQQUETIGSNVSR 701
 EV + + + + A+ R+ LY FVR ELG + G + + G +

Sbjct: 536 EVESARCELENGKPGIANRIKDCRSYSLYKFVRGELGT-----NFLTGKVRSPGEEFDK 590

Query: 702 IYEAIKDGRINHVLVKML 719
 ++ AI +G++ L+ L

Sbjct: 591 VFTAICEGKLIDPLLDCL 608

☐ >gi|11761146|dbj|BAB19128.1| phenylalanine ammonia-lyase [Dianthus caryophyllus]
 Length = 618

Score = 326 bits (835), Expect = 2e-87

Identities = 225/618 (36%), Positives = 323/618 (52%), Gaps = 34/618 (5%)

Query: 116 YGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPPTSVSSFSVGRGLENLPLEVVIRGAM 175
 YGVTTGFG ++ RT+ +LQK LI GV F G +TLP R AM

Sbjct: 10 YGVTTGFGATSHRRTKQGGALQKELIRFLNAGV-----FGNGTETSHTLPHITASRAAM 62

Query: 176 VIRVNSLTRGHSAVRLVLEALTNFLNHRITPIVPLRGSISASGDLSPLSYIAGAITGHP 235
 ++R+N+L +G+S +R +LEA+T+ LNH +TP +PLRG+I+ASGDL PLSYIAG +TG P

Sbjct: 63 LVRINTLLQGYSGIRWEILEAITSLLNHDVTPCLPLRGTTITASGDLVPLSYIAGLLTGRP 122

Query: 236 DVKVHVLHEGTEKIMFAREAISLFGLEAVV--LGPKEGLGLVNGTAVSASMATXXXXXXXX 293
 + K +I+ A EA +E+ L PKEGL +VNGTAV + MA+

Sbjct: 123 NAKAA---GPNGEILTAEAFKAAKIESPFFELQPEGLAMVNGTAVGSGMASIVLYEAN 179

Query: 294 XXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGSSFAXXXXX 353
 E M G+ F + + HPGQ+E A + +L GSS+

Sbjct: 180 ILAVLAEVISAVFAEVMNGKP-EFTDHLTHKLKHHPGQIEAAAIMEHILDGSSYMKAAKE 238

Query: 354 XXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTDNPLLDVENKQTA 413
 +QDRY LRTSPQ +GP +E + A ++ E N+ DNPL+DV +

Sbjct: 239 LHEMDPLQKP-KQDRYALRTSPQCVGPQIEVIRWATKSIEREINSVNDNPLIDVSRNKAL 297

Query: 414 HGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCL-AAEDPSLNYHG 472
 HGGNFQ + + +SM+ TRLA++ IGKL F Q +EL+N N GLPS L A+ DPSL+Y

Sbjct: 298 HGGNFQGTPIGVSMNTRLAISAIKLLFAQFSELVNDFYNNGLPSNLTASRDPSLDYGF 357

Query: 473 KGLDIHIAAYASELGHLANPVTTTFVQPAEMGNQAVNSLALISARRTAEANDVLSLLASH 532
 KG +I +A+Y SEL L NPVT VQ AE NQ VNSL LISAR+T EA ++L L+ ++

Sbjct: 358 KGAEIAMASYCSELQFLGNPVTNHVQSAEQHNQDVNSLGLISARKTFEAVEILKLMSTF 417

Query: 533 LYCTLQAVDLRAMELDFKKQFDPLLPDLLQHLGTGLDVNALALEVKKALNKRL----- 586
 L QAVDLR +E + + + + ++ L TG+ L + K L

Sbjct: 418 LVALCQAVDLRHIEENLQSAVKNTVSQVCKRVLITGVKGE---LHPGRFCEKDLIRVVER 474

Query: 587 EQTTTYDLEP--RWHDAFSYATGTVVELLSSSPSANVTLTAVNAWKVASAEKAIS--LTR 642
 E TY +P + +V+ + A T + K+ + E+ + L +

Sbjct: 475 EHVFTYADDPCSSSTYPLLQKLRQVLVDQALVNGDAEKVATTSSISQKIGAFEEELKARLPK 534

Query: 643 EVRN-RFWQTPSSQAPAHAYLSPRTRVLYSFVREELGVQARRGDVFGVGVQQUETIGSNVSR 701
 E+ R S + R+ LY FVRE L + D+ G + G + +

Sbjct: 535 EIEAVRCAVENGSAITPNRIKECRSYPLYKFVREVL-----KTDLLTGEGVRSPGEEIDK 589

Query: 702 IYEAIKDGRINHVLVKML 719
 ++ A+ +G+I L++ L

Sbjct: 590 VFTALNEGKIVDPLLECL 607

☐ >gi|58618158|gb|AAW80645.1| phenylalanine ammonia lyase [Pellia epiphylla]
Length = 744

Score = 325 bits (834), Expect = 2e-87

Identities = 240/687 (34%), Positives = 347/687 (50%), Gaps = 72/687 (10%)

Query: 66 VELSGYSLTXXXXXXXXXXXXXXXXXQNDDEIRARVDKSVDFL--KAQLQNSVYGVTTGFG 123
V L G SLT ++ E ++RVD+S +++ + YGVTTGFG

Sbjct: 48 VILRGSSLTVGQVTAVTQRASVIVQLDEAEAKSRVDESSNWVLNRTLGTDTYGVTTGFG 107

Query: 124 GSADTRTEDAVSLQKALIEHQLCGVTPTSVSSFSVGRGLEN-TLPLEVVRGAMVIRVNSL 182
++ RT V LQ+ LI GV +GR + +LPL+ R AM++R N+L

Sbjct: 108 ATSHRRTNQVVDLQRELIRFLNAGV-----IGRSDGCSLPLKYARAAMLVRTNTL 158

Query: 183 TRGHSAVRLVVLEALTNFLNHRITPIVPLRGSISASGDLSPLSYIAGAITGHPDVKVHVL 242
+G+S +R +L+A+ + + P +PLRG+I+ASGDL PLSYIAG +TG + K +

Sbjct: 159 MQGYSGIRWDILDAMRKLMCANVIPKLPLRGTTITASGDLVPLSYIAGLLTGRSNSKA-IT 217

Query: 243 HEGTEKIMFAEAISLFGLEAVV-LGPKEGLGLVNGTAVSASMATXXXXXXXXXXXXXXXXX 301
EG E + A EA+ + G++ L PKEGL LVNGT+V A++A

Sbjct: 218 PEGKE--VSAAEALKIAGIDGPFELQPKEGLALVNGTSVGAAVAANVCFDANVLALLSEV 275

Query: 302 XXXXXVEAMVGQQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGSSFAXXXXXXXXXXXXXX 361
E M G+ P H + + HPGQ+E A + LL GSS+

Sbjct: 276 LSAFFCEVMQGKPEFTDPLTHQL-KHHPGQIEAAVMEFLLEGSSYMKAAAKLHETDPLS 334

Query: 362 GILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTNDNPLLDVENKQTAHGGNFQAS 421
+QDRY LRTSPQ+LGP +E + A ++ E N+ DNPL+DV HGGNFQ +

Sbjct: 335 KP-KQDRYALRTSPQWLGPQIEVIRSATHSIEREINSVNDNPLIDVSRDMALHGGNFQGT 393

Query: 422 AVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCLA-AEDPSLNYHGKGLDIHIA 480
+ +SM+ R+ALA IGKL F Q +EL+ N GLPS L+ +PSL+Y KG +I +A

Sbjct: 394 PIGVSMNDMRIAALAAIGKLMFAQFSELVCDYNSGLPSNLSGGPNPSLDYGFKGAEIAMA 453

Query: 481 AYASELGHLANPVTTTFVQPAEMGNQAVNSLALISARRTAEANDVLSLLLASHLYCTLQAV 540
AY SEL +LANPVTT VQ AE NQ VNSL LI+AR+TAEA ++L L+ ++++ QAV

Sbjct: 454 AYCSELQYLANPVTHVQSAEQHNQDVNSLGLIAARKTAEAVEILKLMSSTYMVALCQAV 513

Query: 541 DLRAMELDFKKQFDPLLPTLLQQHLGTGLDVNALALEVKKALNKRLEQTTTYDLEPRWHD 600
DLR +E + ++ L++ + L +L + K L Q D +P

Sbjct: 514 DLRHLE----ENMQAVVKRLVESATKSTLYTENGSLFPTRFSEKDLLQVV--DHQP---- 563

Query: 601 AFSYATGTVVELLSSSPSANVTLTAVNAWKVASAEKAISL-----TREVRNRFWQTPSSQ 655
FSY +S+PS + L + E+A+ +EV F P +

Sbjct: 564 VFSYIDN-----ASNPSYALMLQL----REVLVEQALKTPQDEDCKEVTPLFTTIPKFE 613

Query: 656 APAHAYLSP-----RTRVLYSFVREELGVQARRGDVFGVGVQQ 692
A L RT +Y FVR ELG + R G

Sbjct: 614 AELKKLLDAEVPKARDRYDGGDYAVPNRIKNCRTYPIYKFVRGELGTELLR-----GTAT 668

Query: 693 ETIGSNVSRIYEAIKDGRINHVLVKML 719

++ G ++ +++ AI DG++ L+K L

Sbjct: 669 KSPGEDIEKVFTAILDGKLLPLKCL 695

☐ >gi|60459950|gb|AAX20146.1| phenylalanine aminomutase [Taxus x media]
Length = 687

Score = 324 bits (831), Expect = 5e-87

Identities = 241/645 (37%), Positives = 338/645 (52%), Gaps = 46/645 (7%)

Query: 94 DEIRARVDKSVDFLKAQLQNS--VYGVTTFGGGSADTRTEDAVSLQKALIEHQLCGVTPT 151
++ RARV+ +++ + ++ +YGVTTGFG + RT LQ++LI L GV

Sbjct: 56 EQCRARVETCSSWVQRKAEDGADIYGVTTGFGACSSRRTNQLSELQESLIRCLLAGVFTK 115

Query: 152 SVSSFSVGRGLENLPLEVVIRGAMVIRVNSLTRGHSVAVRLVVLEALTNFLNHRITPIVPL 211
+S SV + LP R AM++R+NS T G S +R V+EAL LN ++P VPL

Sbjct: 116 GCAS-SV-----DELPATATRSAMLLRLNSFTYGCSGIRWEVMEALEKLLNSNVSPKVPL 169

Query: 212 RGSISASGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEAVVLGPKEG 271
RGS+SASGDL PL+YIAG + G P V + G + + A EA+S GL L KEG

Sbjct: 170 RGSVSASGDLIPLAYIAGLLIGKPSVARI---GDDVEVPAPPEALSRVGLRPFKLQAKEG 226

Query: 272 LGLVNGTAVSASMATXXXXXXXXXXXXXXXXXXXXXVEAMVGQQGSFAPFIHDVCRPHPGQ 331
L LVNGT+ + ++A+ E + G++ P IH V +PHPGQ

Sbjct: 227 LALVNGTSFATALASTVMYDANVLLLLVETLCGMFCEVIFGREEFAHPLIHKV-KPHPGQ 285

Query: 332 VEARNIRTLLSGSSFAXXXXXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYST 391
+E A + LL S F +QDRY LR+SPQ+L PLV+ + +A +T

Sbjct: 286 IESAELEWLLRSSPFQDLSREYYSIDKLKKP-KQDRYALRSSPQWLAPLVQTIRNATTT 344

Query: 392 LSLENNTTTDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNA 451
+ E N+ DNP++D N + HG NFQ SAV M+ R+A+A +GKL F Q TEL+

Sbjct: 345 VETEVNSANDNPIIDHANDRALHGANGFQGSAGVFYMDYVRIAVAGLGKLLFAQFTELMIE 404

Query: 452 AMNRGLPSCLA-AEDPSLNYHGKGLDIHIAAYASELGHLANPVTTTFVQPAEMGNQAVNSL 510
+ GLP L+ D S++Y KGLDI +AAY+SEL +LANPVTT V AE NQ +NSL

Sbjct: 405 YYSNGLPGNLSLGPDLSDYGLKGLDIAMAAYSSELQYLANPVTTTHVHSAEQHNQDINS 464

Query: 511 ALISARRTAEANDVLSLLLASHLYCTLQAVDLRAMELDFKKQFDPLLPTLLQQHLGTGLD 570
ALISAR+T EA D+L L++A HL QAV+LR +E K + ++ TL + G D

Sbjct: 465 ALISARKTDEALDILKLMIAPHLTAMCQAVNLRQLEEALVKVVENNVSTLADE-CGLPND 523

Query: 571 VNALALEVKKALNKRLEQTTTYDLEPRWHDFAFSYATGTVVELLSSSPSAN-----VTLTA 625
A L V KA+ TY LE G S S + T T

Sbjct: 524 TKARLLYVAKAV-----PVYTY-LESPCDPTLPLLLGLKQSCFDSILSLHKKDGIETDTL 577

Query: 626 VNAWKVASAEKAIS--LTREV-----RNRFWQTPSSQAPAHAYLSRPRTRVLYSFVREE 676
V+ ++A EK +S L E+ + +T + + Y FVR+E

Sbjct: 578 VD--RLAEFEKRLSDRLNEMTAVRVLYEKKGHKTADNNDALVRIQGSKFLPFYRFVRDE 635

Query: 677 L--GVQARRGDFVGVQQETIGSNVSRIYEAIKDGRINHLVKML 719
L GV + R +++T +V ++++AI DGRI L+ L

Sbjct: 636 LDTGVMSAR-----REQTPQEDVQKVFDAIVDGRITVPLLHCL 673

☐ >gi|1143312|gb|AAA84889.1| phenylalanine ammonia-lyase
gi|1709564|sp|P52777|PALY_PINTA Phenylalanine ammonia-lyase
gi|7437129|pir|T09777 phenylalanine ammonia-lyase (EC 4.3.1.5) - loblolly pine
Length = 754

Score = 324 bits (831), Expect = 5e-87

Identities = 236/677 (34%), Positives = 347/677 (51%), Gaps = 53/677 (7%)

Query: 66 VELSGYSLTXXXXXXXXXXXXXXXXXQNDDEIRARVDKSVDFLKAQLQNSV--YGVTTGFG 123
 + + G SLT + ++RV++S +++ Q+ YGVTTGFG
 Sbjct: 62 ISIEGKSLTISDVAAVARRSQVKVKLDAAAKSRVEESSNWVLTQMTKGTDTYGVTTGFG 121

Query: 124 GSADTRTEDAVSLQKALIEHQLCGVTPPTSVSFSVGRGLENTLPLEVVRGAMVIRVNSLT 183
 ++ RT LQK LI GV +G+ EN L + R AM++R N+L
 Sbjct: 122 ATSHRRTNQGAELQKELIRFLNAGV-----LGKCPENVLSEDTTRAAMLVRTNTLL 172

Query: 184 RGHSAVRLVLEALTNFLNHRITPIVPLRGSISASGDLSPLSYIAGAITGHPDVKVHVLH 243
 +G+S VR +LE + LN +TP +PLRG+I+ASGDL PLSYIAG +TG P+ +V
 Sbjct: 173 QGYSGVRWDILETVEKLLNAWLTPKLPLRGTTASGDLVPLSYIAGLLTGRPNRSRVS-R 231

Query: 244 EGTEKIMFAREAISLFGLEAVV-LGPKEGLGLVNGTAVSASMATXXXXXXXXXXXXXXXXX 302
 +G E M EA+ GLE L PKEGL +VNGT+V A++A+
 Sbjct: 232 DGIE--MSGAEALKKVGLEKPFELQKEGLAIVNGTSVGAALASIVCFDANVLALLSEVI 289

Query: 303 XXXXVEAMVGQQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGSSFAXXXXXXXXXXXXXXG 362
 E M G+ P H + + HPGQ+E A + +L GSS+
 Sbjct: 290 SAMFCEVMNGKPEFTDPLTHKL-KHHPGQMEAAAIMYVLDGSSYMKHAAKLHEMNPLQK 348

Query: 363 ILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTDNPLLDVENKQTAHGGNFQASA 422
 +QDRY LRTSPQ+LGP VE + A + E N+ DNP++DV + HGGNFQ +
 Sbjct: 349 P-KQDRYGLRTSPQWLGPQVEIIRSATHMIEREINSVNDNPVIDVARDKALHGGNFQGTP 407

Query: 423 VSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCLA-AEDPSLNYHGKGLDIHIAA 481
 + +SM+ RL+++ IGKL F Q +EL+N N GLPS L+ +PSL+Y KG +I +A+
 Sbjct: 408 IGVSMNLRLSISAIGKLMFAQFSELVNDYNGGLPSNLSGGPNPSLDYGLKGAEIAMAS 467

Query: 482 YASELGHLANPVTTTFVQPAEMGNQAVNSLALISARRTAEANDVLSLLLASHLYCTLQAVD 541
 Y SEL +LANPVT+ VQ AE NQ VNSL L+SAR++AEA D+L L+L+++L QAVD
 Sbjct: 468 YTSELLYLANPVTSHVQSAEQHNQDVNSLGLVSARKSAEAIDILKMLSTYLTALCQAVD 527

Query: 542 LRAMELDFKKQFDPLLPTLLQQHLGTGLDVNAL-ALEVKKALNKRLEQ-----T 589
 LR +E + ++ + ++ L TGL+ L +K L + ++
 Sbjct: 528 LRHLEENMLATVKQIVSQVAKKTLSTGLNGELLPGRFCEKDLLQVVDNEHVF SYIDDP CN 587

Query: 590 TTYDLEPRWHD-----AFSYATGTVVELLSSSPSANV--TLTAVNAWKVASAEKAISLTR 642
 +Y L + + AF A G P+ ++ + A A E +SL R
 Sbjct: 588 ASYPLTQKLRNILVEHAFKNAEG-----EKDPNTSIFNKIPVFEAELKAQLEPQVSLAR 641

Query: 643 EVNRNRFWQTPSSQAPAHAYLSRPRTRVLYSFVREELGVQARRGDVFGVQQTIGSNVSRI 702
 E + +S P R+ LY FVR +LG + + G + + G + +
 Sbjct: 642 E----SYDKGTSPLPDRIQ-ECRSYPLYEFVRNQLGTK-----LLSGTRTISPGEVIEVV 691

Query: 703 YEAIKDGRINHVLVKML 719
 Y+AI + ++ L K L
 Sbjct: 692 YDAISEDKVIVPLFKCL 708

☐ >gi|49473532|gb|AAT66434.1| phenylalanine ammonia lyase [Pinus pinaster]
 Length = 754

Score = 323 bits (829), Expect = 9e-87

Identities = 233/674 (34%), Positives = 345/674 (51%), Gaps = 47/674 (6%)

Query: 66 VELSGYSLTXXXXXXXXXXXXXXXXXQNDDEIRARVDKSVDFLKAQLQNSV--YGVTTGFG 123
 + + G SL + + ++RV++S +++ Q+ YGVTTGFG
 Sbjct: 62 IYIEGKSLQTSDVAAIARRSQVKVKLDAEAAKSRVEESSNWVLTQMTKGTDTYGVTTGFG 121

Query: 124 GSADTRTEDAVSLQKALIEHQLCGVTPTSVSSFSVGRGLENLPLEVVRGAMVIRVNSLT 183
 ++ RT LQK LI GV +G+ EN L ++ R +M++R N+L
 Sbjct: 122 ATSHRRTNQGAELQKELIRFLNAGV-----LGKCPENVLSEDI TRASMLVRNTNTLL 172

Query: 184 RGHSVRLVLEALTNFLNHRITPIVPLRGSISASGDLSPLSYIAGAITGHPDVKVHVLH 243
 +G+S +R +LE + LN +TP +PLRG+IS+SGDL PLSYIAG +TG P+ +V
 Sbjct: 173 QGYSGIRWDILETVEKLLNAGLTPKLPPLRGITSSSGDLVPLSYIAGLLTGPRNSRVRS-R 231

Query: 244 EGTEKIMFAREAISLFGLEAVV-LGPKEGLGLVNGTAVSASMATXXXXXXXXXXXXXXXXX 302
 +G E M EA+ GLE L PKEGL +VNGT+V A++A+
 Sbjct: 232 DGIE--MSGAEALKKVGLEKPFELQPEGLAIVNGT SVGAALASIVCFDANVLALLSEVI 289

Query: 303 XXXXVEAMVGQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGSSFAXXXXXXXXXXXXXXG 362
 E M G+ P H + + HPGQ+E A + +L GSS+
 Sbjct: 290 SAMFCEVMNGKPEFTDPLTHKL-KHHPGQMEAAAIMEYVLDGSSYMKHAAKLHEMNPLQK 348

Query: 363 ILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTNDNPLLDVENKQTAHGGNFQASA 422
 +QDRY LRTSPQ+LGP VE + A + E N+ DNP++DV + HGGNFQ +
 Sbjct: 349 P-KQDRYALRTSPQWLGPQVEIIRSATHMIEREINSVNDNPVIDVARDKALHGGNFQGT 407

Query: 423 VSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCLA-AEDPSLNYHGKGLDIHIAA 481
 + +SM+ RLA++ IGKL F Q +EL+N N GLPS L+ +PSL+Y KG +I +A+
 Sbjct: 408 IGVSMNDNRLAISAIKLMFAQFSELVNDYNGGLPSNLSGGPNPSLDYGMKGAEIAMAS 467



Query: 482 YASELGHLANPVTTTFVQPAEMGNQAVNSLALISARRTAEANDVLSLLLASHLYCTLQAVD 541
 Y SEL +LANPVTT VQ AE NQ VNSL L SAR++AEA D+L L+L+++L QAVD
 Sbjct: 468 YTSELLYLANPVTTTHVQSAEQHNQDVNSLGLGSARKSAEAIDILKMLSTYLTALCQAVD 527

Query: 542 LRAMELDFKKQFDPLLPTLLQQHLGTGLDVNALALEVKKALNKRLEQTTTYDLEPRWHA 601
 LR +E + ++ + ++ L TGL+ L + K L Q + + D
 Sbjct: 528 LRHLEENMLATVKQIVSQVAKKTLSTGLNGELLP---GRFCEKDLLQVVDNEHVFSYIDD 584

Query: 602 FSYATGTVVELL-----SSSPSANV--TLTAVNAWKVASAEKAISLTREVR 645
 A+ + + L P+ ++ + A A E +SL RE
 Sbjct: 585 PCNASYPLTQKLRNILEHAFKNGEKDPNTSIFNKIPLFEAELKAQLELQVSLARE-- 642

Query: 646 NRFWQTPSSQAPAHAYLSPRTRVLVSFVREELGVQARRGDVFGVQQETIGSNVSRIYEA 705
 + +S P + R+ LY FVR +LG + + G + + G + +Y+A
 Sbjct: 643 --SYDKGTSPLP-NRIQECSYPLYEFVRNQLGTK-----LLSGTRTTSPEVIEVVYDA 694

Query: 706 IKDGRINHVLVKML 719
 I + ++ L K L
 Sbjct: 695 INEDKVIGPLFKCL 708

☐ >gi|9955578|emb|CAC05505.1|  phenylalanine ammonia-lyase PAL3 [Arabidopsis thal
 gi|15237651|ref|NP_196043.1|  phenylalanine ammonia-lyase 3 (PAL3) [Arabidopsis
 Length = 698

Score = 323 bits (828), Expect = 1e-86

Identities = 236/680 (34%), Positives = 341/680 (50%), Gaps = 28/680 (4%)

Query: 49 SQLEIVQELSDPTDDVVELSGYSLTXXXXXXXXXXXXXXXXXQNDDEIRARVDKSVDFLK 108
 S LE V++++ D V+L G +LT + +E R V S D++
 Sbjct: 27 SHLEEKKMKVVDYRKGTQVQLGGETLTIGQVAASGSGPTV--ELSEEARGGVKASSDWVM 84

Query: 109 AQLQNSV--YGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPTSVSSFSVGRGLENL 166

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      +      YG+TTGFG S+  RT+  +LQK LI +  G+  T      +      NTL
Sbjct: 85  ESMNRD TDTYGITTGFGSSSRRTDQGAALQKELIRYLNAGIFATG----NEDDDRNTL 140

Query: 167  PLEVVRGAMVIRVNSLTRGHSVRLVLEALTNFLNHRITPIVPLRGSISASGDLSPLSY 226
      P      R AM+IRVN+L +G+S +R  +LEA+T  LN +ITP++PLRG+I+ASGDL PLSY
Sbjct: 141  PRPATRAAMLIRVNTLLQGYSGIRFEILEAITLLNCKITPLLPLRGTITASGDLVPLSY 200

Query: 227  IAGAITGHPDVKVHVLHEGTEKIMFAREAIISLFGLEAVV-LGPKEGLGLVNGTAVSASMA 285
      IAG + G P+ +  V      G  +I+ A EA  L G+ +  L PKEGL LVNGTAV +++A
Sbjct: 201  IAGFLIGRPNSR-SVGPSG--EILTALEAFKLAGVSSFFELRPKEGLALVNGTAVGSALA 257

Query: 286  TXXXXXXXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGS 345
      +                                E M G+  F  +  + HPGQ+E A  +  +L GS
Sbjct: 258  STVLYDANILVVFSEVASAMFAEVMQGKP-EFTDHLTHKLKHHPGQIEAAIMEHILDGS 316

Query: 346  SFAXXXXXXXXXXXXXXGILRQDRY----PLRTSPQFLGPLVEDMMHAYSTLSLENNTTTD 401
      S+                                +QDRY      LRTSPQ+LGP +E +  A  +  E N+  D
Sbjct: 317  SYVKEALHLHKIDPLQKP-KQDRYVLGYALRTSPQWLGPQIEVIRAATKMIEREINSVND 375

Query: 402  NPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCL 461
      NPL+DV  +  HGGNFQ  +  +  +M+  TRLALA IGKL F Q TEL+N  N GLPS L
Sbjct: 376  NPLIDVSRNKAIHGGNFQGTPIGVAMDNTRLALASIGKLMFAQFTELVDNFYNNGLPSNL 435

Query: 462  A-AEDPSLNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVNSLALISARRTAE 520
      +  +PSL+Y  KG ++ +A+Y SEL  LANPVT  V+ A  NQ VNSL LIS+R TAE
Sbjct: 436  SGGRNPSLDYGLKGAEVAMASYCSELQFLANPVTNHVESASQHNQDVNSLGLISSRTTAE 495

Query: 521  ANDVLSLLASHLYCTLQAVDLRAMELDFKKQFDPLLPTLLQQHLGTGLDVNALALEVKK 580
      A  +L L+  ++L  QA DLR +E  KK  +  ++  +  L  ++  ++
Sbjct: 496  AVVILKLMSTTYLVALCQAFDLRHLEEILKKAVNEVVSHTAKSVL--AIEPFRKHDDILG 553

Query: 581  ALNKRLEQTTTYDLEPRWHDFAFSYATGTVVELLSSSPSANVTLTAVNAWKVASAEKAISL 640
      +N+  +  D  +  +  +  + P  T T  AE  L
Sbjct: 554  VVNREYVFSYVDDPSSLTNPLMQKL RHVLF DKALEPEGE-TDTVFRKIGAFEAE LKFL 612

Query: 641  TREV-RNRFWQTPSSQAPAHAYLSPRTRVLYSFVREELGVQARRGDVFGVQQETIGSNV 699
      +EV R R  +  A+  R+  LY FVR EL  +  +  G  +  G  +
Sbjct: 613  PKEVERVRTEYENGTFNVANRIKKCRSYPLYRFVRNELETR-----LLTGEDVRSPGEDF 667

Query: 700  SRIYEAIKDGRINHVLVKML 719
      +++ AI  G++  L + L
Sbjct: 668  DKVFRAISQGLIDPLFECL 687

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☐ >gi|3024362|sp|Q43052|PAL2_POPKI Phenylalanine ammonia-lyase G2B
 gi|2118317|pir|S60042 phenylalanine ammonia-lyase (EC 4.3.1.5) 2b - Japanese asp
 large-toothed aspen
 gi|1109641|dbj|BAA07860.1| phenylalanine ammonia-lyase [Populus kitakamiensis]
 Length = 710

Score = 322 bits (826), Expect = 2e-86

Identities = 238/696 (34%), Positives = 351/696 (50%), Gaps = 37/696 (5%)

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Query: 40  GLDGHAHQSQLEIVQELLSDPD VVELSGYSLTXXXXXXXXXXXXXXXXXQNDDEIRAR 99
      G+  +  S L+ V+ ++ +  + VV+L G +LT  +  +E RA
Sbjct: 25  GMAAESLKGSHLDEVKRMIEEYRNPVVKLGGETLTIGQVTAIASRDVGVMVELSEEARAG 84

Query: 100  VDKSVDFLKAQLQNSV--YGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPTSVSSFS 157
      V  S D++  +  YGVTTGFG ++  RT+  LQK LI  G+  F

```

Sbjct: 85 VKASSDWVMDSMSKGTDSYGVTTGFGATSHRRTKQGGELOKELIRFLNAGI-----FG 137

Query: 158 VGRGLENLTPLEVVVRGAMVIRVNSLTRGHSAVRLVVLEALTNFLNHRITPIVPLRGSISA 217
 G +TLP R AM++R N+L +G+S +R +LEA+T +NH ITP +PLRG+I+A

Sbjct: 138 NGTESSHTLPRSATRAAMLVRTNTLLQGYSGIRFEMLEAITKMINHNITPCLPLRGTTITA 197

Query: 218 SGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEA--VVLGPKEGLGLV 275
 SGDL PLSYIAG +TG P+ K + E + A EA + G++ L PKEGL LV

Sbjct: 198 SGDLVPLSYIAGLLTGRPNSKA--VGPNGEPLTPA-EAFTQAGIDGGFFELQPKEGLALV 254

Query: 276 NGTAVSASMATXXXXXXXXXXXXXXXXXXXXXVEAMVGQQGSFAPFIHDVCRPHPGQVEVA 335
 NGTAV + +A+ E M G+ F + + HPGQ+ A

Sbjct: 255 NGTAVGSGGLASMLFEANVLAILSEVLSAIFAEMVQKGP-EFTDHLTHKLKHHPGQIVAA 313

Query: 336 RNIRTLSSGSSFAXXXXXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLE 395
 + +L GS++ +QDR+ LRTSPQ+LGPL+E + + + E

Sbjct: 314 AIMEHILDGSAYVKEAQLHEIDPLQKP-KQDRHALRTSPQWLGPLIEVIRTSTKMIERE 372

Query: 396 NNTTTDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNR 455
 N+ DNPL+DV + HGGNFQ + + +SM+ TRLA+A IGKL F Q +EL+N N

Sbjct: 373 INSVDNPLIDVSRNKALHGGNFQGTPIGVSMNTRLAIASIGKLMFAQFSELVNDLYNN 432

Query: 456 GLPSCL-AAEDPSLNYHGKGLDIHIAAYASELGHLANPVTTTFVQPAEMGNQAVNSLALIS 514
 GLPS L +PSL+Y KG +I +A+Y SEL L T VQ AE NQ VNSL LIS

Sbjct: 433 GLPSNLTGGRNPGLDYGFKAELIAMSYSSELQFLDQSCNTHVQSAEQHNQDVNSLGLIS 492

Query: 515 ARRTAEANDVLSLLLASHLYCTLQAVDLRAMELDFK---KQFDPLLPTLLQQHLGTGLDV 571
 +R+TAEA D+L L+ + L +VDLR +E + K K LP +L L

Sbjct: 493 SRKTAEADILKLMSTTFLVGLCHSVDLRHIEENLKNTVKISVSQQLPRVLTMGFNGELHP 552

Query: 572 NALA-LEVKKALNKRLEQTTTYDLEP--RWHDAFSYATGTVVE--LLSSSPSANVTLTAV 626
 + ++ K +++ E +Y +P + +VE L++ N T +

Sbjct: 553 SRFCEKDLLKVVDNR--EHVFSYIDDPSCSATYPLMQKLRQVLVEHALVNGEKVRNSTTSIF 610

Query: 627 NAWKVASAEKAIS--LTREVRN-RFWQTPSSQAPAHAYLSPRTRVLYSFVREELGVQARR 683
 K+ S E+ + L +EV + R + A + R+ LY FVREELG

Sbjct: 611 Q--KIGSFEEELKTLPLKEVESARLEVENGNPAIPNRIKECRSYPLYKFVREELGT----- 664

Query: 684 GDVFGVGVQETIGSNVSRIYEAIKDGRINHLVKML 719
 + G + ++ G +++ AI G++ L++ L

Sbjct: 665 -SLLTGEKVKSPGEEFDKVFITAICAGKLIDPLLECL 699

☐ >gi|478740|pir|S28185 phenylalanine ammonia-lyase (EC 4.3.1.5) - rice
 Length = 716

Score = 322 bits (824), Expect = 3e-86

Identities = 200/507 (39%), Positives = 280/507 (55%), Gaps = 20/507 (3%)

Query: 49 SQLEIVQELLSDPDPTDDVVELSGYSLTXXXXXXXXXXXXXXXXXQNDDEIRARVDKSVDFLK 108
 S L+ V+ ++ D +V++ G SLT + D+ R RV S D++

Sbjct: 42 SHLDEVKRMVEDFRQLVKIEGASLTIAQVAAVAAGAGDARVELDESARGRVKASSDWVM 101

Query: 109 AQLQNSV--YGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPTSVSSFSVGRGLENL 166
 + YGVTTGFG ++ RT++ LQ+ LI G T + L

Sbjct: 102 NSMSEGTDYGVTTGFGATSHRRTKEG-GLQRELIRFLNAGAFGTGTDG-----HVL 152

Query: 167 PLEVVRGAMVIRVNSLTRGHSAVRLVVLEALTNFLNHRITPIVPLRGSISASGDLSPLSY 226
 P E R AM++R+N+L +G+S +R +LEA+T LN +TP +PLRG+I+ASGDL PLSY

Sbjct: 153 PAEATRAAMLVRINTLLQGYSGIRFEILEAITKLLNANVTPCLPLRGTITASGDLVPLSY 212

Query: 227 IAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEA--VVLGPKEGLGLVNGTAVSASM 284
IAG ITG + V V +G + + A EA + G+E L PKEGL +VNGTAV + +

Sbjct: 213 IAGLITGRQN-SVAVAPDGRK--VTAAEAFKIAGIEHGFFELQPKEGLAMVNGTAVGSGL 269

Query: 285 ATXXXXXXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQVEVARNIRTLLSG 344
A+ E M + + + + HPGQ+E A + +L G

Sbjct: 270 ASTVLFEANVLAISPEVLSAVFCEVMTKPE--YTDHLTHKLKHHPGQIEAAAIMEHILEG 327

Query: 345 SSFAXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTDNPL 404
SS+ +QDRY LR +PQ+LGP +E + A ++ E N+ DNPL

Sbjct: 328 SSYMKLAKKLGEIDPLMKP-KQDRYALRRAPQWLGPQIEVIPFATKSIEREINSVNDNPL 386

Query: 405 LDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCLA-A 463
+DV + HGGNFQ + + +SM+ TRLALA IGKL F Q +EL+N N GLPS L+

Sbjct: 387 IDVSRGKALHGGNFQGTPIGVSMNTRLALAAIGKLMFAQFSELVNDFYNGLPSNLSSG 446

Query: 464 EDPSLNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVNSLALISARRTAEAND 523
+PSL+Y KG +I +A+Y SEL L NPVT VQ AE NQ VNSL LIS+R+TAEA D

Sbjct: 447 RNPSLDYGFKGAEIAMASYCSELQFLGNPVTNHVQSAEQHNQDVNSLGLISSRKTAEAID 506

Query: 524 VLSLLLASHLYCTLQAVDLRAMELDFK 550
+L L+ ++ L QA+DLR +E + K

Sbjct: 507 ILKLMSSTFLIALCQAIDLRHLEENMK 533

☐ >gi|1172000|sp|P45731|PAL1_POPKI Phenylalanine ammonia-lyase G1
gi|485810|dbj|BAA06337.1| phenylalanine ammonia-lyase [Populus kitakamiensis]
Length = 682

Score = 322 bits (824), Expect = 3e-86

Identities = 235/684 (34%), Positives = 345/684 (50%), Gaps = 34/684 (4%)

Query: 49 SQLEIVQELLSDPTDDVVELSGYSLTXXXXXXXXXXXXXXXXXQNDDEIRARVDKSVDFLK 108
S L+ V+ ++ + + VV+L G +LT + +E RA V S D++

Sbjct: 9 SHLDEVKRMIEEYRNPVVKLGGETLTIGQVTAIASGHVGMVELSEEARAGVKASNDWVM 68

Query: 109 AQLQNSVYGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPTSVSSFSVGRGLENTLPL 168
+NS + VT GFG ++ +T+ LQK LI G+ F G + LP

Sbjct: 69 DS-KNS-HAVTAGFGATSHRKTQGGELQKELIRFLNVGI-----FGNGTESNHILPR 119

Query: 169 EVVRGAMVIRVNSLTRGHSVRLVLEALTNFLNHRITPIVPLRGSISASGDLSPLSYIA 228
R AM++R N+L +G+S +R +LEA+T LNH ITP +PLRG+I+ASGDL PL+YIA

Sbjct: 120 SATRAAMLVRTNTLLQGYSGIRFEMLEAITKLLNHNITPCLPLRGTITASGDLVPLAYIA 179

Query: 229 GAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEA--VVLGPKEGLGLVNGTAVSASMAT 286
G +TG + K V G + + EA + G+ L PKEGL LVNGTAV + +A+

Sbjct: 180 GLLTGRHNSKA-VGPNGEP--LTSTEAFTQAGINGGFFELQPKEGLALVNGTAVGSGLAS 236

Query: 287 XXXXXXXXXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGSS 346
E M G+ F + + HPGQ+E A + +L GS+

Sbjct: 237 MVLFEANVLAILSEVLSAIFAEVMQKGP-EFTDHLTHKLKHHPGQIEAAAIMEHILDGSA 295

Query: 347 FAXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTDNPLLD 406
+ +QDRY LRTSPQ+LGPL+E + + + E N+ DNPL+D

Sbjct: 296 YVKEAQKLEIDPLQKP-KQDRYALRTSPQWLGPLIEVIRTSTKMIEREINSVNDNPLID 354

Query: 407 VENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCL-AAED 465

V + GGNFQ + + +SM+ TRLA+A IGKL F Q +EL+N N GLPS L +
 Sbjct: 355 VSRSKALQGGNFQGTPIGVSMNTRLAIASIGKLMFAQFSELVNDFYNNGLPSNLTGGRN 414

Query: 466 PSLNYHGKGLDIIHIAAYASELGHLANPVTTTFVQPAEMGNQAVNSLALISARRTAEANDVL 525
 PSL+Y KG +I +A+Y SEL LANPVT VQ AE NQ VNSL LIS+R+TAEA D+L
 Sbjct: 415 PSLDYGFKGAEIAMASYCSELQFLANPVTNHVQSAEQHNQDVNSLGLISSRKTAEAVDIL 474

Query: 526 SLLLASHLYCTLQAVDLRAMELDFKKQFDPLLPTLLQQHLGTGLD-----VNALALEVKK 580
 L+ + L QAVDLR +E + K + + ++ L G + ++ K
 Sbjct: 475 KLMSTTFLVGLCQAVDLRHIEENLKNVTKNVTSQVAKRVLTMGFNGLHPSRLCEKDLLK 534

Query: 581 ALNKRLEQTTTYDLEP--RWHDAFSYATGTVVE--LLSSSPSANVTLTAVNAWKVASAEK 636
 ++K E Y +P + +VE L++ N T + + E
 Sbjct: 535 LVDK--EHVFAYIDDPSCSATYPLMQKLRQVLVEHALVNGERETNSTTSIFQKIRSFEEEL 592

Query: 637 AISLTREVRN-RFWQTPSSQAPAHAYLSRTRVLYSFVREELGVQARRGDVFGVQQETI 695
 L +EV + R + + R+ LY FVREELG + G + ++
 Sbjct: 593 KTLKPKEVESARLEVENGNPVVPNRIKECRSYPLYKFVREELGT-----SLLTGEKVKSP 647

Query: 696 GSNVSRIYEAIKDGRIHVLVKML 719
 G + +++ AI G++ L++ L
 Sbjct: 648 GEDFDKVFTAICAGKLMPLLECL 671

☐ >gi|18539331|gb|AAL74336.1| phenylalanine ammonia-lyase [Pinus sylvestris]
 gi|18539329|gb|AAL74335.1| phenylalanine ammonia-lyase [Pinus sylvestris]
 gi|18539327|gb|AAL74334.1| phenylalanine ammonia-lyase [Pinus sylvestris]
 gi|18539325|gb|AAL74333.1| phenylalanine ammonia-lyase [Pinus sylvestris]
 gi|18539323|gb|AAL74332.1| phenylalanine ammonia-lyase [Pinus sylvestris]
 gi|18539319|gb|AAL74330.1| phenylalanine ammonia-lyase [Pinus sylvestris]
 gi|18539317|gb|AAL74329.1| phenylalanine ammonia-lyase [Pinus sylvestris]
 gi|18539315|gb|AAL74328.1| phenylalanine ammonia-lyase [Pinus sylvestris]
 gi|18539311|gb|AAL74326.1| phenylalanine ammonia-lyase [Pinus sylvestris]
 gi|18539305|gb|AAL74323.1| phenylalanine ammonia-lyase [Pinus sylvestris]
 gi|18539303|gb|AAL74322.1| phenylalanine ammonia-lyase [Pinus sylvestris]
 gi|18539301|gb|AAL74321.1| phenylalanine ammonia-lyase [Pinus sylvestris]
 gi|18539299|gb|AAL74320.1| phenylalanine ammonia-lyase [Pinus sylvestris]
 gi|18539297|gb|AAL74319.1| phenylalanine ammonia-lyase [Pinus sylvestris]
 gi|18539295|gb|AAL74318.1| phenylalanine ammonia-lyase [Pinus sylvestris]
 gi|18539293|gb|AAL74317.1| phenylalanine ammonia-lyase [Pinus sylvestris]
 Length = 681

Score = 321 bits (822), Expect = 6e-86

Identities = 206/548 (37%), Positives = 304/548 (55%), Gaps = 22/548 (4%)

Query: 27 SAAGPTSALRRTPGLDGHAAHQSQLEIVQELLSIPTDDVVELSGYSLTXXXXXXXXXXXXX 86
 S + P + +R ++G +H +++ + + + +E G SLT
 Sbjct: 19 SGSDPLNWWRAAKAMEG--SHFEEVKAMVDSYLGVEKIFIE--GKSLTISDVAAVARRSQ 74

Query: 87 XXXXQNDDEIRARVDKSVDLKAQLQNSV--YGVTTGFGGSADTRTEDAVSLQKALIEHQ 144
 + + ++RV++S +++ Q+ YGVTTGFG ++ RT LQK LI
 Sbjct: 75 VKVKLDAEAAKSRVEESSNWVLTQMTKGTDTYGVTTGFGATSHRRTNQGAELQKELIRFL 134

Query: 145 LCGVTPTS SVSSFSVGRGLENLPLEVVRGAMVIRVNSLTRGHSAVRLVVLEALTNFLNHR 204
 GV +G+ EN L + R AM++R N+L +G+S +R +LE + LN
 Sbjct: 135 NAGV-----LGKCPENVLSEDTTRAAMLVRTNTLLQGYSGIRWDILETVEKLLNAG 185

Query: 205 ITPIVPLRGSISASGDLSPLSYIAGAITGHPDKVHVLHEGTEKIMFAREAISLFGLEAV 264
 +TP +PLRG+I+ASGDL PLSYIAG +TG P+ +V +G E M EA+ GLE

Sbjct: 186 LTPKPLRGTTITASGDLVPLSYIAGLLTGRPNRSRVS-RDGIE--MSGAEALKKVGLEKP 242

Query: 265 V-LGPKEGLGLVNGTAVSASMATXXXXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHD 323
L PKEGL +VNGT+V A++A+ E M G+ P H

Sbjct: 243 FELQPKEGLAIVNGTSVGAALASIVCFDANVLALLSEVISAMFCEVMNGKPEFTDPLTHK 302

Query: 324 VCRPHPGQVEVARNIRTLLSGSSFAXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVE 383
+ + HPGQ+E A + +L GSS+ +QDRY LRTSPQ+LGP VE

Sbjct: 303 L-KHHPGQMEAAAIMEYVLDGSSYMKHAAKLHEMNPLQKP-KQDRYALRTSPQWLGPQVE 360

Query: 384 DMMHAYSTLSLENNTTTNDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFT 443
+ A + E N+ DNP++DV + HGGNFQ + + +SM+ RL+++ IGKL F

Sbjct: 361 IIRSATHMIEREINSVNDNPVIDVARDKALHGGNFQGTPIGVSMNDLRLSISAIGKLMFA 420

Query: 444 QCTELLNAAMNRGLPSCLA-AEDPSLNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEM 502
Q +EL+N N GLPS L+ +PSL+Y KG +I +A+Y SEL +LANPVT+ VQ AE

Sbjct: 421 QFSELVNDYYNGGLPSNLGGPNPSLDYGLKGAEIAMASYTSELLYLANPVTSHVQSAEQ 480

Query: 503 GNQAVNSLALISARRTAEANDVLSLLASHLYCTLQAVDLRAMELDFKKQFDPLLPPLLQ 562
NQ VNSL L+SAR++AEA D+L L+L+++L QAVDLR +E + ++ + +

Sbjct: 481 HNQDVNSLGLVSARKSAEAIDILKMLSTYLTALCQAVDLRHLEENMLATVKQIVSQVAK 540

Query: 563 QHLGTGLD 570
+ L TGL+

Sbjct: 541 KTLSTGLN 548

☐ >gi|18539321|gb|AAL74331.1| phenylalanine ammonia-lyase [Pinus sylvestris]
Length = 681

Score = 320 bits (821), Expect = 8e-86

Identities = 206/548 (37%), Positives = 304/548 (55%), Gaps = 22/548 (4%)

Query: 27 SAAGPTSALRRTPGLDGHAHQSQLEIVQELLSIPTDDVVELSGYSLTXXXXXXXXXXXXX 86
S + P + +R ++G +H +++ + + + +E G SLT

Sbjct: 19 SGSDPLNWWRAAKAMEG--SHFEEVKAMVDSYLGVEIFIE--GKSLTISDVAAVARRSQ 74

Query: 87 XXXXQNDDEIRARVDKSVDFLKAQLQNSV--YGVTTGFGGSADTRTEDAVSLQKALIEHQ 144
+ + ++RV++S +++ Q+ YGVTTGFG ++ RT LQK LI

Sbjct: 75 VKVKLDAAEAASRVEESSNWVLTQMTKGTDTYGVTTGFGATSHRRTNQGAELQKELIRFL 134

Query: 145 LCGVTPTSVSFSVGRGLENLPLEVVRGAMVIRVNSLTRGHSVRLVLEALTNFLNHR 204
GV +G+ EN L + R AM++R N+L +G+S +R +LE + LN

Sbjct: 135 NAGV-----LGKCPENVLSEDTTRAAMLVRTNTLLQGYSGIRWDILETVKLLNAG 185

Query: 205 ITPIVPLRGSIASGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIMFAEAIISLFGLEAV 264
+TP +PLRG+I+ASGDL PLSYIAG +TG P+ +V +G E M EA+ GLE

Sbjct: 186 LTPKPLRGTTITASGDLVPLSYIAGLLTGRPNRSRVS-RDGIE--MSGAEALKKVGLEKP 242

Query: 265 V-LGPKEGLGLVNGTAVSASMATXXXXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHD 323
L PKEGL +VNGT+V A++A+ E M G+ P H

Sbjct: 243 FELQPKEGLAIVNGTSVGAALASIVCFDANVLALLSEVISAMFCEVMNGKPEFTDPLTHK 302

Query: 324 VCRPHPGQVEVARNIRTLLSGSSFAXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVE 383
+ + HPGQ+E A + +L GSS+ +QDRY LRTSPQ+LGP VE

Sbjct: 303 L-KLHPGQMEAAAIMEYVLDGSSYMKHAAKLHEMNPLQKP-KQDRYALRTSPQWLGPQVE 360

Query: 384 DMMHAYSTLSLENNTTTNDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFT 443
+ A + E N+ DNP++DV + HGGNFQ + + +SM+ RL+++ IGKL F

Sbjct: 361 IIRSATHMIEREINSVNDNPVIDVARDKALHGGNFQGTPIGVSMNDLRLSISAIGKLMFA 420

Query: 444 QCTELLNAAMNRGLPSCLA-AEDPSLNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEM 502
Q +EL+N N GLPS L+ +PSL+Y KG +I +A+Y SEL +LANPVT+ VQ AE

Sbjct: 421 QFSELVNDYYNGGLPSNLSGGPNPSLDYGLKGAEIAMASYTSELLYLANPVTSHVQSAEQ 480

Query: 503 GNQAVNSLALISARRTAEANDVLSLLLASHLYCTLQAVDLRAMELDFKKQFDPLLPTLLQ 562
NQ VNSL L+SAR++AEA D+L L+L+++L QAVDLR +E + ++ + +

Sbjct: 481 HNQDVNSLGLVSARKSAEAIDILKLMLSTYLTALCQAVDLRHLEENMLATVKQIVSQVAK 540

Query: 563 QHLGTGLD 570
+ L TGL+

Sbjct: 541 KTLSTGLN 548

☐ >gi|18539309|gb|AAL74325.1| phenylalanine ammonia-lyase [Pinus sylvestris]
gi|18539307|gb|AAL74324.1| phenylalanine ammonia-lyase [Pinus sylvestris]
Length = 681

Score = 320 bits (821), Expect = 8e-86
Identities = 206/548 (37%), Positives = 304/548 (55%), Gaps = 22/548 (4%)

Query: 27 SAAGPTSALRRTPGLDGHAHQSQLEIVQELLSDPTDDVVELSGYSLTXXXXXXXXXXXXX 86
S + P + +R ++G +H +++ + + + +E G SLT

Sbjct: 19 SGSDPLNWVRAAKAMEG--SHFEEVKAMVDSYLGVKEIFIE--GKSLTISDVAAVARRSQ 74

Query: 87 XXXXQNDDEIRARVDKSVDFLKAQLQNSV--YGVTTGFGGSADTRTEDAVSLQKALIEHQ 144
+ + ++RV++S +++ Q+ YGVTTGFG ++ RT LQK LI

Sbjct: 75 VKVKLDVEAAKSRVEESSNWVLTMQTKGTDTYGVTTGFGATSHRRTNQGAELQKELIRFL 134

Query: 145 LCGVTPTSVSSFSVGRGLENLPLEVVRGAMVIRVNSLTRGHSAVRLVVLEALTNFLNHR 204
GV +G+ EN L + R AM++R N+L +G+S +R +LE + LN

Sbjct: 135 NAGV-----LGKCPENVLSEDTTRAAMLVRTNTLLQGYSGIRWDILETVEKLLNAG 185

Query: 205 ITPIVPLRGSISASGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEAV 264
+TP +PLRG+I+ASGDL PLSYIAG +TG P+ +V +G E M EA+ GLE

Sbjct: 186 LTPKLPLRGITITASGDLVPLSYIAGLLTGRPNRVR--RDGIE--MSGAEALKKVGLEKP 242

Query: 265 V-LGPKEGLGLVNGTAVSASMATXXXXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHD 323
L PKEGL +VNGT+V A++A+ E M G+ P H

Sbjct: 243 FELQPKEGLAIVNGTSVGAALASIVCFDANVLALLSEVISAMFCEVMNGKPEFTDPLTHK 302

Query: 324 VCRPHPGQVEVARNIRTLLSGSSFAXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVE 383
+ + HPGQ+E A + +L GSS+ +QDRY LRTSPQ+LGP VE

Sbjct: 303 L-KHHPGQMEAAAIMEYVLDGSSYMKHAAKLHEMNPLQKP-KQDRYALRTSPQWLGPQVE 360

Query: 384 DMMHAYSTLSLENNTTTDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFT 443
+ A + E N+ DNP++DV + HGGNFQ + + +SM+ RL+++ IGKL F

Sbjct: 361 IIRSATHMIEREINSVNDNPVIDVARDKALHGGNFQGTPIGVSMNDLRLSISAIGKLMFA 420

Query: 444 QCTELLNAAMNRGLPSCLA-AEDPSLNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEM 502
Q +EL+N N GLPS L+ +PSL+Y KG +I +A+Y SEL +LANPVT+ VQ AE

Sbjct: 421 QFSELVNDYYNGGLPSNLSGGPNPSLDYGLKGAEIAMASYTSELLYLANPVTSHVQSAEQ 480

Query: 503 GNQAVNSLALISARRTAEANDVLSLLLASHLYCTLQAVDLRAMELDFKKQFDPLLPTLLQ 562
NQ VNSL L+SAR++AEA D+L L+L+++L QAVDLR +E + ++ + +

Sbjct: 481 HNQDVNSLGLVSARKSAEAIDILKLMLSTYLTALCQAVDLRHLEENMLATVKQIVSQVAK 540

Query: 563 QHLGTGLD 570

+ L TGL+
Sbjct: 541 KTLSTGLN 548

□>gi|129589|sp|P14166|PAL1_IPOBA Phenylalanine ammonia-lyase
gi|168272|gb|AAA33389.1| phenylalanine ammonia-lyase
Length = 707

Score = 320 bits (820), Expect = 1e-85

Identities = 236/693 (34%), Positives = 347/693 (50%), Gaps = 47/693 (6%)

Query: 49 SQLEIVQELLSDPTDDVVELSGYSLTXXXXXXXXXXXXXXXXXQNDDEIRARVDKSVDFLK 108
S L+ V+ ++++ V+L G +LT + +E RA V S D++
Sbjct: 29 SHLDEVKRMVAEFRKPAVKLGGETLTVAQVARIASRDNAVAVELSEEARAGVKASSDWVM 88

Query: 109 AQLQNSV--YGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPTSVSSFSVGRGLENLTL 166
+ YGVTTGFG ++ RT+ +LQK LI G+ + S +TL
Sbjct: 89 DSMNKGTD SYGVTTGFGATSHRRTKQGGALQKELIRFLNAGIFGNATESC-----HTL 141

Query: 167 PLEVVRGAMVIRVNSLTRGHSAVRLVLEALTNFLNHRITPIVPLRGSISASGDLSPLSY 226
P R AM++R+N+L +G+S +R +LEA+T LNH ITP +PLRG+I+ASGDL PLSY
Sbjct: 142 PHSATRAAMLVRINTLLQGYSGIRFEILEAITKLLNHNITPCLPLRGITITASGDLVPLSY 201

Query: 227 IAGAITGHPDVKVHVLHEGT----EKIMFAREAISLFGLEAVVLGPKEGLGLVNGTAVSA 282
IAG ITG P+ K + T E + +R +F V P++GL + +
Sbjct: 202 IAGLITGRPNKAVGPNGETLNAEEALRLSRSGRRIFR----VASPRKGLPSLMAPPLVL 257

Query: 283 SMATXXXXXXXXXXXXXXXXXXXXXVEAMVGQQGSFAPFIHDVCRPHPGQVEVARNIRTLL 342
MA+ E M G+ F + + HPGQ+E A + +L
Sbjct: 258 GMASMLFEANVLAVLSEVLSAIFAEMNGKP-EFTDHLTHKLKHHHPGQIEAAAIMEHIL 316

Query: 343 SGSSFAXXXXXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTDN 402
GSS+ +QDRY LRTSPQ+LGP +E + A + E N+ DN
Sbjct: 317 DGSSYVKAQKLHEMDPLQKP-KQDRYALRTSPQWLGPQIEVIRAATKMIEREINSVNDN 375

Query: 403 PLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCL- 461
PL+DV + HGGNFQ + + +SM+ +RLALA IGKL F Q +EL+N N GLPS L
Sbjct: 376 PLIDVARSKALHGGNFQGTPIGVSMDNSRLALASIGKLLFAQFSELVNDYNNGLPSNLT 435

Query: 462 AAEDPSLNYHGKGLDIHIAAYASELGHLANPVTTTFVQPAEMGNQAVNSLALISARRTAEA 521
A +PSL+Y KG +I +A+Y SEL LANPVT VQ AE NQ VNSL LISAR+TAEA
Sbjct: 436 AGRNP SLDYGFKGAEIAMASYCSELQFLANPVTNHVQSAEQHNQDVNSLGLISARKTAEA 495

Query: 522 NDVLSLLLASHLYCTLQAVDLRAMELDFKKQFDPLLPTLLQQHLGTGLDVNA-LALEVKK 580
DVL L+ +++L QA+DLR +E + + + + ++ L G + A +K
Sbjct: 496 VDVLKMSSTYLVALCQAIDLRFLLENLRNAVKNVAVTQVAKRTLTVGANGELHPARFCEK 555

Query: 581 ALNKRLEQ-----TTTTYDLEPRWHDASFYATGTVVVELLSSSPSANVTLTAVNAW 629
L + +++ + Y L + A V L + + T T++
Sbjct: 556 DLLRVVDREYVFAYADDPCSANYPLMQKLRQAL-----VDHALQNGENEKNTGTSTI-FL 608

Query: 630 KVASAEKAIS--LTREVR-NRFWQTPSSQAPAHAYLSPRTRVLYSFVREELGVQARRGDV 686
KVA+ E + L +EV R + A + R+ LY FVRE LG ++
Sbjct: 609 KVAAFEDELKAVLPKEVEAARIAVESGNPAIPNRIKECRSYPLYKFVREGLGT-----EL 663

Query: 687 FVG VQ QETIGSNVSRIYEAIKDGRINHVLVKML 719
G + + G +++ A+ +G I L++ L
Sbjct: 664 LTGEKVRSPGEECDKVFAMCEGSIIDPLECL 696

☐ >gi|129586|sp|P19143|PAL3_PHAVU Phenylalanine ammonia-lyase class III
 gi|81878|pir|S04128 phenylalanine ammonia-lyase (EC 4.3.1.5) class III - kidney
 Length = 710

Score = 320 bits (820), Expect = 1e-85

Identities = 231/691 (33%), Positives = 347/691 (50%), Gaps = 44/691 (6%)

Query: 49 SQLEIVQELLSIPTDDVVELSG-YSLTXXXXXXXXXXXXXXXXXQNDDEIRARVDKSVDFL 107
 S LE V+ +++++ + V+ + G +LT + R VD S ++
 Sbjct: 34 SHLEEVKGMVAEYREAVIHVGGGETLTVSKVAAVANQYLQAKVDLSESAREGVDSSCKWI 93

Query: 108 KAQLQNSV--YGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPTSVSSFSVGRGLENT 165
 + + YGVTTGFG +++ +T++ ++LQK ++ C + F L +T
 Sbjct: 94 VDNIDKGIPIYGVTTGFGANSNRQTQEGALQKEMVRFLNCAI-----FGYQTELSHT 146

Query: 166 LPLEVVRGAMVIRVNSLTRGHSVRLVLEALTNFLNHRITPIVPLRGSISASGDLSPLS 225
 LP R AM++RVN+L +G+S +R +LEA+T LNH +TPI+PLRG+I+ASGDL PLS
 Sbjct: 147 LPKSATRAAMLVRVNTLLQGYSGIRFEILEAITKLLNHNVTPIPLRGTTITASGDLIPLS 206

Query: 226 YIAGAITGHPDVKVHVLHEGTEKIMFAEAIISLFGLEA--VVLGPKEGLGLVNGTAVSAS 283
 YIA + G + K V G + A+EA L G++ L PKEGL LVNGTAV +
 Sbjct: 207 YIAALLIGRRNSKA-VGPSGES--LNAKEAFHLAGVDGGFFELKPKEGLALVNGTAVGSG 263

Query: 284 MATXXXXXXXXXXXXXXXXXXXXXVEAMVGQQGSFAPFIHDVCRPHPGQVEVARNIRTLLS 343
 +A+ E M G+ IH + + HPGQ+E A + +L
 Sbjct: 264 VASMVLFEANILALLAEVLSAVFAEVMQGKPEFTDHLIHLK-KYHPGQIEAAAIMEHILD 322

Query: 344 GSSFAXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTDNP 403
 GSS+ R+DRY L TSPQ+LGP +E + + ++ E N+ DNP
 Sbjct: 323 GSSYVKNALQPDPLQKP--RKDRYALVTSPQWLGPQIEIIRFSTKSIEREINSVNDNP 380

Query: 404 LLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELNAAAMNRGLPSCLA- 462
 L+DV + GGNFQ + + +SM+ RLA+A IGKL F Q TEL N N GLPS L+
 Sbjct: 381 LIDVTRNKAVSGGNFQGTPIGVSMNARLAVASIGKLIFAQFTELANDLYNNGLPNSLSV 440

Query: 463 AEDPSLNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVNSLALISARRTAEAN 522
 +PSL+Y K ++ +AAY SEL +LANPVT+ VQ E NQ VNSL LISA +T EA
 Sbjct: 441 GRNPSLDYGFKADEVAMAAYCSELQYLANPVTSHVQSTEQHNQDVNSLGLISALKTVEAI 500

Query: 523 DVLSTLLASHLYCTLQAVDLRAMELDFKKQFDPLLPPTLLQQHLGT--GLDVNALAL---E 577
 ++L L+ +++L QA+DLR +E FK + + + L T + N E
 Sbjct: 501 EILKLMSSSTYLVALCQAIDLRHLEEIFKNTVKNTVSRVALKTTLTTEDKEETNPFRFSEEE 560

Query: 578 VKKALNKRL-----EQTTTYDLEPRWHDA-FSYATGTVVELLSSSPSANVTLTAVNAW 629
 + K +++ Y L P+ + A +V+ NV+L
 Sbjct: 561 LLKVVVDREYVFSYIDDPNVRYPLMPKLKQVLYEQAHTSVIN-----DKNVSLLVFEKI 614

Query: 630 KVASAEKAISLTREVRN-RFQWTPSSQAPAHAYLSRPRTRVLYSFVREELGVQARRGDVVF 688
 E L +EV + R + A + R+ LY FVREELG++ G+ +
 Sbjct: 615 GAFEDELKSLLPKEVESARVAYENGPNPATPNRIKECRSYPLYKFVREELGIRLLTGEKAL 674

Query: 689 GVQQETIGSNVSRIYEAIKDGRINHVLVKML 719
 +E ++Y A+ +I +++ L
 Sbjct: 675 SPDEE-----FEKVYTAMCQAKIIDPILECL 700

☐ >gi|228615|prf|1807329B Phe ammonia lyase
Length = 711

Score = 320 bits (820), Expect = 1e-85

Identities = 231/691 (33%), Positives = 347/691 (50%), Gaps = 44/691 (6%)

Query: 49 SQLEIVQELLSDPTDDVVELSG-YSLTXXXXXXXXXXXXXXXXXQNDDEIRARVDKSVDL 107
S LE V+ ++++ + V+ + G +LT + R VD S ++

Sbjct: 34 SHLEEVKGMVAEYREAVIHVGGGETLTVSKVAAVANQYLQAKVDLSESAREGVDSSCKWI 93

Query: 108 KAQLQNSV--YGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPTSVSSFSVGRGLENT 165
+ + YGVTTGFG +++ +T++ ++LQK ++ C + F L +T

Sbjct: 94 VDNIDKGIPIYGVTTGFGANSNRQTQEGALQKEMVRFLNCAI-----FGYQTELSHT 146

Query: 166 LPLEVVRGAMVIRVNSLTRGHSVRLVLEALTNFLNHRITPIVPLRGSISASGDLSPLS 225
LP R AM++RVN+L +G+S +R +LEA+T LNH +TPI+PLRG+I+ASGDL PLS

Sbjct: 147 LPKSATRAAMLVRVNTLLQGYSGIRFEILEAITKLLNHNVTPIPLRGTTITASGDLIPLS 206

Query: 226 YIAGAITGHPDVKVHVLHEGTEKIMFAEAISLFGLEA--VVLGPKEGLGLVNGTAVSAS 283
YIA + G + K V G + A+EA L G++ L PKEGL LVNGTAV +

Sbjct: 207 YIAALLIGRRNSKA-VGPSGES--LNAKEAFHLAGVDGGFFELKPKEGLALVNGTAVGSG 263

Query: 284 MATXXXXXXXXXXXXXXXXXXXXXVEAMVGQQGSFAPFIHDVCRPHPGQVEVARNIRTLLS 343
+A+ E M G+ IH + + HPGQ+E A + +L

Sbjct: 264 VASMLFEANILALLAEVLSAVFAEVMQKPEFTDHLIHKL-KYHPGQIEAAAIMEHILD 322

Query: 344 GSSFAXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTDNP 403
GSS+ R+DRY L TSPQ+LGP +E + + ++ E N+ DNP

Sbjct: 323 GSSYVKNALQQPDPLQKP--RKDRYALVTSPQWLGPQIEIIRFSTKSIEREINSVNDNP 380

Query: 404 LLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCLA- 462
L+DV + GGNFQ + + +SM+ RLA+A IGKL F Q TEL N N GLPS L+

Sbjct: 381 LIDVTRNKAVSGGNFQGTPIGVSMNARLAVASIGKLIFAQFTELANDLYNNGLPNSLSV 440

Query: 463 AEDPSLNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVNSLALISARRTAEAN 522
+PSL+Y K ++ +AAY SEL +LANPVT+ VQ E NQ VNSL LISA +T EA

Sbjct: 441 GRNPSLDYGFKADEVAMAAYCSELQYLANPVTSHVQSTEQHNQDVNSLGLISALKTVEAI 500

Query: 523 DVLSLLASHLYCTLQAVDLRAMELDFKKQFDPDLLPTLLQQHLGT--GLDVNALAL---E 577
++L L+ ++L QA+DLR +E FK + + + L T + N E

Sbjct: 501 EILKLMSSTYLVALCQAIDLRHLEEIFKNTVKNTVSRVALKTLTTEDKEETNPFRFSEEE 560

Query: 578 VKKALNKRL-----EQTTTYDLEPRWHD-AFSYATGTVVELLSSSPSANVTLTAVNAW 629
+ K +++ Y L P+ + A +V+ NV+L

Sbjct: 561 LLKVVDREYVFSYIDDPNVRYPLMPKQVLYEQAHTSVIN-----DKNVSLLVFEKI 614

Query: 630 KVASAEKAISLTREVRN-RFWQTPSSQAPAHAYLSPRTRVLYSFVREELGVQARRGDV 688
E L +EV + R + A + R+ LY FVREELG++ G+ +

Sbjct: 615 GAFEDELKSLLPKEVESARVAYENGNPATPNRIKECRSYPLYKFVREELGIRLLTGEKAL 674

Query: 689 GVQQETIGSNVSRIYEAIKDGRINHVLVKML 719
+E ++Y A+ +I +++ L

Sbjct: 675 SPDEE-----FEKVYTAMCQAKIIDPILECL 700

☐ >gi|18539313|gb|AAL74327.1| phenylalanine ammonia-lyase [Pinus sylvestris]
Length = 681

Score = 318 bits (815), Expect = 4e-85

Identities = 205/548 (37%), Positives = 303/548 (55%), Gaps = 22/548 (4%)

Query: 27 SAAGPTSALRRTPGLDGHAAHQSQLEIVQELLSDPD VVELSGYSLTXXXXXXXXXXXXX 86
S + P + +R ++G +H +++ + + + +E G SLT

Sbjct: 19 SGSDPLNWVRAAKAMEG--SHFEVKAMVDSYLGVEIFIE--GKSLTISDVA AVARRSQ 74

Query: 87 XXXXQNDDEIRARVDKSVDFLKAQLQNSV--YGVTTGFGGSADTRTEDAVSLQKALIEHQ 144
+ + ++RV++S +++ Q+ YGVTTGFG ++ RT LQK LI

Sbjct: 75 VKVKLDAAAKSRVEESSNWVLTQMTKGTDTYGVTTGFGATSHRRTNQGAELQKELIRFL 134

Query: 145 LCGVTPTS SVSSFSVGRGLENLTPLEVVRGAMVIRVNSLTRGHS AVRLVVLEALTNFLNHR 204
GV +G+ EN L + R AM++R N+L +G+S +R +LE + LN

Sbjct: 135 NAGV-----LGKCPENVLSEDTTAAAMLVTRNTLLQGYSGIRWDILETVEKLLNAG 185

Query: 205 ITPIVPLRGSISASGDLSPLSYIAGAITGHPDKVHVLHEGTEKIMFARE AISLFGLEAV 264
+TP +PLRG+I+ASGDL PLSYIAG +TG P+ +V +G E M EA+ GLE

Sbjct: 186 LTPKLPLRGITITASGDLVPLSYIAGLLTGRPNRVR--RDGIE--MSGAEALKKVGLEKP 242

Query: 265 V-LGPKEGLGLVNGTAVSASMATXXXXXXXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHD 323
L PKEGL + NGT+V A++A+ E M G+ P H

Sbjct: 243 FELQPKEGLAIGNGTSGAALASIVCFDANVLALLSEVISAMFCEVMNGKPEFTDPLTHK 302

Query: 324 VCRPHPGQVEVARNIRTLTSGSSFAXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVE 383
+ + HPGQ+E A + +L GSS+ +QDRY LRTSPQ+LGP VE

Sbjct: 303 L-KHHPGQMEAAIMEYVLDGSSYMKHA AKLHEMNPLQKP-KQDRYALRTSPQWLGPQVE 360

Query: 384 DMMHAYSTLSLENNTTT DNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFT 443
+ A + E N+ DNP++DV + HGGNFQ + + +SM+ RL+++ IGKL F

Sbjct: 361 IIRSATHMIEREINSVNDNPVIDVARDKALHGGNFQGTPIGVSM DNRLSISAIGKLMFA 420

Query: 444 QCTELLNAAMNRGLPSCLA-AEDPSLNYHGKGLDIHIAAYASELGH LANPVTTFVQPAEM 502
Q +EL+N N GLPS L+ +PSL+Y KG +I +A+Y SEL +LANPVT+ VQ AE

Sbjct: 421 QFSELVNDYYNGGLPSNLGGPNPSLDYGLKGA EIAMASYTSELLYLANPVTSHVQSAEQ 480

Query: 503 GNQAVNSLALISARRTAEANDVLSLLASHLYCTLQAVDLRAMELDFKKQFDPLLP TLLQ 562
NQ VNSL L+SAR++AEA D+L L+L+++L QAVDLR +E + ++ + +

Sbjct: 481 HNQDVNSLGLVSARKSAE AIDILKMLSTYLTALCQAVDLRHLEENMLATVKQIVSQVAK 540

Query: 563 QHLGTGLD 570
+ L TGL+

Sbjct: 541 KTLSTGLN 548

☐ >gi|44889624|gb|AAS48415.1| phenylalanine lyase [Allium cepa]
Length = 708

Score = 317 bits (811), Expect = 1e-84

Identities = 203/512 (39%), Positives = 279/512 (54%), Gaps = 19/512 (3%)

Query: 40 GLDGHAAHQSQLEIVQELLSDPD VVELSGYSLTXXXXXXXXXXXXXQNDDEIRAR 99
G A S LE V+ +++ + V+L G +L D+ R

Sbjct: 24 GAAAKAMSGSHLEEVKRMVNEYREKSVKLEGATLKVAQVA AAGEIKEVVL-DEGAREG 82

Query: 100 VDKSVDFLKAQLQNSV--YGVTTGFGGSADTRTEDAVSLQKALIEHQ LCGVTPTS SVSSFS 157
V S D++ + YGVTTGFG ++ RT++ V+LQ LI G+ + S

Sbjct: 83 VKASSDWVMDSMCKGTDSYGVTGFGATSHRRTKNGVALQNELIRFLNAGIFGSPNSG-- 140

Query: 158 VGRGLENLTPLEVVRGAMVIRVNSLTRGHS AVRLVVLEALTNFLNHRITPIVPLRGSISA 217

N+LP R AM++RVN+L +G+S +R +LE++T LN ITP +PLRG+I+A
 Sbjct: 141 -----NSLPSTTTTRAAMLVRVNTLLQGYSGIRFEILESITRLNANITPCLPLRGTTITA 194
 Query: 218 SGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEA--VVLGPKEGLGLV 275
 SGDL PLSYIA +TG P+ K V + T ++ EA L G+ + L PKEGL LV
 Sbjct: 195 SGDLVPLSYIAALLTGRPNK-SVTSNDT--LLTPSEAFQLAGITSGFFQLQPKEGLALV 251
 Query: 276 NGTAVSASMATXXXXXXXXXXXXXXXXXXVEAMVGQQGSFAPFIHDVCRPHPGQVEVA 335
 NGTAV + +A+ E M G+ F + + HPGQ+E A
 Sbjct: 252 NGTAVGSGLASIVLYETNVLAVLAEVMSALFCEVMQKGP-EFTDHLTHKLKHHPGQIEAA 310
 Query: 336 RNIRTLGSSSFAXXXXXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLE 395
 + +L GSS+ +QDRY LRTSPQ+LGP +E + A ++ E
 Sbjct: 311 AIMEHILEGSSYMKMAKKLHDTDPLQKP-KQDRYALRTSPQWLGPQIEVIRAATKSIERE 369
 Query: 396 NNTTTDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNR 455
 N+ DNPL+DV + HGGNFQ + + +SM+ TRLA+A IGKL F Q +EL+N N
 Sbjct: 370 INSVDNPLIDVSRNKAVHGGNFQGTPIGVSMONTRLAFAAIGKLMFAQFSELVNDFYNN 429
 Query: 456 GLPSCL-AAEDPSLNYHGKGLDIIHIAAYASELGHLANPVTTFVQPAEMGNQAVNSLALIS 514
 GLPS L +PSL+Y KG +I +A+Y SEL LANPVT VQ AE NQ VNSL LIS
 Sbjct: 430 GLPSNLTGGRNPGLDYGFKAELIAMASYCSELQFLANPVTNHVQSAEQHNQDVNSLGLIS 489
 Query: 515 ARRTAEANDVLSLLASHLYCTLQAVDLRAME 546
 AR+T EA +L L+ + L QA+DLR +E
 Sbjct: 490 ARKTEEAVTILKLMSTTFLVALCQAIDLRHLE 521

☐ >gi|32491955|gb|AAP85251.1| phenylalanine ammonia-lyase [Pinus pinaster]
 Length = 727

Score = 313 bits (803), Expect = 9e-84

Identities = 228/677 (33%), Positives = 339/677 (50%), Gaps = 52/677 (7%)

Query: 66 VELSGYSLTXXXXXXXXXXXXXXXXXQNDDEIRARVDKSVDFLKAQLQNSV-----YGVTT 120
 V + G SLT + +ARVD+S +++ LQN + YGVTT
 Sbjct: 68 VSIEGKSLTIADVTAVARRPEAKVRLDAVSAKARVDESSNWV---LQNMLKGTDTYGVTT 124
 Query: 121 GFGGSADTRTEDAVSLQKALIEHQLCGVTPPTSVSFSVGRGLENTLPLEVVRGAMVIRVN 180
 GFG ++ RT LQK LI GV N LP E R AM++R N
 Sbjct: 125 GFGATSHRRTNQGAELQKELIRFLNSGVLTGEG-----NILPQETTRAAMLVRTN 173
 Query: 181 SLTRGHSVRLVVLEALTNFLNHRITPIVPLRGSSISASGDLSPLSYIAGAITGHPDVKVH 240
 +L +G+S +R +LE + LN I P +P++G+IS+SGDL PLSYIAG ITG P+ +
 Sbjct: 174 TLMQGYSGIRWEILETIQKLLNAGIIPKLPVKGTISSSGDLVPLSYIAGFITGRPNRAR 233
 Query: 241 VLHEGTEKIMFAREAISLFGLEAVV-LGPKEGLGLVNGTAVSASMATXXXXXXXXXXXXX 299
 + +G E + A EA+ G+E L PKEGL +V G + A++A+
 Sbjct: 234 CI-DGKE--LGALEALQQIGVEKPFELQPKGLAIVTGPRLGAALASIVCFDANIICIAA 290
 Query: 300 XXXXXXXXVEAMVGQQGSFAPFIHDVCRPHPGQVEVARNIRTLGSSSFAXXXXXXXXXXXXXX 359
 E M+G+ P H + + HP Q+E A + +L GSS+
 Sbjct: 291 EVLSAMFCEVMLGKPEFTDPLTHRL-KHHPAQMEAAAIMEYVLDGSSYMKNAKKHEMNP 349
 Query: 360 XXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTDNPLLDVENKQTAHGGNFQ 419
 +QDRY LRTSPQ+LGP +E + A + E N+ DNP++DV + HGGNFQ
 Sbjct: 350 LQKP-KQDRYALRTSPQWLGPQIEVIRSATHMIQREINSVDNPNVIDVARDKALHGGNFQ 408
 Query: 420 ASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCLA-AEDPSLNYHGKGLDIH 478

```

      + + +SM+  RLALA IGKL F Q +EL+N   N GLPS L+   +PSL+Y  KG +I
Sbjct: 409 GTPIGVSMNDLRLALAAIGKLMFAQFSELVNDYYNGGLPSNLSGGPNPSLDYGFKGAEIA 468

Query: 479 IAAYASELGHLANPVTTTFVQPAEMGNQAVNSLALISARRTAEANDVLSLLLASHLYCTLQ 538
      +A+Y SEL +LA+PVTT VQ AE  NQ VNSL LISAR++AEA D+L+L+++++L   Q
Sbjct: 469 MASYTSELLYLASPVTHVQSAEQHNQDVNSLGLISARKSAEAIIDILNLMVSTYLLALCQ 528

Query: 539 AVDLRAMELDFKKQFDPLLPTLLQQHLGTGLDVNALALEVKKALNKRLEQTT----- 590
      A DLR +E +      ++ + ++ L T   N   L   +   K L Q
Sbjct: 529 AADLRHLEENMLSTVKHVVS HVAKKTLSTH---NGELLTAGRFCEKDLLQAVENLHVFAV 585

Query: 591 -----TYDLEPRWHDFAF-SYATGTVVVELLS SSPSANVTLTAVNAWKVASAEKAISLTR 642
      Y L +      ++A      ++ + + S+      + A++      E+ +
Sbjct: 586 VDDPCNENYPLMQQLRQVLVAHALTETAQIQQTQTQSS--IFNKIPAFEKELKEQMEAEIG 643

Query: 643 EVNRNRFWQTPSSQAPAHAYLSPRTRVLYSFVREELGVQARRGDVFGVQVQETIGSNVSRI 702
      R +++ + + +      R+ LY F R +LG Q   GD   + + G + ++
Sbjct: 644 RARQDYERGVAGSIPNRIQECRSFPLYDFARSQQLGTQLLSGD-----RVTSPGEYIEKV 698

Query: 703 YEAIKDGRINHLVVKML 719
      Y I+DG+I   L K L
Sbjct: 699 YTGIRDGKIISPLFKCL 715

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☐ >gi|32491953|gb|AAP85250.1| phenylalanine ammonia-lyase [Pinus pinaster]
Length = 727

Score = 312 bits (800), Expect = 2e-83

Identities = 227/677 (33%), Positives = 339/677 (50%), Gaps = 52/677 (7%)

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Query: 66 VELSGYSLTXXXXXXXXXXXXXXXXXQNDDEIRARVDKSVDFLKAQLQNSV-----YGVTT 120
      V + G SLT      +      +ARVD+S +++   LQN +      YGVTT
Sbjct: 68 VSIEGKSLTIADVTAVARRPEAKVRLDAVSAKARVDESSNWV---LQNMLKGTDTYGVTT 124

Query: 121 GFGGSADTRTEDAVSLQKALIEHQLCGVTPTSVSSFSVGRGLENTLPLEVVRGAMVIRVN 180
      GFG ++ RT   LQK LI   GV      N LP E   R AM++R N
Sbjct: 125 GFGATSHRRTNQGAELQKELIRFLNSGVLTG-----NILPQETTRAAMLVRTN 173

Query: 181 SLTRGHSARVLVLEALTNFLNHRITPIVPLRGSISASGDLSPLSYIAGAITGHPDVKVH 240
      +L +G+S +R +LE +   LN I P +P++G+IS+SGDL PLSYIAG ITG P+ +
Sbjct: 174 TLMQGYSGIRWEILETIQKLLNAGIIPKLPVKGTISSSGDLVPLSYIAGFITGRPNRRAR 233

Query: 241 VLHEGTEKIMFAREAISLFGLEAVV-LGPKEGLGLVNGTAVSASMATXXXXXXXXXXXXX 299
      + +G E + A EA+   G+E   L PKEGL +V G + A++A+
Sbjct: 234 CI-DGKE--LGALEALQQIGVEKPFELQPKGLAIVTGPRLGAAALASIVCFDANIICIAA 290

Query: 300 XXXXXXXXVEAMVGQQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGSSFAXXXXXXXXXXXXX 359
      E M+G+      P H + + HP Q+E A + +L GSS+
Sbjct: 291 EVLSAMFCEVMLGKPEFTDPLTHRL-KHHPAQMEAAAIMEYVLDGSSYMKNAAKKHEMN 349

Query: 360 XXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTNDNPLLDVENKQTAHGGNFQ 419
      +QDRY LRTSPQ+LGP +E + A + E N+ DNP++DV + HGGNFQ
Sbjct: 350 LQKP-KQDRYALRTSPQWLGPQIEVIRSATHMIQREINSVNDNPVIDVARDKALHGGNFQ 408

Query: 420 ASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCLA-AEDPSLNYHGKGLDIH 478
      + + +SM+  RLALA IGKL F Q +EL+N   N GLPS L+   +PSL+Y  KG +I
Sbjct: 409 GTPIGVSMNDLRLALAAIGKLMFAQFSELVNDYYNGGLPSNLSGGPNPSLDYGFKGAEIA 468

Query: 479 IAAYASELGHLANPVTTTFVQPAEMGNQAVNSLALISARRTAEANDVLSLLLASHLYCTLQ 538

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+A+Y SEL +LA+PVTT VQ AE NQ VNSL LISAR++AEA D+L+L++++L Q
 Sbjct: 469 MASYTSELLYLASPVTTTHVQSAEQHNQDVNSLGLISARKSAEAIIDILNLMVSTYLLALCQ 528
 Query: 539 AVDLRAMELDFKKQFDPLLPTLLQQHLGTGLDVNALALEVKKALNKRLEQTT----- 590
 A DLR +E + ++ + ++ L T N L + K L Q
 Sbjct: 529 AADLRHLEENMLSTVKHVSHVAKKTLSTH---NGELLTAGRFCEKDLLQAVENLHVFAV 585
 Query: 591 -----TYDLEPRWHDFAF-SYATGTVVELLSSSPSANVTLTAVNAWKVASAEKAISLTR 642
 Y L + ++A ++ + + S+ + A++ ++ +
 Sbjct: 586 VDDPCNENYPLMQQLRQVLVAHALTETAQIQTTQTQSS--IFNKIPAFEKELKDQMEAEIG 643
 Query: 643 EVRNRFWQTPSSQAPAHAYLSPRTRVLYSFVREELGVQARRGDVFGVQQTIGSNVSRI 702
 R +++ + + + R+ LY F R +LG Q GD + + G + ++
 Sbjct: 644 RARQDYERGVAGSIPNRIQECRSFPLYDFARSQGLTQLLSGD-----RVTSPGEYIEKV 698
 Query: 703 YEAIKDGRINHVLVKML 719
 Y I+DG+I L K L
 Sbjct: 699 YTGIRDGKIISPLFKCL 715

☐ >gi|1220270|emb|CAA34715.1| unnamed protein product [Petroselinum crispum]
 Length = 580

Score = 310 bits (793), Expect = 1e-82

Identities = 212/575 (36%), Positives = 303/575 (52%), Gaps = 27/575 (4%)

Query: 159 GRGLENLPLEVVRGAMVIRVNSLTRGHSVRLVLEALTNFLNHRITPIVPLRGSISAS 218
 G G +NTLP R AM++R+N+L +G+S +R +LEA+T FLN ITP +PLRG+I+AS
 Sbjct: 8 GNGSDNTLPHSATRAAMLVRINTLLQGYSGIRFEILEAITKFLNQNITPCLPLRGITITAS 67
 Query: 219 GDLSPLSYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEA--VVLGPKEGLGLVN 276
 GDL PLSYIAG +TG P+ K T I+ EA L G+E L PKEGL LVN
 Sbjct: 68 GDLVPLSYIAGLLTGRPNKAV---GPTGVILSPEEAFKLAGVEGGFFELQPKEGLALVN 124
 Query: 277 GTAVSASMATXXXXXXXXXXXXXXXXXXXXXVEAMVGQQGSFAPFIHDVCRPHPGQVEVAR 336
 GTAV + MA+ E M G+ F + + HPGQ+E A
 Sbjct: 125 GTAVGSGMASMVLFEANILAVLAEVMSAIFAEVMQGP-EFTDHLTHKLKHHHPGQIEAAA 183
 Query: 337 NIRTLLSGSSFAXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLEN 396
 + +L GS++ +QDRY LRTSPQ+LGP +E + + + E
 Sbjct: 184 IMEHILDGSAYVKAQKLHEMDPLQKP-KQDRYALRTSPQWLGPQIEVIRSSTKMIEREI 242
 Query: 397 NTTTDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRG 456
 N+ DNPL+DV + HGGNFQ + + +SM+ TRLA+A IGKL F Q +EL+N N G
 Sbjct: 243 NSVNDNPLIDVSRNKAIHGGNFQGTPIGVSMDNTRLAIAAIGKLMFAQFSELVNDFYNNG 302
 Query: 457 LPSCLA-AEDPSLNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVNSLALISA 515
 LPS L+ +PSL+Y KG +I +A+Y SEL LANPVT VQ AE NQ VNSL LIS+
 Sbjct: 303 LPSNLSGGRNPGLDYGFKAIEAMASYCSELQFLANPVTNHVQSAEQHNQDVNSLGLISS 362
 Query: 516 RRTAEANDVLSLLLASHLYCTLQAVDLRAMELDFKKQFDPLLPTLLQQHLGTGLDVNALA 575
 R+T+EA ++L L+ + L QA+DLR +E + K + ++ ++ L G++
 Sbjct: 363 RKTSEAVEILKLMSTTFLVGLCQAIDLRHLEENLKSTVKNTVSSVAKRVLTMGVNGE--- 419
 Query: 576 LEVKKALNKRLEQTTTYDLEPRWHDFAFSYAT-----GTVVELLSSSPSANVTLTAVN 627
 L + K L + + + D AT T+VE + L+
 Sbjct: 420 LHPSRFCEKDLLRVVDREYIFAYIDDPSCATYPLMQKLRQTLVEHALKNGDNERNLSTSI 479
 Query: 628 AWKVASAEKAIS--LTREVRN-RFWQTPSSQAPAHAYLSPRTRVLYSFVREELGVQARRG 684

K+A+ E + L +EV + R + A + R+ LY FVR+ELG
 Sbjct: 480 FQKIATFEDELKALLPKEVESARAALESGNPAIPNRIEECRSYPLYKFVRKELGT----- 534
 Query: 685 DVFGVGVQQETIGSNVSRIYEAIKDGRINHVLVKML 719
 + G + + G +++ A+ G I L++ L
 Sbjct: 535 EYLTGEKVTSPGEEFEKVFIAMSKGEIIDPLLECL 569

>gi|1171999|sp|P45727|PALY_PERAE Phenylalanine ammonia-lyase
 gi|563243|gb|AAA51873.1| phenylalanine ammonia lyase
 Length = 620

Score = 309 bits (791), Expect = 2e-82
 Identities = 220/618 (35%), Positives = 319/618 (51%), Gaps = 33/618 (5%)

Query: 116 YGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPTSVSSFSVGRGLENLTPLEVVRGAM 175
 YGVTTGFG ++ RT+ +L K LI G+ T+ S +TL R AM
 Sbjct: 11 YGVTTGFGATSHRRTKQGGALHKELIRFLNAGIFGTNGES-----GHTLAPSATRAAM 63
 Query: 176 VIRVNSLTRGHSVRLVLEALTNFLNHRITPIVPLRGSISASGDLSPLSYIAGAITGHP 235
 ++R+N+L +G+S +R +LEA+T+ LNH ITP +PLRG+I+ASGDL PLSYIAG +TG P
 Sbjct: 64 LVRINTLLQGYSGIRFEILEAITSLLNHSITPCLPLRGTTITASGDLVPLSYIAGMLTGRP 123
 Query: 236 DVKVHVLHEGTEKIMFAEASISLFGLEA--VVLGPKEGLGLVNGTAVSASMATXXXXXXX 293
 + K +G E + A EA L G+ + L PKEGL LVNGTAV + +A+
 Sbjct: 124 NSKGD-WPDGKE--IDAGEAFRLAGIPSGFFELQKEGLALVNGTAVGSGGLASMLVFEAN 180
 Query: 294 XXXXXXXXXXXXXXXVEAMVGQQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGSSFAXXXXX 353
 E M G+ F + + HPGQ+E A + +L GSS+
 Sbjct: 181 VLSVLSEVISAIKFCEVMQGKP-EFTDHLTHKLKHHPGQIEAAAIMEHILDGSSYMKVAKK 239
 Query: 354 XXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTNDNPLLDVENKQTA 413
 + LRTSPQ+LGP +E + +A ++ E N+ DNPL+DV +
 Sbjct: 240 LHELDPLQKPKQDPYAALRTSPQWLGPQIEVIRNATLSIEREINSVNDNPLIDVSRNKAL 299
 Query: 414 HGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCLA-AEDPSLNYHG 472
 HG NFQ + + +SM+ TRLA+A IGKL F Q +EL+N N GLPS L+ +PSL+Y
 Sbjct: 300 HGRNFQGTPIGVSMONTRLAIAAIGKLMFAQFSELVNDFYNNGLPSNLSGGRNPPLDYGF 359
 Query: 473 KGLDIHIAAYASELGHLANPVTTTFVQPAEMGNQAVNSLALISARRTAEANDVLSLLASH 532
 KG +I +AAY SEL LANPVT VQ AE NQ VNSL LIS+R+TAEA ++L L+ ++
 Sbjct: 360 KGAEIAMAAYCSELQFLANPVTNHVQSAEQHNQDVNSLGLISSRKTAEAIVEILKLMSSTF 419
 Query: 533 LYCTLQAVDLRAMELDFKKQFDPLLPTLLQQHLGTGLDVNALALEVKKALNKRL----- 586
 L QA+DLR +E + K + + ++ L G++ L + K L
 Sbjct: 420 LVGLCQAIDLRHLEENLKSTVKNTVSQVAKRVLTIGVNGE---LHPSRFCEKDLIKVVVDG 476
 Query: 587 EQTTTYDLEP--RWHDAFSYATGTVVE--LLSSSPSANVTLTAVNAWKVASAEKAI SLTR 642
 E Y +P + +VE L++ + + + E L +
 Sbjct: 477 EHLFAYIDDPSCCTYPLMQKLRQVLVEHALINGEKEKDSSTSIFQKIGAFEEELKTHLPK 536
 Query: 643 EVRN-RFWQTPSSQAPAHAYLSPRTRVLYSFVREELGVQARRGDVFGVGVQQETIGSNVSR 701
 EV + R + A + R+ LY FVREEL + + G + + G +
 Sbjct: 537 EVESARIELERGN SAIPNRIKECRSYPLYKFVREEL-----KTSLLTGEKVRSPGEEFDK 591
 Query: 702 IYEAIKDGRINHVLVKML 719
 ++ AI G++ L++ L
 Sbjct: 592 VFSAICQGKVIDPLLECL 609

☐ >gi|2118318|pir|S60043 phenylalanine ammonia-lyase (EC 4.3.1.5) 4 - Japanese as
large-toothed aspen (fragment)
Length = 582

Score = 308 bits (788), Expect = 5e-82

Identities = 211/569 (37%), Positives = 299/569 (52%), Gaps = 29/569 (5%)

Query: 159 GRGLENT--LPLEVVRGAMVIRVNSLTRGHSAVRLVVLEALTNFLNHRITPIVPLRGSIS 216
G G E+T LP R AM++R+N+L +G+S +R +LEA+T LNH ITP +PLRG+I+
Sbjct: 8 GNGTESTHTLPHSASRAAMLVRINTLLQGYSGIRFEILEAITKLLNHNITPCLPLRGTTIT 67

Query: 217 ASGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEA--VVLGPKEGLGL 274
ASGDL PLSYIAG +TG P+ K V G + M A EA +L G+ L PKEGL L
Sbjct: 68 ASGDLVPLSYIAGLLTGRPNKA-VGPNG--ETMAAAEAFTLAGINGGFFELQPKEGLAL 124

Query: 275 VNGTAVSASMATXXXXXXXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQVEV 334
VNGTAV + +A+ E M G+ F + + HPGQ+E
Sbjct: 125 VNGTAVGSGLASMVLFTNVLAILSEVLSAIFAEMVQKQP-EFTDHLTHKLKHHPGQIEA 183

Query: 335 ARNIRTLLSGSSFAXXXXXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSL 394
A + +L GSS+ +QDRY LRTSPQ+LGPL+E + + +
Sbjct: 184 AAVMEHILDGSSYVKAQKLHEIDPLQK-PKQDRYALRTSPQWLGPLIEVIRTSTKMIER 242

Query: 395 ENNTTTDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMN 454
E N+ DNPL+DV + HGGNFQ + + +SM+ TRLA+A IGKL F Q +EL+N N
Sbjct: 243 EINSVNDNPLIDVSRNKALHGGNFQGTPIGVSMDNTRLAIASIGKLMFAQFSELVNDYYN 302

Query: 455 RGLPSCL-AAEDPSLNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVNSLALI 513
GLPS L +PSL+Y KG +I +A+Y SEL LANPVT VQ AE NQ VNSL LI
Sbjct: 303 NGLPSNLTGGRNPSLDYGFKAIEAMASYCSELQFLANPVTNHVQSAEQHNQDVNSLGLI 362

Query: 514 SARRTAEANDVLSLLLASHLYCTLQAVDLRAMELDFKKQFDPLLPTLLQQHLGTGLDVNA 573
SAR+TAEA ++L+++ + L QA+DLR +E + K + + ++ L G +
Sbjct: 363 SARKTAEAVEILNMSTTWLVALCQAIDLRHIEENLKN TVKN TVSQVAKRVLTMGFNGE- 421

Query: 574 LALEVKKALNKRLEQT'TTYDLEPRWHDAFSYATGTVVE-----LLSSSPSANVTL 623
L + K L + + + D AT +++ L++ N +
Sbjct: 422 --LHPSRFCEKDLLKVVDREYVFTYIDDPSCATYPLMQKLRQVLVDHALMNGEKEQNSST 479

Query: 624 TAVNAWKVASAEKAISLTREVRN-RFQWTPSSQAPAHAYLSPRTRVLYSFVREELGVQAR 682
+ E I L +EV + R + A + R+ LY FVREELG
Sbjct: 480 SIFQKIGAFEEELKILLPKEVESARLELENGNPAIPNRITDRRSYPLYKFVREELGTV-- 537

Query: 683 RGDVFGVGQQETIGSNVSRIYEAIKDGRI 711
+ G + + G +++ AI G++
Sbjct: 538 ---LLTGEKVGSPGEEFDKVFTAICAGKL 563

☐ >gi|58618154|gb|AAW80643.1| phenylalanine ammonia lyase [Blechnum spicant]
Length = 745

Score = 300 bits (767), Expect = 1e-79

Identities = 233/676 (34%), Positives = 342/676 (50%), Gaps = 36/676 (5%)

Query: 53 IVQELLSIPTDDVVELSGYSLTXXXXXXXXXXXXXXXXXXQNDDEIRARVDKSVDFLKAQLQ 112
+V+E L T +VV L G LT ++ + +ARVD+S D++ L+

Sbjct: 48 MVREFLD--TKEVV-LRGSGLTVGQVAAVTDRVGIHVALDEADAKARVDESADWV---LK 101

Query: 113 NSVYGVTTGFGGS-ADTRTEDAVSLQKALIEHQLCGVTPTS SVSSFSVGRGLENTPLEV 171
 N V TTGFG S A+ + A+ Q A ++++L V + LP + V

Sbjct: 102 N-VGKFTTGF GASSANPSSSGALISQAADLQNELIRFLNAGVIGHD-----DVCLPPKFV 155

Query: 172 RGAMVIRVNSLTRGHSVRLVLEALTNFLNHRITPIVPLRGSISASGDLSPSYIAGAI 231
 + +M+IR N+L +G S +R +L+AL ++ I P +PLRGS++ASGDL PL+YIA +

Sbjct: 156 KASMLIRANTLLQGFSGIRWEILDALAKLVSAHILPKIPLRGS LTASGD LIPLAYIAALL 215

Query: 232 TGHDPVKVHVLHEGTEKIMFAREAISLFGLEAVV-LGPKEGLGLVNGTAVSASMATXXXX 290
 G P+ + + +G E + A A+ L G++A L PKEG+ LVNGT V +++A

Sbjct: 216 IGRPNC-IALTPQGEE--IRAIAALKLAGIDAPFQLLPKEGIALVNGTTVGS AVAAKVCF 272

Query: 291 XXXXXXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGSSFAXX 350
 E M G+ P H + + HPGQ+E A + LL GSS+

Sbjct: 273 DANVLVLLAEVLSALFCEVMQKPEFTDPLTHQL-KHHPGQIEAAVMEYLLEGSSYMRA 331

Query: 351 XXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTT DNPLLDVENK 410
 +QDRY LRTSPQ+LGP VE + A ++ E N+ DNPL+DV

Sbjct: 332 AAKLNATNPLSKP-KQDRYALRTSPQWLGPQVEVIRAATHSIEREINSVNDNPLIDVSRN 390

Query: 411 QTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCLA-AEDPSLN 469
 GGNFQ + + +SM+ R+A+A IGKL F Q +EL+ N GLPS L+ D SL+

Sbjct: 391 LLLKGGNFQGTPIGVSMNMRIA VAAIGKLMFAQFSELVCDY YNSGLPSNLGGPDLSLD 450

Query: 470 YHGKGLDIHIAAYASELGH LANPVTTTFVQPAEMGNQAVNSLALISARRTAEANDVLSLLL 529
 Y KG +I +AAY SEL +LANPVTT VQ AE N+ VNSL LI+AR+TAEA D+L L+

Sbjct: 451 YSFKGAEIAMAAYCSELQYLANPVTTTHVQSAEQHNEDVNSLGLIAARKTAEAVDILKLMS 510

Query: 530 ASHLYCTLQAVDLRAMELDFKKQFDPLLPTLL-----QQHLGTGLDVNALALEVKKALN 583
 ++ L QAVDLR ME + LL + + H GT ++ L E+ K +

Sbjct: 511 STFLIALCQAVDLRHMEETMQAVVKHLLTDAIKATLYTENHEGTM PNLFLEGELMKVVE 570

Query: 584 KRLEQTTTTYDLEPRWHD AFSYATGTVVELLS SSPSANVTLTAVNAWKVASAEKAISLTRE 643
 + + + + T+VE S + A ++ + RE

Sbjct: 571 YQPIFSYIDNPSNP NYALMMQLRET LVEQAMKDTSLFRRIPIFE AHLKKRLDEEVPKARE 630

Query: 644 VRNRFWQTPSSQAPAHAYLS PRTRVLYSFVREELGVQARRGDV FVG VQ QETIGSNVSR IY 703
 RF A A RT LY FVREELG RG+ + G ++ +++

Sbjct: 631 ---RF--EKGDYAMASRISKRTYPLYKFVREELGTDLLRGNA-----SRSPGEDIEKLF 680

Query: 704 EAIKDGRINHVLVKML 719
 A+ DG++ ++K +

Sbjct: 681 MAMVDGKVLLPMMKCM 696

☐ >gi|3024358|sp|Q40910|PAL4_POPKI Phenylalanine ammonia-lyase G4
 gi|1374783|dbj|BAA07861.1| phenylalanine ammonia-lyase [Populus kitakamiensis]
 Length = 571

Score = 298 bits (763), Expect = 4e-79
 Identities = 207/563 (36%), Positives = 294/563 (52%), Gaps = 28/563 (4%)

Query: 164 NTLPLEVVRGAMVIRVNSLTRGHSVRLVLEALTNFLNHRITPIVPLRGSISASGDLSP 223
 +TLP R AM++R+N+L +G+S +R +LEA+T LNH ITP +PLRG+I+ASGDL P

Sbjct: 3 HTLPHSASRAAMLVRINTLLQGYSGIRFEILEAITKLLNHNITPCLPLRG TITASGDLPV 62

Query: 224 LSYIAGAITGHDPVKVHVLHEGTEKIMFAREAISLFGLEA--VVLGPKEGLGLVNGTAVS 281

LSYIAG +TG P+ K V G + M A EA +L G+ L PKEGL LVNGTAV
 Sbjct: 63 LSYIAGLLTGRPNKA-VGPNG--ETMAAAEAFTLAGINGGFFELQPKEGLALVNGTAVG 119

Query: 282 ASMATXXXXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQVEVARNIRTL 341
 + +A+ E M G+ F + + HPGQ+E A + +
 Sbjct: 120 SGLASMLVFETNVLAILSEVLSAIFAEVMQGKP-EFTDHLTHKLKHHPGQIEAAAVMEHI 178

Query: 342 LSGSSFAXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTD 401
 L GSS+ +QDRY LRTSPQ+LGPL+E + + + E N+ D
 Sbjct: 179 LDGSSYVKAQKLHEIDPLQK-PKQDRYALRTSPQWLGPLIEVIRTSTKMIEREINSVND 237

Query: 402 NPLLDVENKQTAHGGNFQASAVSISMEKTR-LALALIGKLNFTQCTELLNAAMNRLPSC 460
 NPL+DV + HGGNF S + +SM+ T LA+A IGKL F Q +EL+N N GLPS
 Sbjct: 238 NPLIDVSRNKALHGGNFPGPSPIGVSMNDTLVLAIASIGKLMFAQFSELVNDYYNGLPSN 297

Query: 461 L-AAEDPSLNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVNSLALISARRTA 519
 L +PSL+Y KG +I +A+Y SEL LANPVT VQ AE NQ VNSL LISAR+TA
 Sbjct: 298 LTGGRNPSLDYGFKAIEAMASYCSELQFLANPVTNHVQSAEQHNQDVNSLGLISARKTA 357

Query: 520 EANDVLSLLLASHLYCTLQAVDLRAMELDFKKQFDPLLPTLLQQHLGTGLDVNALALEVK 579
 EA ++L+++ + L QA+DLR +E + K + + ++ L G + L
 Sbjct: 358 EAVEILNVMSSTWLVALCQAIDLRHIEENLKNVTNKTVSQVAKRVLTMGFNGE---LHPS 414

Query: 580 KALNKRLEQTTTYDLEPRWHDASFYATGTVE-----LLSSSPSANVTLTAVNAW 629
 + K L + + + D AT +++ L++ N + +
 Sbjct: 415 RFCEKDLLKVVDREYVFTYIDDPSCSATYPLMQKLRQVLVDHALMNGEKEQNSSTSIFQKI 474

Query: 630 KVASAEKAISLTREVRN-RFWQTPSSQAPAHAYLSRPRVLYSFVREELGVQARRGDV 688
 E I L +EV + R + A + R+ LY FVREELG +
 Sbjct: 475 GAFEEELKILLPKEVESARLEENGPAIPNRITDRRSYPLYKFVREELGTV-----LLT 529

Query: 689 GVQQETIGSNVSRIYEAIKDGRI 711
 G + + G +++ AI G++
 Sbjct: 530 GEKVGSPGEEFDKVF TAICAGKL 552

☐ >gi|18072847|emb|CAC81822.1| phenylalanine ammonia-lyase [Beta vulgaris]
 Length = 396

Score = 280 bits (717), Expect = 9e-74

Identities = 170/395 (43%), Positives = 226/395 (57%), Gaps = 15/395 (3%)

Query: 116 YGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPTSVSSFSVGRGLENLPLEVVRGAM 175
 YGVTTGFG ++ RT+ +LQK LI GV F G +TLP R AM
 Sbjct: 14 YGVTTGFGATSHRRTKQGGALQKELIRFLNAGV-----FGNGTESSHTLPHTATRAAM 66

Query: 176 VIRVNSLTRGHSAVRLVLEALTNFLNHRITPIVPLRGSISASGDLSPLSYIAGAITGHP 235
 ++R+N+L +G+S +R +LEA+T LN+ ITP +PLRG+I+ASGDL PLSYIAG +TG P
 Sbjct: 67 LVRINTLLQGYSGIRFEILEAITGLLNNNITPCLPLRGITITASGDLVPLSYIAGLLTGRP 126

Query: 236 DVKVHVLHEGTEKIMFAREAI SLFGLEA--VVLGPKEGLGLVNGTAVSASMATXXXXXXX 293
 + K V G +++ A +A + + L PKEGL LVNGTAV + MA+
 Sbjct: 127 NSKA-VGPNG--EVLNAEQAFKAAQISSGFFELQPKEGLALVNGTAVSGMASIVLFETN 183

Query: 294 XXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQVEVARNIRTL LSGSSFAXXXXX 353
 E M G+ F + + HPGQ+E A + +L GSS+
 Sbjct: 184 ILAVLAEVISAVFAEVMNGKP-EFTDHLTHKLKHHPGQIEAAAIMHILDGSSYMKAACA 242

Query: 354 XXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTDNPLLDVENKQTA 413

+QDRY LRTSPQ+LGP +E + A ++ E N+ DNPL+DV +
 Sbjct: 243 LHELDPLQKP-KQDRYALRTSPQWLGPQIEVIRFATKSIEREINSVNDNPLIDVSRNKAL 301

Query: 414 HGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCL-AAEDPSLNYHG 472
 HGGNFQ + + +SM+ RLA+A IGKL F Q +EL+N N GLPS L A+ DPSL+Y
 Sbjct: 302 HGGNFQGTPIGVSMNARLAIAAIGKLLFAQFSELVNDYNNGLPSNLTA SRDPSLDYGF 361

Query: 473 KGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAV 507
 KG +I +A+Y SEL L NPVT VQ AE NQ V
 Sbjct: 362 KGAEIAMASYCSELQFLGNPVTNHVQSAEQHNQDV 396

☐ >gi|3513758|gb|AAC33966.1| phenylalanine ammonia-lyase [Capsicum chinense]
 Length = 532

Score = 269 bits (687), Expect = 3e-70

Identities = 186/530 (35%), Positives = 276/530 (52%), Gaps = 21/530 (3%)

Query: 201 LNHRITPIVPLRGSISASGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIMFAEAISLFG 260
 +N ITP +PLRG+I+ASGDL PLSYIAG +TG P+ K + EK+ A EA + G
 Sbjct: 2 INSNITPCLPLRGTTITASGDLVPLSYIAGLLTGRPNKA--VGPNGEKLN-AEEAFRVAG 58

Query: 261 LEA--VVLGPKEGLGLVNGTAVSASMATXXXXXXXXXXXXXXXXXXXXXVEAMVGQGSFA 318
 + L PKEGL LVNGTAV + MA+ E M G+ F
 Sbjct: 59 VSGGFELQPKGLALVNGTAVGSGMASMVLFESENILAVMSEVLSVIFAEMNGKP-EFT 117

Query: 319 PFIHDVCRPHPGQVEVARNIRTLLSGSSFAXXXXXXXXXXXXXXGILRQDRYPLRTSPQFL 378
 + + HPGQ+E A + +L GSS+ +QDRY LRTSPQ+L
 Sbjct: 118 DHLTHKLKHHPGQIEAAIMEHILDGSSYVKAQKLHGNDPLQKP-KQDRYALRTSPQWL 176

Query: 379 GPLVEDMMHAYSTLSLENNTTTNDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIG 438
 GP +E + A + E N+ DNPL+DV + HGGNFQ + + +SM+ TRALA IG
 Sbjct: 177 GPQIEVIRAATKMIEREINSVNDNPLIDVSRNKALHGGNFQGTPIGVSMNTRLALASIG 236

Query: 439 KLNFTQCTELLNAAMNRGLPSCL-AAEDPSLNYHGKGLDIHIAAYASELGHLANPVTTFV 497
 KL F Q +EL+N N GLPS L A +PSL+Y KG +I +A+Y SEL LANPVT V
 Sbjct: 237 KLMFAQFSELVNDYNNGLPSNLTAGRNPSLDYGFKAIEIAMASYCSELQFLANPVTNHV 296

Query: 498 QPAEMGNQAVNSLALISARRTAEANDVLSLLLASHLYCTLQAVDLRAMELDFKKQFDPLL 557
 Q AE NQ VNSL LIS+R+TAEA D+L L+ +++L QA+DLR +E + K +
 Sbjct: 297 QSAEQHNQDVNSLGLISSRKTAEAVIDILKMSSTYLVALCQAIDLRHLEENLKNVKNVT 356

Query: 558 PTLQHLGTGLD-----VNALALEVKKALNKRLEQTTTYDLEPRWHDFAFSYATGTVVEL 612
 + ++ L G + E+ + +++ D + +V+
 Sbjct: 357 SQVAKRTLTMGANGELHPARFCEKELLRVVDREYLFAYADDPSCSSTYPLMQKLRQVLVDH 416

Query: 613 LSSSPSANVTLTAVNAWKVASAEKAIS--LTREVRN-RFWQTPSSQAPAHAYLSRTRVL 669
 ++ + + K+A+ E + L +EV + R + + + R+ L
 Sbjct: 417 ALNNGESEKNVNSSIFQKIAAFEDELKAVLPKEVESARITLESNPSIPNRITECRSYPL 476

Query: 670 YSFVREELGVQARRGDVFGVQQETIGSNVSRIYEAIKDGRINHVLVKML 719
 Y VR+ELG ++ G + + G + +++ A+ +G++ L++ L
 Sbjct: 477 YRLVRKELGT-----ELLTGERVRSPEGEEIDKVFTAMCNGQVIDPILLECL 521

☐ >gi|29424039|gb|AA073468.1| phenylalanine ammonia-lyase [Ginkgo biloba]
 Length = 380

Score = 266 bits (681), Expect = 1e-69

Identities = 164/389 (42%), Positives = 221/389 (56%), Gaps = 13/389 (3%)

Query: 116 YGVTTGFGGSADTRTEDAVSLQKALIEHQLCG--VTPTSVSFSVGRGLENLPLEVVVRG 173
 YGVTTGFG + RT LQ++LI L G + P+S S+ S G L R
 Sbjct: 1 YGVTTGFGACSSKRTNQLSLLQESLIRCLLAGAFMRPSSASTSSTGE-----LATSTTRC 55

Query: 174 AMVIRVNSLTRGHSVRLVLEALTNFLNHRITPIVPLRGSISASGDLSPLSYIAGAITG 233
 AM++R+NS RG S +R VLEAL LNH ITP PLRGS+SASGDL PL+YIAG + G
 Sbjct: 56 AMLLRINSFMRGCSGIRWEVLEALKELLNHITPKCPLRGSVSASGDLVPLAYIAGLLIG 115

Query: 234 HPDVKVHVLHEGTEKIMFAREAISLFGLEAVVLGPKEGLGLVNGTAVSASMATXXXXXXXX 293
 P VK + + A +A++ GL+ L KEGL LVNGT+ + ++A+
 Sbjct: 116 RPTVKART---ADHQELTAPQALAKVGLKPKFLQAKEGLALVNGTSFATALASTVIYDAK 172

Query: 294 XXXXXXXXXXXXXVEAMVGQQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGSSFAXXXXX 353
 E + G++ P IH + +PHPGQ+E A + LL+ S F
 Sbjct: 173 VLLFVEILTGMFCEVVFGRREEFAHPLIHRM-KPHPGQIESAALLEWLLNDSPFMELSRE 231

Query: 354 XXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTNDNPLLDVENKQTA 413
 RQDRY LR+SPQ+LGPLV+ + A +T+ +E N+ DNP++D + +
 Sbjct: 232 YYSTDKLKKP-RQDRYALRSSPQWLGPLVQIIREATATIQVEINSANDNPIIDHLHDKAL 290

Query: 414 HGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCLA-AEDPSLNYHG 472
 HG NFQ SA+ M+ R+ALA +GKL F Q TEL+ + GLP L+ D ++Y
 Sbjct: 291 HGANFQGSAGFYMDNVRIALAGLGKLMFAQFTELMIEFYSNGLPGNLSLGPDLGVDYGY 350

Query: 473 KGLDIHIAAYASELGHLANPVTTTFVQPAE 501
 KG+DI +A+Y SEL +LANPVTT VQ AE
 Sbjct: 351 KGVDIAMASYCSELQYLANPVTTTHVQSAE 379

☐ >gi|9965440|gb|AAG02280.1| inducible phenylalanine ammonia-lyase [Triticum aesti
 Length = 544

Score = 266 bits (680), Expect = 2e-69

Identities = 159/365 (43%), Positives = 216/365 (59%), Gaps = 8/365 (2%)

Query: 189 VRLVLEALTNFLNHRITPIVPLRGSISASGDLSPLSYIAGAITGHDPDKVHVLHEGTEK 248
 +R +LEA+T LN +TP +PLRG+I+ASGDL PLSYIAG ITG + V V +G++
 Sbjct: 2 IRFEILEAITKLLNANVTCLPLRGITITASGDLVPLSYIAGLITGRQN-SVAVAPDGSK- 59

Query: 249 IMFAREAISLFGLEA--VVLGPKEGLGLVNGTAVSASMATXXXXXXXXXXXXXXXXXXXX 306
 + A EA + G+E L PKEGL +VNGTAV + +A+
 Sbjct: 60 -VTAAEAFKIAGIEHGFFELQPKGLAMVNGTAVGSGLASTVLFANVLSVLAEVL SAVF 118

Query: 307 VEAMVGQQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGSSFAXXXXXXXXXXXXXXGILRQ 366
 E M G+ F + + HPGQ+E A + +L GSS+ +Q
 Sbjct: 119 CEVMNGKP-EFTDHLTHKLKHHPGQIEAAAIMHILEGSSYMKQAKKLGELDPLMKP-KQ 176

Query: 367 DRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTNDNPLLDVENKQTAHGGNFQASAVSIS 426
 DRY LRTSPQ+LGP +E + A ++ E N+ DNPL+DV + HGGNFQ + + +S
 Sbjct: 177 DRYALRTSPQWLGPQIEVIRFATKSIEREINSVNDNPLIDVSRGKAIHGGNFQGTPIGVS 236

Query: 427 MEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCLA-AEDPSLNYHGKGLDIHIAAYASE 485
 M+ TRLA+A IGKL F Q +EL+N N GLPS L+ +PSL+Y KG +I +A+Y SE
 Sbjct: 237 MDNTRLAIAAIGKLMFAQFSELVNDFYNNGLPSNLSGGRNPSLDYGFKAIEIAMASYCSE 296

Query: 486 LGHLANPVTTFVQPAEMGNQAVNSLALISARRTAEANDVLSLLLASHLYCTLQAVDLRAM 545
 L L NPVT VQ AE NQ VNSL LIS+R+T EA D+L ++ ++ L QA+DLR +
 Sbjct: 297 LQFLGNPVTNHVQSAEQHNQDVNSLGLISSRKTPEAIDILKIMSSTFLVALCQAIDLRHI 356

Query: 546 ELDFK 550
 E + K
 Sbjct: 357 EENMK 361

☐ >gi|10732813|gb|AAG22550.1| phenylalanine ammonia-lyase 2 [Rubus idaeus]
 Length = 362

Score = 259 bits (663), Expect = 2e-67
 Identities = 156/369 (42%), Positives = 212/369 (57%), Gaps = 15/369 (4%)

Query: 129 RTEDAVSLQKALIEHQLCGVTPTSVSSFSVGRGLENLPLEVVRGAMVIRVNSLTRGHSA 188
 RT+ +LQK LI GV S +TLP R AM++R+N+L +G+S
 Sbjct: 6 RTKQGAALQKELIRFLNAGVLRNGTES-----AHTLPHSATRAAMLVRINTLLQGYSG 58

Query: 189 VRLVVLEALTNFLNHRITPIVPLRGSISASGDLSPLSYIAGAITGHPDVKVHVLHEGTEK 248
 +R +LEA++ FLNH ITP +PLRG+I+ASGDL PLSYIAG +TG P+ K V +G +
 Sbjct: 59 IRFEILEAISKFLNHNITPCLPLRGITITASGDLVPLSYIAGPLTGRPNKA-VGPKG--E 115

Query: 249 IMFAEAISLFGLEA--VVLGPKEGLGLVNGTAVSASMATXXXXXXXXXXXXXXXXXXXXX 306
 + A EA + G+ + L PKEGL LVNGTAV + +A+
 Sbjct: 116 TLNAAEAFAQVGISGFFELQPKEGLALVNGTAVGSGLASTVLFETNILALLSEILSAIF 175

Query: 307 VEAMVGQQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGSSFAXXXXXXXXXXXXXXXXXXGILRQ 366
 E M G+ F + + HPGQ+E A + +L GSS+ +Q
 Sbjct: 176 AEVMQGKP-EFTDHLTHKLKHHPGQIEAAIMEHILDGSSYVKA AEKLHEQDPLQKP-KQ 233

Query: 367 DRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTNDNPLLDVENKQTAHGGNFQASAVSIS 426
 DRY LRTSPQ+LGP +E + + ++ E N+ DNPL+DV + HGGNFQ + + +S
 Sbjct: 234 DRYALRTSPQWLGPQIEVIRFSTKSIEREINSVNDNPLIDVSRNKALHGGNFQGTPIGVS 293

Query: 427 MEKTRLALALIGKLNFTQCTELLNAAMNRLPSCLA-AEDPSLNYHGKGLDIHIAAYASE 485
 M+ TRLA+A IGKL F Q +EL+N N GLPS L+ DPSL+Y KG +I +A+Y SE
 Sbjct: 294 MDNTRLAIASIGKLMFAQFSELVNDFYNNGLPSNLSGGRDPSLDYGFKA EIAMASYCSE 353

Query: 486 LGHLANPVT 494
 L LANPVT
 Sbjct: 354 LQFLANPVT 362

☐ >gi|10732811|gb|AAG22549.1| phenylalanine ammonia-lyase 1 [Rubus idaeus]
 Length = 363

Score = 249 bits (636), Expect = 2e-64
 Identities = 153/369 (41%), Positives = 211/369 (57%), Gaps = 15/369 (4%)

Query: 129 RTEDAVSLQKALIEHQLCGVTPTSVSSFSVGRGLENLPLEVVRGAMVIRVNSLTRGHSA 188
 RT++ +LQ+ LI G+ +S+ S + LP R AM++R+N+L +G+S
 Sbjct: 6 RTKNGGALQRELIRFLNAGIFGSSLD-----THKLPHATATRAAMLVRINTLLQGYSG 58

Query: 189 VRLVVLEALTNFLNHRITPIVPLRGSISASGDLSPLSYIAGAITGHPDVKVHVLHEGTEK 248
 +R +LEA+T FLN ITP +PLRG+I+ASGDL PLSYIAG + G P+ K V +G +
 Sbjct: 59 IRFEILEAITKFLNGNITPCLPLRGITITASGDLVPLSYIAGLLIGRPNSK-SVGPKG--E 115

Query: 249 IMFAREAI SLFGLEA--VVLGPKEGLGLVNGTAVSASMATXXXXXXXXXXXXXXXXXXXXX 306
+ EA L G++ L PKEGL LVNGTAV + MA+
Sbjct: 116 TLSPAEAFKLAGIDGGFFELQPKEGLALVNGTAVGSGMASMVLFDANTLAVLSEVMSAIF 175

Query: 307 VEAMVGQQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGSSFAXXXXXXXXXXXXXXXXXGILRQ 366
E M G+ F + + HPGQ+E A + +L GSS+ +Q
Sbjct: 176 AEVMQGKP-EFTDHLTHKLKHHPGQIEAAAIMHILEGSSYVKEAKKVHEMDPLQKP-KQ 233

Query: 367 DRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTNDNPLLDVENKQTAHGGNFQASAVSIS 426
DRY LRTSPQ+LGP +E + A + E N+ DNPL+DV + HGGNFQ + + ++
Sbjct: 234 DRYALRTSPQWLGPQIEVIRAATKMIEREINSVNDNPLIDVSRNKALHGGNFQGTPIGVA 293

Query: 427 MEKTRLALALIGKLNFTQCTELLNAAMNRLPSCL-AAEDPSLNYHGKGLDIHIAAYASE 485
M+ TRLA+A IGKL F Q +EL+N N GLPS L + +PSL+Y KG +I +A+Y SE
Sbjct: 294 MDNTRLAIASIGKLIFAQFSELVNDYYNGLPSNLTGSSNP SLDYGFKGAEIAMASYCSE 353

Query: 486 LGHLANPVT 494
L LANPVT
Sbjct: 354 LQFLANPVT 362

☐ >gi|46102036|gb|EAK87269.1| hypothetical protein UM06509.1 [Ustilago maydis 521]
gi|49081430|ref|XP_404124.1| hypothetical protein UM06509.1 [Ustilago maydis 521]
Length = 790

Score = 244 bits (623), Expect = 7e-63
Identities = 223/782 (28%), Positives = 339/782 (43%), Gaps = 129/782 (16%)

Query: 42 DGHAHQSQLEIVQELLSDPD--DVVELSGYSLTXXXXXXXXXXXXXXXXXQNDDEIRAR 99
+GHAA S L+ + + +D + L G SL D R
Sbjct: 17 NGHAAASSWLD TARNGWAPQSDLNSGITLDGSSDLARLMGLVVYRRTPLATDR--RED 74

Query: 100 VDKSVDFLKAQ--LQNSVYGVTTFGGGSADTRTEDAVSLQKALIEHQLCGV----- 148
+D SV L+++ +N++YGV FG A T + Q+ I+ L +
Sbjct: 75 MDASVASLESERKTENAIYGVNIPFGAGAYTTLDHQQLQQQQRIDRALITLINGDLGADM 134

Query: 149 -----TPTSVSSFSV-----GRGLEN---TLPLEVVRGAMVIRVNSLTRGHSVRL 191
TP S S+ G +N T+P+ VR AMV+R+NSL R S R
Sbjct: 135 LRLTQTPQVASQASMPPLPAPAPISAFGPDNSRLTMPVAWVRAAMVLRINSLRAASGCRW 194

Query: 192 VVLEALTNFLNHRITPIVPLRGSISASGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIMF 251
V+E L + L+ + P++P+R SISASGDLSP+Y+A A G KV +L+ T K+
Sbjct: 195 EVVERLRDLLDRELYPVIPIRNSISASGDLSP+Y+A A G KV +L+ T K+ 252

Query: 252 AREAISLFGLEAVV-LGPKEGLGLVNGTAVSASMATXXXXXXXXXXXXXXXXXXXXXVEAM 310
A A++ LE V L P+E L +NGT +++ EA+
Sbjct: 253 ADSALAAAKLEPVFQLRPREMLACINGTGACLAVSALALDRLQGLAFATHVVTAVMCEAL 312

Query: 311 VGQQGSFAPFIHDVCRPHPGQVEVARNIRTLL----- 342
+ P++HDV RPHPGQ E A +R LL
Sbjct: 313 LASPSFLDPYLDHVARPHPGQCESASILRQLLGTESAGLRNELLRHHDQDPLEFIWSLTA 372

Query: 343 -----SGSSFAXXXXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYS 390
+GSSFA LRQDRY LR +PQ++GP +E++ A+
Sbjct: 373 QPVLEQRFASKRNGSSFAAPTQVGPAAASY--LRQDRYHLRCAPQYIGPALEELRAAHD 430

Query: 391 TSLLENNTTTNDNPLLDVE-----NKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQ 444
T+ +E N+ TDNPLL N HGGNF AS+V S E+ R +G+L Q

Sbjct: 431 TVQIELNSVTDNPLLKPGTTSSSINTAMVHGGNFMASSVGHSAEQMRATTCTLGRLLEHQ 490

Query: 445 CTELLNAAMNRGLPSCLAA---EDPSLNYHGKGLDIHIAAYASELGHLANPVTTTFVQPAE 501
 T ++ + GLP+ LAA ++P++ + LDI ++Y +EL L + + AE

Sbjct: 491 LTGAIDPCKSNGLPAYLAAYGADNPAMTGGLRSLDIASSSYLAELTFLGQRLIHLNRNAE 550

Query: 502 MGNQAVNSLALISARRTAEANDVLSLLLASHLYCTLQAVDLRAMELDFKKQFDPLLPTLL 561
 GNQ+VNS+AL SAR T EA D+L+ + AS L QA+DLR + + F + + LL

Sbjct: 551 CGNQSVNSMALASARYTLEAVDLLTMCASLLAACQALDLRRLTVRFFRALSEHVLALL 610

Query: 562 Q---QHLGTGLDVNALALEVKKALNKRLEQTTTYDLEPRWHDFAFSYATGTVVELLSSSPS 618
 + Q +GT L L++ T + L W+ + V +

Sbjct: 611 EIAGQKMG-----PGLPADLQRDTLFRLFATWNAHPVQLEERVRRAVEAAL 658

Query: 619 ANVTLTAVNAWKVASAEKAI-----SLTREVRNRFWQT-----PSSQAP 657
 ++ + A+ + AS+ + + LT + + T S A

Sbjct: 659 PSLAVWALTQVQDASSPQTVQSALADLDQGLTNWMTAWANTMDMYTAQSAAGNAESAAL 718

Query: 658 AHAYLSPRTRVLYSFVREELGVQARRGDVFGVQQE-----TIGSNVSRIYEAIKDGR 710
 + S + + FVR +LG+ G + + T G +VS++ A +D R

Sbjct: 719 IDLHSAASLRILRFVRRDLGIPLDAGGGLQAMHSDKAQHAFATYGHVSQSLAAAFDRRR 778

Query: 711 IN 712
 I+

Sbjct: 779 ID 780

☐ >gi|129583|sp|P07218|PAL1_PHAVU Phenylalanine ammonia-lyase class I
 Length = 506

Score = 238 bits (607), Expect = 5e-61

Identities = 178/508 (35%), Positives = 261/508 (51%), Gaps = 27/508 (5%)

Query: 226 YIAGAITGHPDVKVHVLHEGTEKIMFAREAI SLFGL--EAVVLGPKEGLGLVNGTAVSAS 283
 YIAG +TG P+ K V G ++ A++A L + E L PKEGL LVNGTAV +

Sbjct: 1 YIAGLLTGRPNKA-VGPSGV--VLTAKQAFELANINSEFYELQPKEGLALVNGTAVGSG 57

Query: 284 MATXXXXXXXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQVEVARNIRTLLS 343
 MA+ E M G+ F + + HPGQ+E A + +L

Sbjct: 58 MASIVLFDANILAVLSEVLSAIFAEVMQGKP-EFTDHLTHKLKHHPGQIEAAAIMEHILD 116

Query: 344 GSSFAXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTDNP 403
 GSS+ +QDRY LRTSPQ+LGPL+E + + ++ E N+ DNP

Sbjct: 117 GSSYMKDAKKLHEIDPLQKP-KQDRYALRTSPQWLGPLIEVIRFSTKSIEREINSVNDNP 175

Query: 404 LLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCL-A 462
 L+DV + HGGNFQ + + +SM+ TR LALA IGKL F Q +EL+N N GLPS L A

Sbjct: 176 LIDVSRNKALHGGNFQGTPIGVSMNTRLALASIGKLMFAQFSELVNDFYNNGLPSNLTA 235

Query: 463 AEDPSLNYHGKGLDIHIAAYASELGHLANPVTTTFVQPAEMGNQAVNSLALISARRTAEAN 522
 + +PSL+Y KG +I +A+Y SEL +LANPVT+ VQ AE NQ VNSL LISAR+T E+

Sbjct: 236 SRNPSLDYGFKGAEIAMASYCSELQYLANPVTSHVQSAEQHNQDVNSLDLISARKTNEST 295

Query: 523 DVLSLLLASHLYCTLQAVDLRAMELDFKKQFDPLLPTLLQHLGTGLDVNALALEVKKAL 582
 ++L L+ ++ L QA+DLR +E + K + + ++ L TG + L +

Sbjct: 296 EILKLMSSFTMLGLCQAIDLRHLEENLKSSVKNTVSQVSKRTLTTGGNGE---LHPSRFC 352

Query: 583 NKRLEQTTTYDLEPRWHDFAFSYATGTVVELLSSSPSANVTLTAVNA-----WKVASA 634
 K L + + + D T +++ L + + A N K+A+

Sbjct: 353 EKDLLKVVDREYVFSYIDDPYSGTYPLMQKLRQVLVDHALINAENEKDVNTSIFQKIATF 412

Query: 635 EKAIS--LTREVRNRFWQTPSSQAPAHAYLSP-RTRVLYSFFVREELGVQARRGDVFGVQ 691
 E+ + L +EV + S +A + R+ LY FVREELG + G +

Sbjct: 413 EEELKTILPKEVESTRAAYESGKAAIPNKIKECRSYPLYKFVREELGT-----GLLTGEK 467

Query: 692 QETIGSNVSRIYEAIKDGRINHLVKML 719
 ++ G +++ AI G+I L++ L

Sbjct: 468 VKSPGEEFDKLFATAICQGKIIDPLLECL 495

☐ >gi|81875|pir|A24727 phenylalanine ammonia-lyase (EC 4.3.1.5) - kidney bean (f
 gi|169357|gb|AAA33770.1| phenylalanine ammonia-lyase (EC 4.3.1.5)
 gi|224727|prf|1111326A ammonia lyase,Phe
 Length = 505

Score = 236 bits (601), Expect = 2e-60
 Identities = 177/507 (34%), Positives = 261/507 (51%), Gaps = 27/507 (5%)

Query: 227 IAGAITGHPDVKVHVLHEGTEKIMFAEAISLFG--EAVVLGPKEGLGLVNGTAVSASM 284
 IAG +TG P+ K V G +++ A++A L + E L PKEGL LVNGTAV + M

Sbjct: 1 IAGLLTGRPNKA-VGPGS--EVLTAQAFELANINSEFYELQPKEGLALVNGTAVGSGM 57

Query: 285 ATXXXXXXXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQVEVARNIRTLLSG 344
 A+ E M G+ F + + HPGQ+E A + +L G

Sbjct: 58 ASIVLFDANILAVLSEVLSAIFAEMQKGP-EFTDHLTHKLKHHPGQIEAAIMEHILDG 116

Query: 345 SSFAXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTDNPL 404
 SS+ +QDRY LRTSPQ+LGPL+E + + ++ E N+ DNPL

Sbjct: 117 SSYMKDAKKLHEIDPLQKP-KQDRYALRTSPQWLGPLIEVIRFSTKSIEREINSVNDNPL 175

Query: 405 LDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELNNAAMNRGLPSC-L-AA 463
 +DV + HGGNFQ + + +SM+ TRALA IGKL F Q +EL+N N GLPS L A+

Sbjct: 176 IDVSRNKALHGGNFQGTPIGVSMDNTRLALASIGKLMFAQFSELVNDFYNNGLPSNLTAS 235

Query: 464 EDPSLNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVNSLALISARRTAEAND 523
 +PSL+Y KG +I +A+Y SEL +LANPVT+ VQ AE NQ VNSL LISAR+T E+ +

Sbjct: 236 RNPSLDYGFKAIEAMASYCSELQYLANPVTSHVQSAEQHNQDVNSLDLISARKTNESESIE 295

Query: 524 VLSLLLASHLYCTLQAVDLRAMELDFKKQFDPLLPTLLQQHLGTGLDVNALALEVKKALN 583
 +L L+ ++ L QA+DLR +E + K + + ++ L TG + L +

Sbjct: 296 ILKLMSSTFLMGLCQAIDLRHLEENLKSSVKNTVSQVSKRTLTTGGNGE---LHPSRFCE 352

Query: 584 KRLEQTTTYDLEPRWHDFAFSYATGTVEVLLSSSPSANVTLTAVNA-----WKVASAE 635
 K L + + + D T +++ L + + A N K+A+ E

Sbjct: 353 KDLLKVVDREYVFSYIDDPYSGTYPLMQKLRQVLVDHALINAENEKDVNTSIFQKIATFE 412

Query: 636 KAIS--LTREVRNRFWQTPSSQAPAHAYLSP-RTRVLYSFFVREELGVQARRGDVFGVQ 692
 + + L +EV + S +A + R+ LY FVREELG + G +

Sbjct: 413 EELKTILPKEVESTRAAYESGKAAIPNKIKECRSYPLYKFVREELGT-----GLLTGEKV 467

Query: 693 ETIGSNVSRIYEAIKDGRINHLVKML 719
 ++ G +++ AI G+I L++ L

Sbjct: 468 KSPGEEFDKLFATAICQGKIIDPLLECL 494

☐ >gi|23123897|ref|ZP_00105927.1| COG2986: Histidine ammonia-lyase [Nostoc punctif

Length = 569

Score = 229 bits (583), Expect = 3e-58

Identities = 165/495 (33%), Positives = 239/495 (48%), Gaps = 25/495 (5%)

Query: 59 SDPTDDVVELSGYSLTXXXXXXXXXXXXXXXXXQNDDEIRARVDKSVDFLKAQLQNS--VY 116
 ++ +D +V + +LT ++ ++ V S D++ ++ + +Y
 Sbjct: 19 TNSSDSIVTVGDRNLTIDEVNVARHGTQVRLTDNADVIRGVQASCDYINNAVETAQPIY 78

Query: 117 GVTTFGGGSADT--RTEDAVSLQKALIEHQLCGVTPTSVSSFSVGRGLENTLPLEVVRGA 174
 GVT+GFGG AD E A LQ LI + + G N L L VR A
 Sbjct: 79 GVTSGFGGMADVVISREQAAELQTNLI-----WFLKSGAGNKLSLADVRAA 124

Query: 175 MVIRVNSLTRGHSAVRLVLEALTNFLNHRITPIVPLRGSISASGDLSPLSYIAGAITGH 234
 M++R NS G S +RL +++ + FLN +TP V GSI ASGDL PLSYI GA+ G
 Sbjct: 125 MLLRANSHLYGASGIRLELIQRIETFLNAGVTPHVEFGSIGASGDLVPLSYITGALIGL 184

Query: 235 PDVKVHVLHEGTEKIMFAEAI SLFGLEAVVLGPKEGLGLVNGTAVSASMATXXXXXXXXX 294
 D V +G E M A A+S GL + L PKEGL ++NGT+V +A
 Sbjct: 185 -DPSFTVDFDGKE--MDAVTALSRLGLPKLQLQKEGLAMMNGTSVMTGIAANCVDYDAKV 241

Query: 295 XXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGSSFAXXXXXX 354
 ++ + G SF PFIH C+PHPGQ+ A + +LL SS
 Sbjct: 242 LLALTMGVHALAIQGLYGTNQSFHPFIHQ-CKPHPGQLWTADQMFSLKDSLVREELDG 300

Query: 355 XXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTNDNPLLDVENKQTAH 414
 ++ QDRY LR QF+GP+V+ + + +E N+ TDNPL+DVEN+ + H
 Sbjct: 301 KHEYRGKDLI-QDRYSLRCLAQFIGPIVDGVSEITKQIEVEMNSVTDNPLIDVENQVSYH 359

Query: 415 GGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGL-PSCLAAEDPSLNHYHGK 473
 GGNF V ++M++ R + L+ K Q L++ + GL PS + D +N K
 Sbjct: 360 GGNFLGQYVGVTMDRLRYIIGLLAKHIDVQIALLVSPFNSGLPPLSVGNVSDRKNMGLK 419

Query: 474 GLDIHIAAYASELGHLANPVT-TFVQPAEMGNQAVNSLALISARRTAEANDVLSLLASH 532
 GL I + L N + F AE NQ +NS ISA T + D+ +A
 Sbjct: 420 GLQISGNSIMPLLSFYGNLADRFPTHAEQFNQININSQGYISANLTRRSVDIFQNYMAIA 479

Query: 533 LYCTLQAVDLRAMEL 547
 L +QAVDLR ++
 Sbjct: 480 LMFGVQAVDLRTYKM 494

☐ >gi|2052090|emb|CAA89005.1| phenylalanine ammonia-lyase [Hordeum vulgare subsp.
 gi|7437113|pir|T05966 phenylalanine ammonia-lyase (EC 4.3.1.5) - barley (fragmen
 Length = 475

Score = 221 bits (564), Expect = 5e-56

Identities = 165/473 (34%), Positives = 237/473 (50%), Gaps = 36/473 (7%)

Query: 266 LGPKEGLGLVNGTAVSASMATXXXXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVC 325
 L PKEGL +VNGTAV + +A+ E M G+ H +
 Sbjct: 9 LQPKEGLAMVNGTAVGSGLASMLFEANILSLLAEVLSAVFCEVMNGKPEYTDHLTHKL- 67

Query: 326 RPHPGQVEVARNIRTLLSGSSFAXXXXXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDM 385
 + HPGQ+E A + +L GSS+ +QDRY LRTSPQ+LGP +E +
 Sbjct: 68 KHHPGQIEAAIMEHILEGSSYMLAKKLGEPLMKP-KQDRYALRTSPQWLGPQIEVI 126

Query: 386 MHAYSTLSLENNTTTNDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQC 445
 A ++ E N+ DNPL+DV + HGGNFQ + + +SM+ TRLA+A IGKL F Q

Sbjct: 127 RAATKSIEREINSVNDNPLIDVSRGKAIHGGNFQGTPIGVSMNTRLAIAAIGKLMFAQF 186

Query: 446 TELLNAAMNRGLPSCLA-AEDPSLNYHGKGLDIHIAAYASELGH LANPVTTFVQPAEMGN 504
 +EL+N N GLPS L+ +PSL+Y KG +I +A+Y SEL L NPVT VQ AE N

Sbjct: 187 SELVNDFYNNGLPSNLSGGRNP SLDYGFKGAEIAMASYCSELQFLGNPVTNHVQSAEQHN 246

Query: 505 QAVNSLALISARRTAEANDVLSLLLASHLYCTLQAVDLRAMELDFKKQFDPLLPTLLQQH 564
 Q VNSL LIS+R+TAEA D+L L+ ++ L QA+DLR +E + K + T+ ++

Sbjct: 247 QDVNSLGLISSRKTAEAIDILKLSSTFLVALCQAIDLRHLEENVKNAVKSCVKT VARKT 306

Query: 565 LGTGLDVNALALEVKKALNKRLEQTTTYDLEPRWHDAFSYATG-----TV 609
 L T D N + KA + T D E F+YA V

Sbjct: 307 LST--DNNG---HLHKARFCEKDLLLTIDREA----VFAYADDPSCSVNYPLMQMRAVLV 357

Query: 610 VELLSSSPSANVTLTAVNAWKVASAE---KAISLTREVRNRFWQTPSSQAPAHAYLSPRT 666
 L++ + + T+V A K+A+ E +A+ T R + A + R+

Sbjct: 358 EHALANGEAEHDVETSVFA-KLATFEQELRAVLPTVEEAARSAVENGTAAQQNRRISECRS 416

Query: 667 RVLYSFVREELGVQARRGDVFGVGVQETIGSNVSRIYEAIKDGRINHVLVKML 719
 LY FVR+ELG + G + + G V +++ A+ G+ L++ L

Sbjct: 417 YPLYRFVRKELGT-----EYLTGEKTRSPGEEVDKVFVAMNQKHHIDALLECL 464

☐ >gi|1944573|emb|CAA89006.1| phenylalanine ammonia-lyase [Hordeum vulgare subsp.
 gi|7437123|pir||T05968 probable phenylalanine ammonia-lyase (EC 4.3.1.5) - barley
 (fragment)
 Length = 497

Score = 217 bits (552), Expect = 1e-54

Identities = 166/491 (33%), Positives = 239/491 (48%), Gaps = 51/491 (10%)

Query: 252 AREAISLFGLEA--VVLGPKEGLGLVNGTAVSASMATXXXXXXXXXXXXXXXXXXXXXVEA 309
 A EA G+E L PKEGL +VNGT+V +++A E

Sbjct: 14 AAFAKAGIEGGFFKLNPKGLAIVNGTSVGSALAATVLFDCNVLAVLSEVLSAVFCEV 73

Query: 310 MVGQQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGSSFAXXXXXXXXXXXXXXGILRQDRY 369
 M G+ F + + HPG +E A + +L+GS+F +QDRY

Sbjct: 74 MNGKP-EFTDHLTHKLKHHPGSIEAAIMEHILAGSAFMGHAKKVNEIDTQLKP-KQDRY 131

Query: 370 PLRTSPQFLGPLVEDMMHAYSTLSLENNTTTDNPLLDVENKQTAHGGNFQASAVSISMEK 429
 LRTSPQ+LGP +E + A ++ E N+ DNP++DV + HGGNFQ + + +SM+

Sbjct: 132 ALRTSPQWLGPQIEVIRSATKSIEREVNSVNDNPVIDVHRGKALHGGNFQGTPIGVSMND 191

Query: 430 TRLLALALIGKLNFTQCTELLNAAMNRGLPSCLA-AEDPSLNYHGKGLDIHIAAYASELGH 488
 TRLA+A IGKL F Q +EL+N N GL S LA + +PSL+Y KG +I +A+Y SEL +

Sbjct: 192 TRLAIANIGKLMFAQFSELVNEFYNNGLTSNLAGSRNP SLDYGFKGTEIAMASYCSELQY 251

Query: 489 LANPVTTFVQPAEMGNQAVNSLALISARRTAEANDVLSLLLASHLYCTLQAVDLRAMELD 548
 LANPVT VQ AE NQ VNSL L+SAR+TAEA D+L L+ +++ QA+DLR +E +

Sbjct: 252 LANPVTNHVQSAEQHNQDVNSLGLVSARKTAEAVDILKLSSTYTMVALCQAIDLRHLEEN 311

Query: 549 FKKQFDPLLPTLLQQHL---GTGLDVNALALEVKKALNKRLEQTTTYDLEPRWHDAFSYA 605
 K + + ++ L TG D+++ K + T D E FSYA

Sbjct: 312 IKTSVKNCVTQVSKKVLTMNPTG-DLSSARFSEKSLI-----TAIDREA----VFSYA 359

Query: 606 TGT-----VVELLSSSP-SANVTLTAVNAWKVASAEKAISLTREVRNRFW 649
 V L++ P A T + E +L RE+

Sbjct: 360 DDACSANYPLMQKLRAVLVDHALTAGPGEAESEATVFSKINKFEEELRSALPREIEAARV 419

Query: 650 QTPSSQAP-AHAYLSPRTRVLYSFVREELGVQARRGD-----VFVGVQQETIGS 697
 + AP + R+ LY FVREELG G+ VF+G+ Q +
 Sbjct: 420 AFENGTAIPNLIKESRSFPLYRFVREELGCVYLTGEKLLSPGEECTKVFLGISQNKL-- 477

Query: 698 NVSRIYEAIKD 708
 + + E +K+
 Sbjct: 478 -IDPMLECLKE 487

☐ >gi|53763481|ref|ZP_00158715.2| COG2986: Histidine ammonia-lyase [Anabaena variabilis]
 Length = 567

Score = 215 bits (548), Expect = 3e-54
 Identities = 156/459 (33%), Positives = 224/459 (48%), Gaps = 27/459 (5%)

Query: 92 NDDEIRARVDKSVDFLKAQLQNS--VYGVTTGFGGSADTRT--EDAVSLQKALIEHQLCG 147
 N+ +I + S D++ +++ +YGVTTGFGG A+ E A LQ L+
 Sbjct: 52 NNTDILQGIQASCDYINNAVESGEPIYGVTSFGFGGMANVAISREQASELQTNLV----- 105

Query: 148 VTPTSVSFSVGRGLENLTPLEVVIRGAMVIRVNSLTRGHSVRLVVLEALTNFLNHRITP 207
 + + G N LPL VR AM++R NS RG S +RL +++ + FLN +TP
 Sbjct: 106 -----WFLKTGAGNKLPLADVRAAMLRLANSHMRGASGIRLELIKRMELFLNAGVTP 157

Query: 208 IVPLRGSISASGDLSPLSYIAGAITG-HPDVKVHVLHEGTEKIMFAREAISLFGLEAVVL 266
 V GSI ASGDL PLSYI G++ G P KV + K M A A+ L + L
 Sbjct: 158 YVYEFSGSIGASGDLVPLSYITGSLIGLDPSPFKV----DFNGKEMDAPTALRQLNLSPLTL 213

Query: 267 GPKEGLGLVNGTAVSASMATXXXXXXXXXXXXXXXXXXXXVEAMVGQQGSFAPFIHDVCR 326
 PKEGL ++NGT+V +A ++A+ G SF PFIH+ +
 Sbjct: 214 LPKEGLAMNGTSVMTGIAANCVYDTQILTAIAMGVHALDIQALNGTNQSFHPFIHN-SK 272

Query: 327 PHPGQVEVARNIRTLLSGSSFAXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMM 386
 PHPGQ+ A + +LL+ S ++ QDRY LR PQ+LGP+V+ +
 Sbjct: 273 PHPGQLWAADQMISLLANSQLVRLDELGKHLDYRDHELI-QDRYSLRCLPQYLGPVVDGIS 331

Query: 387 HAYSTLSLENNTTTDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCT 446
 + +E N+ TDNPL+DV+N+ + HGGNF V + M+ R + L+ K Q
 Sbjct: 332 QIAKQIEIEINSVTDNPLIDVDNQASYHGGNFLGQYVGMGMMDHLRYIYIGLLAKHLDVQIA 391

Query: 447 ELLNAAMNRGL-PSCLAEDPSLNYHGKGLDIHIAAYASELGHLANPVT-TFVQPAEMGN 504
 L + + GL PS L + +N KGL I + L N + F AE N
 Sbjct: 392 LLASPEFSNGLPPSLGNRERKVNMGKGLQICGNSIMPLLTIFYGNSIADRFPHTAEQFN 451

Query: 505 QAVNSLALISARRTAEANDVLSLLLASHLYCTLQAVDLR 543
 Q +NS SA + D+ +A L +QAVDLR
 Sbjct: 452 QNINSQGYTSATLARRSVDIFQNYVAIALMFGVQAVDLR 490

☐ >gi|46107082|ref|ZP_00188602.2| COG2986: Histidine ammonia-lyase [Rubrobacter xylophilus]
 Length = 543

Score = 209 bits (533), Expect = 2e-52
 Identities = 146/450 (32%), Positives = 219/450 (48%), Gaps = 36/450 (8%)

Query: 112 QNSVYGVTTGFGGSADTRTEDA--VSLQKALIEHQLCGVTPPTSVSFSVGRGLENLTPLE 169
 + +YGVTTGFG SA + A LQK ++ +G G+ P E

Sbjct: 62 ERPIYGVTTGFGDSAHRQISPARTAELQKNILRF-----LGNGIGPLAPPE 107

Query: 170 VVRGAMVIRVNSLTRGHSAVRLVLEALTNFLNHRITPIVPLRGSISASGDLSPLSYIAG 229
VVR M++R N + RG+S VR ++E L F+NH + P +P RGS ASGDL PLSY+

Sbjct: 108 VVRATMLLRANCMARGNSGVRRELVELLALAFVNHDVLPPIPERGSCGASGDLVPLSYLGS 167

Query: 230 AITGHPDVKVHVLHEGTEKIMFAREAISLFGLEAVVLGPKEGLGLVNGTAVSASMATXXX 289
A+TGH + VLH G + + E + GL + L KEGL + NGT+ ++ A

Sbjct: 168 ALTGHGE----VLHRGEWRPV--GEVLEELGLAPLELEAKEGLAITNGTSFMSAFAALAV 221

Query: 290 XXXXXXXXXXXXXXXXXXXXVEAMVGQQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGSSFAX 349
EA++G + F PFIH+ +PHPGQVE AR IR LL GS +

Sbjct: 222 WDAGELAFVCDLCTAMASEALLGNRAHFHPFIHE-NKPHPGQVESARVIRGLLEGSGSLST 280

Query: 350 XXXXXXXXXXXXXG-----ILR--QDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTND 402
G + R QD+Y +R +P G L + + + +E N++ DN

Sbjct: 281 EIDQVLSGDGLGGRGYRELERNIQDKYSIRCAPHVNGVLRDTLWVRRWVEVEMNSSDDN 340

Query: 403 PLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGL-PSCL 461
PL D E + GGNF + +M+ ++ALA + L Q +++ N GL P+ +

Sbjct: 341 PLFDAEGRAVHSGGNFYGGHIVQAMDSLKVALASVADLMDRQLELVVDEKFNNGLTNPNI 400

Query: 462 AAEDP-----SLNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVNSLALISAR 516
DP L++ KG+ + ++ +E L++PV+ + E NQ S+ I+AR

Sbjct: 401 PFFDPEGPQAGLHHGFKGMQLACSSSLVAEACKLSSPVSVHSRSTEAHNQDKVSMGTIAAR 460

Query: 517 RTAEANDVLSLLLASHLYCTLQAVDLRAME 546
++ + A HL QA+DLR +

Sbjct: 461 DARTIVELAQNVAAIHLIAVCQALDLRGTQ 490

☐ >gi|52009699|ref|ZP_00337061.1| COG2986: Histidine ammonia-lyase [Silicibacter s
Length = 507

Score = 208 bits (529), Expect = 5e-52

Identities = 143/432 (33%), Positives = 207/432 (47%), Gaps = 31/432 (7%)

Query: 115 VYGVTTGFGGSADTRT--EDAVSLQKALIEHQLCGVTPTSVSSFSVGRGLENTLPLEVVR 172
VYG+ TGFG A T+ ED +LQ+ LI CGV L + R

Sbjct: 51 VYGINTEGFKLASTKIAPEDTATLQRNLILSHSCGVG-----EPLAEDKTR 96

Query: 173 GAMVIRVNSLTRGHSAVRLVLEALTNFLNHRITPIVPLRGSISASGDLSPLSYIAGAIT 232
MV+++ SL RG S VR V+E + L +TP+VP +GS+ ASGDL+PL+++ A+

Sbjct: 97 LMMVLKLLSLGRGASGVRWAVIEQIQEMLARGVTPVVP SQSGVGASGDLAPLAHMTAAMI 156

Query: 233 GHPDVKVHVLHEGTEKIMFAREAISLFGLEAVVLGPKEGLGLVNGTAVSASMATXXXXXX 292
G + + + + EA+ GLE +VLGPKEGLGL+NGT S + A

Sbjct: 157 GEGEATIDGVR-----LPGAELRRAGLEPIVLGPKEGLGLINGTQFSTACALTGLFEA 210

Query: 293 XXXXXXXXXXXXXXXXXXXXVEAMVGQQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGSSFAXXXX 352
+A++G IH + R H GQ+EVA +R +++GS

Sbjct: 211 LEMARASMAIASLTDAIMGSTAPLVADIHSL-RGHAGQMEVAATMRDIMAGSEIRESHR 269

Query: 353 XXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTNDNPLLDVENKQT 412
QD Y +R PQ +G ++ + A TL +E N TDNPL+ VE Q

Sbjct: 270 EGDTRV-----QDPYCIRCQPQVVGAAALDVLMAARTLEIEANAVTDNPLVLVEAGQI 322

Query: 413 AHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCLAEDPSLNYHG 472
GGNF A V + ++ LA+A IG + + +++ ++ LP L +P LN

Sbjct: 323 VSGGNFHAIEYVGFAADQIALAVAEIGAIQRRVALMVDPTLSHDLPPFL-TPNPGLNSGF 381

Query: 473 KGLDIHIAAYASELGHLANPVTTTFVQPAEMGNQAVNSLALISARRTAEANDVLSLLASH 532
 ++ AA SE HLANP T P + S+A A R A+ N LS++L

Sbjct: 382 MIAEVTTAALMSENKHLANPCVTDSTPTSANQEDHVSMAAHGALRLAKMNANLSVILGVE 441

Query: 533 LYCTLQAVDLRA 544
 + C Q V+ RA

Sbjct: 442 MLCAAQGVEARA 453

☐ >gi|8249014|emb|CAB93138.1| phenylalanine ammonia-lyase [Betula pendula]
 Length = 435

Score = 205 bits (521), Expect = 5e-51

Identities = 136/378 (35%), Positives = 193/378 (51%), Gaps = 20/378 (5%)

Query: 66 VELSGYSLTXXXXXXXXXXXXXXXXXQNDDEIRARVDKSVDFLKAQLQNSV--YGVTTGFG 123
 +++ G SLT N+ R RV KS +++ + YGVTTGFG

Sbjct: 64 IDIEGTSLTVAQVTAIARRSEVKVNLNEAAARDRAKSAWVADNISRGTDITYGVTTGFG 123

Query: 124 GSADTRTEDAVSLQKALIEHQLCGVTPPTSVSSFSVGRGLENLPLEVVRGAMVIRVNSLT 183
 ++ RT V LQ LI GV +G+ +LP + AM++R N+L

Sbjct: 124 ATSHRRTNKTVDLQTELIRFLNAGV-----IGK---ESLPSTYSKVAMLRANTLM 171

Query: 184 RGHSAVRLVLEALTNFLNHRITPIVPLRGSISASGDLSPSYIAGAITGHPDVKVHVLH 243
 +G+S +R +LEA+ +N + P +PLRG+I+ASGDL PLSYIAG +TG + KV V

Sbjct: 172 QGYSGIRWEILEAMAKLMNKNLIPKLPLRGITITASGDLVPLSYIAGLLTGRHNSKV-VTP 230

Query: 244 EGTEKIMFAREAISLFGLEAVV-LGPKEGLGLVNGTAVSASMATXXXXXXXXXXXXXXXXX 302
 E E + + EA+ G+ A L KEGL LVNGTAV +++A

Sbjct: 231 EDEE--ITSIEALKRAGIPAPFELQAKEGLALVNGTAVGSAVAATVCFDANILSLFAEIL 288

Query: 303 XXXXVEAMVGQGSFAPFIHDVCRPHPGQVEVARNIRTLTLLSGSSFAXXXXXXXXXXXXXXG 362
 E M+G P H++ + HPGQ+E A + LL S +

Sbjct: 289 SALFCEVMLGNSEFTDPLTHEL-KHHPGQIEAAAIMFLLDESDYMKEAKLRYEKDPLTK 347

Query: 363 ILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTDNPLLDVENKQTAHGGNFQASA 422
 +QDRY LRTSPQ+LGP +E + A ++ E N+ DNPL+DV HGGNFQ +

Sbjct: 348 P-KQDRYALRTSPQWLGPQIEVIRMATHSIEREINSVNDNPLIDVARDIALHGGNFQGT 406

Query: 423 VSISMEKTRLALALIGKL 440
 + +SM+ R+A+A IGKL

Sbjct: 407 IGVSMNDNLRIAVAAIGKL 424

☐ >gi|8249041|emb|CAB93139.1| phenylalanine ammonia-lyase [Betula pendula]
 Length = 436

Score = 204 bits (519), Expect = 8e-51

Identities = 137/378 (36%), Positives = 191/378 (50%), Gaps = 20/378 (5%)

Query: 66 VELSGYSLTXXXXXXXXXXXXXXXXXQNDDEIRARVDKSVDFLKAQLQNSV--YGVTTGFG 123
 V++ G SLT ++ R RV KS +++ + YGVTTGFG

Sbjct: 72 VDIQGTSLTVAQVTAIARRSEVKVNLDEAAARERVAKSANWVAENISRGTDITYGVTTGFG 131

Query: 124 GSADTRTEDAVSLQKALIEHQLCGVTPPTSVSSFSVGRGLENLPLEVVRGAMVIRVNSLT 183

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      ++ RT      LQ LI      GV      +G+      +LP      + AM++R N+L
Sbjct: 132 ATSHRRNTNKTADLQTELRFLNAGV-----IGK---ESLPSTYSKVAMLVRTNTLM 179

Query: 184 RGHSAVRLVVLEALTNFLNHRITPIVPLRGSISASGDLSPLSYIAGAITGHPDVKVHVLH 243
      +G S +R +LEA+ N +N + P +PLRG+I+ASGDL PLSYIAG +TG + KV V
Sbjct: 180 QGFSGIRWEILEAMANLMNKNLIPKPLPLRGITITASGDLVPLSYIAGLLTGRHNSKV-VTP 238

Query: 244 EGTEKIMFAREAISLFGLEAVV-LGPKEGLGLVNGTAVSASMATXXXXXXXXXXXXXXXXX 302
      E E + A EA+ G+ A L KEGL LVNGTAV +++A
Sbjct: 239 EDEE--ITALEALKRAGIPAPFELQAKEGLALVNGTAVGSAVAATVCFDANILALFAEIL 296

Query: 303 XXXXVEAMVGQQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGSSFAXXXXXXXXXXXXXXG 362
      E M+G P H + + HPGQ+E A + LL S +
Sbjct: 297 SALFCEVMLGNAEFTDPLTHGL-KHHPGQIEAAAIMFEFLDESDYMKEAKLRYEKDPLTK 355

Query: 363 ILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTNDNPLLDVENKQTAHGGNFQASA 422
      +QDRY LRTSPQ+LGP +E + A ++ E N+ DNPL+DV HGGNFQ +
Sbjct: 356 P-KQDRYALRTSPQWLGPQIEVIRMATHSIEREINSVNDNPLIDVARDIALHGGNFQGTG 414

Query: 423 VSISMEKTRLALALIGKL 440
      + +SM+ R+A+A IGKL
Sbjct: 415 IGVSMDNLRIAIAAIGKL 432

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☐ >gi|19073338|gb|AAL84767.1| phenylalanine ammonia lyase 1 [Cucumis sativus]
Length = 395

Score = 202 bits (514), Expect = 3e-50

Identities = 135/364 (37%), Positives = 199/364 (54%), Gaps = 21/364 (5%)

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Query: 365 RQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTNDNPLLDVENKQTAHGGNFQASAVS 424
      +QDRY LRT+PQ+LGPL+E + + ++ E N+ DNPL+DV + HGGNFQ + +
Sbjct: 32 KQDRYALRTAPQWLGPLIEVIRFSTKSIEREINSVNDNPLIDVSRNKALHGGNFQGTPIG 91

Query: 425 ISMEKTRLALALIGKLNFTQCTELLNAAMNRLPSCL-AAEDPSLNYHGKGLDIHIAAYA 483
      +SM+ TRLA+A IGKL F Q +EL+N N GLPS L A+ +PSL+Y KG +I +A+Y
Sbjct: 92 VSMDNTRLAIASIGKLMFAQFSELVNDFYNNGLPSNLSASRNPSLDYGFKAIEIAMASYC 151

Query: 484 SELGHLANPVTTTFVQPAEMGNQAVNSLALISARRTAEANDVLSLLLASHLYCTLQAVDLR 543
      SEL +LANPVTT VQ AE NQ VNSL LIS+R+TAEA D+L L+ ++ L QA+DLR
Sbjct: 152 SELQYLANPVTTTHVQSAEQHNQDVNSLGLISSRKTAEAIDILKLMSSSTFLVALCQAILR 211

Query: 544 AMELDFKKQFDPLLPTLLQQHLGTGLDVNALALEVKKALNKRLEQTTTYDLEPRWHDAFS 603
      +E + K + + Q+ L T + AL+ + K L + + + D
Sbjct: 212 HLEENLKSARKSTIILVAQKVLITSTNG---ALDPSRLFENLLKVVDREYTFAYIDDP 268

Query: 604 YATGTVVE-----LLSSSPSANVTLTAVNAWKVASAEKAIISLTREVRNRFWQTPS 653
      .AT +++ L +S N + AE L+ +V + S
Sbjct: 269 SATYPLMQGLRQVFVEHTLANSDDENNADTPIFQKIAIFEAEKAILS NKVESTRLAYES 328

Query: 654 SQAPAHAYLSP-RTRVLYS FVREELGVQARRGDVFGVQQETIGSNVSRIYEAIKDGR-I 711
      A + R+ LY FVREELG++ G+ + + G +++ A+ G+ I
Sbjct: 329 GNALIKNQIEECRSYPLYRFVREELGIKLLTGEKVI-----SPGEECEKVFAALCKGKMI 383

Query: 712 NHVL 715
      N +L
Sbjct: 384 NSIL 387

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☐ >gi|48784800|ref|ZP_00281105.1| COG2986: Histidine ammonia-lyase [Burkholderia
Length = 531

Score = 200 bits (509), Expect = 1e-49

Identities = 147/485 (30%), Positives = 222/485 (45%), Gaps = 40/485 (8%)

Query: 66 VELSGYSLTXXXXXXXXXXXXXXXXQNDDEIRARVDKSVDFLKAQLQN--SVYGVTTGFG 123
V + G LT D RAR+ + DFL+ L +VYGV TG+G
Sbjct: 21 VVIGGRKLTIEEVVAIARHRAPVALSADPAWRARIQRGADFLRRHLAAGATVYGVNTGYG 80

Query: 124 GSA--DTRTEDAVSLQKALIEHQLCGVTPPTSVSFSVGRGLENTLPLEVVVRGAMVIRVNS 181
+ D E +L L + CG+ G+ L+ L V+ R+NS
Sbjct: 81 DACVVDVPMELVEALPLQLTRYHGCGM-----GQYLDEAQLAVIAA----RLNS 126

Query: 182 LTRGHSVRLVLEALTNFLNHRITPIVPLRGSISASGDLSPLSYIAGAITGHPDVKVHV 241
L G S VR V+LE L + +NHR+ P +P GS+ ASGDL+PLSY+A A+ G D V
Sbjct: 127 LAYGFSGVRPVLLERLADLVNHRVLPRIPEGSVGASGDLTPLSYVAAALAGERD----V 182

Query: 242 LHEGTEKIMFAREAISLFGLEAVVLGPKEGLGLVNGTAVSASMATXXXXXXXXXXXXXXXXX 301
+ EG ++ RE + G + L PKEGL L+NGTAV +A
Sbjct: 183 MFEG--QLRNVREVWTELGGTPLTLAPKEGLALMNGTAVMTGLACLAFAHADHLTRLTAR 240

Query: 302 XXXXXVEAMVGQQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGSSFAXXXXXXXXXXXXXXXXX 361
A+ G+ F + +V +PH GQ E A IR L+G
Sbjct: 241 LTALCTVALDGRAAHFDAMLFEV-KPHAGQAEAAAWIRDDLAGRD-----DTP 287

Query: 362 GILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTNDPLLDVENKQTAHGGNFQAS 421
G QDRY +R +P +G + + + E N+ DNPL+D +N++ HGGNF
Sbjct: 288 GHRLQDRYSIRCAPHVIGVARDALSWVRDIENELNSANDNPLIDPDNERVLHGGNFYGG 347

Query: 422 AVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCLA---AEDPSLNYHGKGLDIH 478
++ +M+ ++A+A + L Q L++ N GLP L+ + ++N+ K + I
Sbjct: 348 HIAFAMDSLKVAVANLADLMDRQLALLVDVNFNGLPRNLGATSARAAINHGFKAVQIS 407

Query: 479 IAAYASELGHLANPVTTFVQPAEMGNQAVNSLALISARRTAEANDVLSLLASHLYCTLQ 538
+A+ +E P + F + E NQ S+ I+AR ++ + A+H T+Q
Sbjct: 408 SSAWTAEALKNTMPASVFSRSTEAHNQDKVSMGTIAARDCLRVLELTEQVAAAHTLATVQ 467

Query: 539 AVDLR 543
A LR
Sbjct: 468 AARLR 472

☐ >gi|56459245|ref|YP_154526.1| ☒ Histidine ammonia-lyase [Idiomarina loihiensis I
gi|56178255|gb|AAV80977.1| ☒ Histidine ammonia-lyase [Idiomarina loihiensis L2TR]
Length = 515

Score = 200 bits (508), Expect = 1e-49

Identities = 145/487 (29%), Positives = 223/487 (45%), Gaps = 35/487 (7%)

Query: 62 TDDVVELSGYSLTXXXXXXXXXXXXXXXXQNDDEIRARVDKSVDFLKAQLQNS--VYGV 119
T ++ G LT + E +VD V FL L+ +YGV
Sbjct: 2 TTIIAFGGRPLTIKDVVEIANGKAQIALSDAPEFVEKVDAGVRFLDELLEQDGVYGV 61

Query: 120 TGFGGSADTRTEDAVSLQKALIEHQLCGVTPPTSVSFSVGRGLENTLPLEVVVRGAMVIRV 179
TG+G S VS+ + L+ P ++ F G GL +T + R + R+
Sbjct: 62 TGYGDSC-----TVSPENLVNE-----LPIHLTRFH-GCGLGDTFDEQETRAILATRL 109

Query: 180 NSLTRGHSASVRLVVLEALTNFLNHRITPIVPLRGSISASGDLSPLSYIAGAITGHPDVKV 239
 +SL +G+S V +LE L LN + P++P GS+ ASGDL+PLSYIAGA+ G DV+
 Sbjct: 110 SSLAQGYSGVSWELLERLVVMLNENMLPLIPKEGSGVASGDLTPLSYIAGALIGERDVRF 169

Query: 240 HVLHEGTEKIMFAREAIISLFGLEAVVLGPKEGLGLVNGTAVSASMATXXXXXXXXXXXXX 299
 K+M + EA L G+ L PKEGL ++NGTAV ++A
 Sbjct: 170 R-----NKVMNSAEAFELLGMSVHKLRPKEGLAIMNGTAVMTALACLAWDRAEYLTRLS 223

Query: 300 XXXXXXXVEAMVGQQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGSSFAXXXXXXXXXXXXXX 359
 A+ G F + V +PH GQ +VA I+ L+
 Sbjct: 224 SRITSLASIALEGNSNHFDLLFAV-KPHKGQQQVASWIQQDLNHVEHPRNSSRL----- 277

Query: 360 XXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTNDNPLLDVENKQTAHGGNFQ 419
 QDRY +R +P +G L + + T+ E N+ DNP++D + HGG+F
 Sbjct: 278 -----QDRYSIRCAPHVIGVLKDSLPWFKETIENELNSANDNPIIDGLGEHVLHGGHFY 331

Query: 420 ASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCLA---EDPSLNYHGKGLD 476
 +++ M+ + A+A + L+ Q L++ MN GLPS L+A E S+N+ K +
 Sbjct: 332 GGHIAMVMSMKTAVANLADLHQRQALLMDTKMNHGLPSNLSAAEGERKSINHGFKAVQ 391

Query: 477 IHIAAYASELGHLANPVTTFVQPAEMGNQAVNSLALISARRTAEANDVLSLLASHLYCT 536
 I +A+ +E L P + F + E NQ S+ I+AR ++ ++ + L
 Sbjct: 392 IGCSAWTAEALKLTMPASVFSRSTECHNQDKVSMGTIAARDCIRILELTEQVVVATLLAA 451

Query: 537 LQAVDLR 543
 Q V+LR
 Sbjct: 452 YQGVELR 458

☐ >gi|60299943|gb|AAx18625.1| phenylalanine ammonia-lyase [Nerium oleander]
 Length = 289

Score = 199 bits (507), Expect = 2e-49

Identities = 125/293 (42%), Positives = 163/293 (55%), Gaps = 8/293 (2%)

Query: 218 SGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIMFAREAIISLFGLEA--VVLGPKEGLGLV 275
 SGDL PLSYIAG +TG P+ K + G ++ A EA L G+ L PKEGL LV
 Sbjct: 2 SGDLVPLSYIAGLLTGRPNKCVGPNGG---LLDAGEAFRLAGINGGFELQPKEGLALV 58

Query: 276 NGTAVSASMATXXXXXXXXXXXXXXXXXXXXVEAMVGQQGSFAPFIHDVCRPHPGQVEVA 335
 NGTAV + +A+ E M G+ F + + HPGQ+E A
 Sbjct: 59 NGTAVGSGLASMVLFDANVLAVLCEVLSAIFAEVMQGKP-EFTDHLTHKLKHHPGQIEAA 117

Query: 336 RNIRTLLSGSSFAXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLE 395
 + +L GS F +QDRY LRTSPQ+LGP +E + + ++ E
 Sbjct: 118 AIMEHILDGS-FCVKAARKLHEMDPLQPKQDRYALRTSPQWLGPQIEVIRTSTKSIERE 176

Query: 396 NNTTTNDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNR 455
 N+ DNPL+DV + HGGNFQ + + +SM+ TRLA+A IGKL F Q +EL+N N
 Sbjct: 177 INSVDNPLIDVSRNKALHGGNFQGTPIGVSMNTRLAIASIGKLMFAQFSELVNDFFYN 236

Query: 456 GLPSCLA-AEDPSLNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAV 507
 GLPS L+ ++PSL+Y KG +I +AAY SEL LANPVT VQ AE NQ V
 Sbjct: 237 GLPSNLGGQNPSLDYGFKAELIAAAYCSELQFLANPVTNHVQSAEQHNQDV 289

☐ >gi|81807|pir|JQ1070 phenylalanine ammonia-lyase (EC 4.3.1.5) - soybean (fragr
Length = 416

Score = 199 bits (506), Expect = 3e-49

Identities = 143/405 (35%), Positives = 216/405 (53%), Gaps = 23/405 (5%)

Query: 328 HPGQVEVARNIRTLLSGSSFAXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMH 387
HPGQ+E A + +L GSS+ +QDRY LRTSPQ+LG L+E +
Sbjct: 11 HPGQIEAAAMEHILEGSSYVKAACKLHEIDPLQKP-KQDRYALRTSPQWLGHLEIVIRF 69

Query: 388 AYSTLSLENNTTTDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTE 447
+ ++ E N+ DNPL+DV + HGGNFQ + + +SM+ TRLALA IGKL F Q +E
Sbjct: 70 STKSIEREINSVNDNPLIDVSRNKALHGGNFQGTPIGVSMNTRLALASIGKLMFAQFSE 129

Query: 448 LLNAAMNRGLPSCL-AAEDPSLNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQA 506
L+N N GLPS L A+ +P L+Y KG +I +A+Y SEL +LANPVT+ VQ AE NQ
Sbjct: 130 LVNDYYNGLPSNLTASRNPRLDYGFKAELAMASYCSELQYLANPVTSHVQSAEQHNQD 189

Query: 507 VNLSALISARRTAEANDVLSLLLASHLYCTLQAVDLRAMELDFKKQFDPLLPTLLQQHLG 566
VNLS LIS+R+T EA ++L L+ ++ L QA+DLR +E + K ++ + ++ L
Sbjct: 190 VNLSGLISSRKTHEAIEILKLMSSTFLVGLWQAIDLRHLEDNLKNTVKNVVSQVAKRTL 249

Query: 567 TGLDVNALALEVKKALNKRLEQT'TYDLEPRWHDAFSYATGTVVE-----LLSSSP 617
TG++ L + K L + + + D T +++ L++
Sbjct: 250 TGVNGE---LHPSRFCEKDLLKVVVDREYTFAYIDDPSCGTYPLMQKLQVLVDYALANGE 306

Query: 618 SANVTLTAVNAWKVASAEKAIS--LTREVRNRFWQTPSSQ-APAHAYLSPRTRVLYSFVR 674
+ T T++ K+AS E+ + L +EV + Q A + R+ LY FVR
Sbjct: 307 NEKNTNTSI-FQKIASFEEELKTLLPKEVEGARVAYENDQCAIPNKIKECRSYPLYKFVR 365

Query: 675 EELGVQARRGDVFGVGQQETIGSNVSRIYEAIKDGRINHVLVKML 719
EELG G+ + + G +++ A+ G I L++ L
Sbjct: 366 EELGTALLTGERVI-----SPGEECDKVFTALCQGNIIDPLLECL 405

☐ >gi|17548586|ref|NP_521926.1| ☒ PROBABLE HISTIDINE AMMONIA-LYASE PROTEIN [Ralstonia
GMI1000]

gi|17430834|emb|CAD17516.1| ☒ PROBABLE HISTIDINE AMMONIA-LYASE PROTEIN [Ralstonia
Length = 528

Score = 198 bits (503), Expect = 6e-49

Identities = 142/457 (31%), Positives = 216/457 (47%), Gaps = 36/457 (7%)

Query: 93 DDEIRARVDKSVDFLKAQLQN--SVYGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTP 150
D+ R R+++ FL+ QL +VYGV TG+G + + +S+ AL+ Q +
Sbjct: 46 DEAWRDRIERGARFLQEQLAQGATVYGVNTGYGDACE-----ISVPPALV--QALPLQL 97

Query: 151 TSVSSFSVGRGLENLTPLEVVRGAMVIRVNSLTRGHSVRLVLEALTNFLNHRITPIVP 210
T +GR L + L V+ R+NSL G+S VR +L+ L + +NH I P +P
Sbjct: 98 TRYHCGMGRYLAPSETLAVIAA----RLNSLAHGYSGVRYTLLQRLADLINHDILPRIP 153

Query: 211 LRGSISASGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEAVVLGPKE 270
GS+ ASGDL+PLSY+A A+ G D VL +G K+ A + G L PKE
Sbjct: 154 AEGSVGASGDLTPLSYVAAALVGERD----VLFDG--KVRAASDVWRALGHSPFELAPKE 207

Query: 271 GLGLVNGTAVSASMATXXXXXXXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHPG 330
GL L+NGTAV +A A+ G+ G F I +PH G
Sbjct: 208 GLALMNGTAVMTGLACLAYARAEHLIRLATRLTALATVALDGRSGHFDATIFQ-AKPHAG 266

Query: 331 QVEVARNIRTLLSGSSFAXXXXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYS 390
 Q +VA +R L+G G QDRY +R +P +G + M
 Sbjct: 267 QADVAAWLREDLAG-----WDDTGGHRLQDRYSIRCAPHVIGVAQDAMSWIRR 314

Query: 391 TLSLENNTTTDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLN 450
 + E N+ DNPL+D + ++ HGGNF ++ +M+ + A+A + L Q L++
 Sbjct: 315 DIENELNSANDNPLIDPDARRILHGGNFYGGHIAFAMDALKTAIANLADLMDRQLALLVD 374

Query: 451 AAMNRGLPSCLAEDPS---LNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAV 507
 + GLP L+ P +N+ K + I ++A+ +E P + F + E NQ
 Sbjct: 375 DRYSNGLPRGLSGASPDRAPIINHGFKAQISVSAWTAEALKHTMPASVFSRSTESHNQDK 434

Query: 508 NSLALISARRTAEANDVLSLLLASHLYCTLQAVDLRA 544
 S+ I+AR ++ + A+H T QAV LRA
 Sbjct: 435 VSMGTIAARDCLRVLLELTEQVAAHATLATAQAVRLRA 471

☐ >gi|1345583|emb|CAA53581.1| phenylalanine ammonium lyase [Vitis vinifera]
 gi|1172004|sp|P45735|PALY_VITVI Phenylalanine ammonia-lyase
 Length = 416

Score = 197 bits (501), Expect = 1e-48

Identities = 139/405 (34%), Positives = 212/405 (52%), Gaps = 21/405 (5%)

Query: 328 HPGQVEVARNIRTLLSGSSFAXXXXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMH 387
 HPGQ+E A + +L GSS+ +QDRY LRTSPQ+LGP +E +
 Sbjct: 11 HPGQIEAAAIMEHILDGSSYVKEAKKLHEMDPLQKP-KQDRYALRTSPQWLGPHEVIRA 69

Query: 388 AYSTLSLENNTTTDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTE 447
 + ++ E N+ DNPL+DV + HGGNFQ + + +SM+ TRLA+A IGKL F Q +E
 Sbjct: 70 STKSIEREINSVNDNPLIDVSRNKALHGGNFQGTPIGVSMNDNRLAIAAIGKLMFAQFSE 129

Query: 448 LLNAAMNRGLPSCLA-AEDPSLNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQA 506
 L+N N GLPS L+ + +PSL+Y KG +I +A+Y SEL LANPVT V+ AE NQ
 Sbjct: 130 LVNDFYNNGLPSNLGSRNP SLDYGFKGAEIAMASYCSELQFLANPVTNHVESAEQHNQD 189

Query: 507 VNSLALISARRTAEANDVLSLLLASHLYCTLQAVDLRAMELDFKKQFDPLLPTLLQQHLG 566
 VNSL LIS+R+TAEA D+L L+ ++L QA+DLR +E + K + + ++ L
 Sbjct: 190 VNSLGLISSRKTAEAVIDILKLMSTTYLVALCQAIDLRHLEENLKSTVKKTVSHVAKKTLT 249

Query: 567 TGLDVNALALEVKKALNKRL-----EQTTTYDLEP--RWHDAFSYATGTVVELLSSSPS 618
 G + L + K L E Y +P + +VE ++
 Sbjct: 250 IGANGE---LHPSRFCEKDLLKVVDREHVFAYIDDPSCSATYPLMQKVRQVLVEHALNNGE 306

Query: 619 ANVTLTAVNAWKVASAEKAIS--LTREVRN-RFWQTPSSQAPAHAYLSPRTRVLYSFVRE 675
 + + K+ + E+ + L +EV + R + + + R+ LY FVRE
 Sbjct: 307 SEKNGSTSIFQKIGAFEEELKAVLPKEVESARDGVESGNPSIPNRIKECRSYPLYKFBVRE 366

Query: 676 ELGVQARRGDVFGVQQETIGSNVSRIYEAIKDGRINHLVKMLA 720
 ELG + G + + G + +++ A+ +G+I L+ L+
 Sbjct: 367 ELGT-----GLLTGEKVRSPGEDFDKVFMTAMCEGKIIDPLLDCLS 406

☐ >gi|28872212|ref|NP_794831.1| ☒ histidine ammonia-lyase [Pseudomonas syringae pv
 DC3000]
 gi|28855466|gb|AA058526.1| ☒ histidine ammonia-lyase [Pseudomonas syringae pv. to

DC3000J
Length = 515

Score = 197 bits (500), Expect = 1e-48
Identities = 154/513 (30%), Positives = 233/513 (45%), Gaps = 41/513 (7%)

Query: 91 QNDDEIRARVDKSVDFLKAQLQNS--VYGVTTGFGGSADTRTEDAVSLQKALIEHQLCGV 148
Q DDE RAR+ + FL + L +YGVTTG+G S +EH
Sbjct: 34 QGDDEFARARIARGAQFLDSLKSKEGVYGVTTGYGDSVCVAVP-----LEH--VEA 82

Query: 149 TPTSVSFSVGRGLENTLPLEVVRGAMVIRVNSLTRGHSVAVRLVVLEALTNFLNHRITPI 208
P + +F G GL L + R + R+ SL +G S VR+ +LE L F++ + P+
Sbjct: 83 LPRYLTFH-GCGLGKLLDAQATRAVLAARLQSLCQGVSGVRVELLERLQAFIDQDVLPL 141

Query: 209 VPLRGSISASGDLSPSYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEAVVLGP 268
+P GS+ ASGDL+PLSY+A ++G + V+ G ++ A + G +VL P
Sbjct: 142 IPEEGSVGASGDLTPSYVAATLSGERE---VMFRGERRL--ASDVHRELGWTPVLVLRP 195

Query: 269 KEGLGLVNGTAVSASMATXXXXXXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPH 328
KE L L+NGTAV +A V A+ G F + +PH
Sbjct: 196 KEALALMNGTAVMTGIACLAFAARADYLLQLATRITAMNVVALQGNPEHFDERLF-AAKPH 254

Query: 329 PGQVEVARNIRTLLSGSSFAXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHA 388
PGQ++VA +R L+ + QDRY LR +P LG L + +
Sbjct: 255 PGQMVAAWLRQDLAIDAPTAPLHRL-----QDRYSLRCAPHVLGVLADSLNWL 303

Query: 389 YSTLSLENNTTTNDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTEL 448
S + +E N+ DNP++D E ++ HGG+F ++ +M+ + +A + L Q L
Sbjct: 304 RSFIEIELNSANDNPIIDAEAERVLHGGHFYGGHIAFAMDLSKTLVANVADLLDRQLALL 363

Query: 449 LNAAMNRGLPSCL---AAEDPSLNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQ 505
++ N GLPS L +AE LN+ K + I +A+ +E P + F + E NQ
Sbjct: 364 VDERYNHGLPSNLGASAEARMLNHGFKAVQIGTSAWTAELKNTMPASVFSRSTECHNQ 423

Query: 506 AVNSLALISARRTAEANDVLSLLLASHLYCTLQAVDLRAMELDFKKQFDPLLPTLLQQHL 565
S+ I+AR ++ + A+ L Q V LR+ D + PL P L H
Sbjct: 424 DKVSMGTIAARDAIRVLELTEQVAAATLIAANQGVWLRSGADAR----PLPPALASMAHA 479

Query: 566 GTGLDVNALALEVKKALNKRLEQTTTYDLEPRW 598
G D A +E +AL L + RW
Sbjct: 480 ELGEDF-APVIE-DRALESELRLCLKHIANRRW 510

☐ >gi|60299945|gb|AAx18626.1| phenylalanine ammonia-lyase [Pittosporum tobira]
Length = 289

Score = 196 bits (499), Expect = 2e-48
Identities = 122/294 (41%), Positives = 162/294 (55%), Gaps = 8/294 (2%)

Query: 217 ASGDLSPSYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEA--VVLGPKEGLGL 274
ASGDL PLSYIAG +TG P+ K T + + +A S G++ L PKEGL L
Sbjct: 1 ASGDLVPLSYIAGLLTGRPNKCV---GPTGESLDPGKAFSFAIDGGFFELQPKGLAL 57

Query: 275 VNGTAVSASMATXXXXXXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQVEV 334
VNGTAV + + + E M G+ F + + HPGQ+E
Sbjct: 58 VNGTAVGSLTSSVLFETNVLALLSEVLSAIFAEMVQKGP-EFTDHLTHKLKHHHPGQIEA 116

Query: 335 ARNIRTLLSGSSFAXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSL 394
A + +L GSS+ +QDRY LRTSPQ+LGP +E + + ++

Sbjct: 117 AAIMEHILDGSSYVKAACKLHEMDPLQKP-KQDRYALRTSPQWLGPQIEVIRASTKSIER 175

Query: 395 ENNTTTDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMN 454
E N+ DNPL+DV + HGGNFQ + + +SM+ TRLA+A IGKL F Q +EL+N N

Sbjct: 176 EINSVNDNPLIDVSRNKALHGGNFQGTPIGVSMDNTRLAIASIGKLMFAQFSELVNDNFYN 235

Query: 455 RGLPSCLA-AEDPSLNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAV 507
GLPS L+ +PSL+Y KG +I +A+Y SEL LANPVT VQ AE NQ V

Sbjct: 236 NGLPSNLSGGRNPSLDYGFKAIEAMASYCSELQFLANPVTNHVQSAEQHNQDV 289

☐ >gi|24575109|gb|AAL06680.1| putative ammonia lyase/transferase [Streptomyces glc
Length = 539

Score = 196 bits (498), Expect = 2e-48
Identities = 143/475 (30%), Positives = 214/475 (45%), Gaps = 43/475 (9%)

Query: 98 ARVDKSVDFLK--AQLQNSVYGVTTFGFGGSADTRTEDA--VSLQKALIEHQLCGVTPPTSV 153
A+ KS + + A+ +YGVTTG+G + + + V LQ L+ GV P

Sbjct: 43 AKAQKSREIFEGIAEQNIPIYGVTTGYGEMIYMQVDKSKEVELQTNLVRSHSAGVGPLFA 102

Query: 154 SSFSVGRGLENLPLEVVRGAMVIRVNSLTRGHSAVRLVVLEALTNFLNHRITPIVPLRG 213
+ R + R+N+L +GHSVR ++LE L +LN ITP +P G

Sbjct: 103 E-----DEARAIVAARLNTLAKGHSVRPIILERLAQYLNNEGITPAIPEIG 148

Query: 214 SISASGDLSPSYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEAVVLGPKEGLG 273
S+ ASGDL+PLS++A + G + +VL +G + + + ++ G+E + L KEGL

Sbjct: 149 SLGASGDLAPLSHVASTLIG----EGYVLRDG--RPVETAQVLAERGIEPLELRFKEGLA 202

Query: 274 LVNGTAVSASMATXXXXXXXXXXXXXXXXXXXXXVEAMVGQQGSFAPFIHDVCRPHPGQVE 333
L+NGT+ + + +EA+ G F HD+ RPH GQ++

Sbjct: 203 LINGTSGMTGLGSLVVGRALEQAQQAEIVTALLIEAVRGSTSPFLAEGHDIARPHEGQID 262

Query: 334 VARNIRTLLSGSSFAXXXX-----XXXXXXXXXXGILRQDRYPLRTSPQFLGPLVE 383
A N+R L+ GS I Q Y LR PQ +G + +

Sbjct: 263 TAANMRALMRGSLTVEHADLRRELQKDKEAGKDVQRSEIYLQKAYSLRAIPQVVGAVRD 322

Query: 384 DMMHAYSTLSLENNTTTDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFT 443
+ HA L +E N+ DNPL E K+ HG NF ++ +M+ +AL +G L

Sbjct: 323 TLYHARHKLRIELNSANDNPLF-FEGKEIFHGANFHGQPIAFAMDFVTIALTQLGVLAER 381

Query: 444 QCTELLNAAMNRGLPSCLAEDPSLNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMG 503
Q +LN ++ GLP L + DP L+ G A +E P +T P+

Sbjct: 382 QINRVLNRHLSYGLPEFLVSGDPGLHSGFAGAQPATALVAE-NRTIGPASTQSVPSNGD 440

Query: 504 NQAVNSLALISARRTAEANDVLSLLLASHLYCTLQAVDLRAMELDFKKQFDPLLP 558
NQ V S+ LISAR + +LA QAVD+ +FD L P

Sbjct: 441 NQDVVSMGLISARNARRVLSNNNKILAVEYLAAAQAVDISG-----RFDGLSP 488

☐ >gi|27361857|gb|AA010763.1| ☒ Histidine ammonia-lyase [Vibrio vulnificus CMCP6]
gi|27365708|ref|NP_761236.1| ☒ Histidine ammonia-lyase [Vibrio vulnificus CMCP6]
gi|33301173|sp|Q8DA21|HUTH_VIBVU Histidine ammonia-lyase (Histidase)
Length = 513

Score = 195 bits (495), Expect = 5e-48
Identities = 139/433 (32%), Positives = 217/433 (50%), Gaps = 32/433 (7%)

Query: 114 SVYGVTTGFGGSADTRT--EDAVSLQKALIEHQLCGVTPTSVSSFSVGRGLENLTPLEV 171
 +VYG+ TGFG A+TR ED +LQ++++ S G+ + E V
 Sbjct: 54 TVYGINTGFGLLANTRIAPEDLETLQRSIV-----LSHAAGIGEFMADETV 99

Query: 172 RGAMVIRVNSLTRGHSAVRLVVLEALTNFLNHRITPIVPLRGSISASGDLSPLSYIAGAI 231
 R MV+++NSL+RG+S +RL V++ L + +N ++ P VP +GS+ ASGDL+PL++++ +
 Sbjct: 100 RLMMVLKINSLSRGYSGIRLNVIQMLIDLVAQVYPCVPQKGSVGASGDLAPLAHMSTVL 159

Query: 232 TGHPDVKVHVLHEGTEKIMFAREAISLFGLEAVVLGPKEGLGLVNGTAVSASMATXXXXX 291
 G + H G KI+ EA+ + GLE + L PKEGL L+NGT S + A
 Sbjct: 160 LGEGQAR----HNG--KIISGLEALKIAGLEPITLAPKEGLALLNGTQASTAFLEGLFI 213

Query: 292 XXXXXXXXXXXXXXXXVEAMVGQQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGSSFAXXX 351
 VEA +G + F P IH V R H Q++ A R LL SS
 Sbjct: 214 AEDLFASATVCGAMSVEAALGSRRPFDPRIHRV-RGHRSQMDSAMAYRHLLDTSSEIGQS 272

Query: 352 XXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTNDNPLLDVENKQ 411
 QD Y LR PQ +G ++ + ++ L +E+N+ +DNPL+ E+
 Sbjct: 273 HSNCEKV-----QDPYSLRCQPQVMGACLQQIRNSAEILLVESNSVSDNPLVFAEDDD 325

Query: 412 TAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCLAEDPSLNYH 471
 GGNF A V+++ + LA+A IG L+ + L+++A+++ LP L ++ +N
 Sbjct: 326 IISGGNFHAEPVAMAADNLALAEIGSLSERRMALLIDSALSK-LPPFL-VDNGGVNSG 383

Query: 472 GKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVNSLALISARRTAEANDVLSLLLAS 531
 + AA ASE LA+P + P + S+A +ARR E + +LA
 Sbjct: 384 FMIAQVTSAAASENKTLAHPASVDSLPTSANQEDHVSMTFAARRLREMGENTRGILAV 443

Query: 532 HLYCTLQAVDLRA 544
 Q +D RA
 Sbjct: 444 EYLSAAQGLDFRA 456

☐ >gi|37680136|ref|NP_934745.1| ☒ histidine ammonia-lyase [Vibrio vulnificus YJ016]
 gi|61213549|sp|Q7MK58|HUTH_VIBVY Histidine ammonia-lyase (Histidase)
 gi|37198882|dbj|BAC94716.1| ☒ histidine ammonia-lyase [Vibrio vulnificus YJ016]
 Length = 513

Score = 195 bits (495), Expect = 5e-48

Identities = 139/433 (32%), Positives = 217/433 (50%), Gaps = 32/433 (7%)

Query: 114 SVYGVTTGFGGSADTRT--EDAVSLQKALIEHQLCGVTPTSVSSFSVGRGLENLTPLEV 171
 +VYG+ TGFG A+TR ED +LQ++++ S G+ + E V
 Sbjct: 54 TVYGINTGFGLLANTRIAPEDLETLQRSIV-----LSHAAGIGEFMADETV 99

Query: 172 RGAMVIRVNSLTRGHSAVRLVVLEALTNFLNHRITPIVPLRGSISASGDLSPLSYIAGAI 231
 R MV+++NSL+RG+S +RL V++ L + +N ++ P VP +GS+ ASGDL+PL++++ +
 Sbjct: 100 RLMMVLKINSLSRGYSGIRLNVIQMLIDLVAQVYPCVPQKGSVGASGDLAPLAHMSTVL 159

Query: 232 TGHPDVKVHVLHEGTEKIMFAREAISLFGLEAVVLGPKEGLGLVNGTAVSASMATXXXXX 291
 G + H G KI+ EA+ + GLE + L PKEGL L+NGT S + A
 Sbjct: 160 LGEGQAR----HNG--KIISGLEALKIAGLEPITLAPKEGLALLNGTQASTAFLEGLFI 213

Query: 292 XXXXXXXXXXXXXXXXVEAMVGQQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGSSFAXXX 351
 VEA +G + F P IH V R H Q++ A R LL SS
 Sbjct: 214 AEDLFASATVCGAMSVEAALGSRRPFDPRIHRV-RGHRSQMDSAMAYRHLLDTSSEIGQS 272

Query: 352 XXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTDNPLLDVENKQ 411
 QD Y LR PQ +G ++ + ++ L +E+N+ +DNPL+ E+
 Sbjct: 273 HSNCEKV-----QDPYSLRCQPQVMGACLQQIRNSAEILLVESNSVSDNPLVFAEDDD 325

Query: 412 TAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRLPSCLAEDPSLNYH 471
 GGNF A V+++ + LA+A IG L+ + L+++A+++ LP L ++ +N
 Sbjct: 326 IISGGNFHAEPVAMAADNLALATAEIGSLSERRMALLIDSALSK-LPPFL-VDNGGVNSG 383

Query: 472 GKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVNSLALISARRTAEANDVLSLLLAS 531
 + AA ASE LA+P + P + S+A +ARR E + +LA
 Sbjct: 384 FMIAQVTSAAALASENKTLAHPASVDSLPTSANQEDHVSMTAARRLREMGENTRGILAV 443

Query: 532 HLYCTLQAVDLRA 544
 Q +D RA
 Sbjct: 444 EYLSAAQGLDFRA 456

☐ >gi|49364851|gb|AAT65681.1| phenylalanine ammonia-lyase [Ginkgo biloba]
 Length = 287

Score = 194 bits (493), Expect = 8e-48
 Identities = 123/289 (42%), Positives = 162/289 (56%), Gaps = 7/289 (2%)

Query: 221 LSPLSYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEAVV-LGPKEGLGLVNGTA 279
 L PLSYIAG +TG P+ KV +G E M EA+ GLE L PKEGL +VNGT+
 Sbjct: 4 LGPLSYIAGLLTGRPNKSVRT-RDGAE--MSGLEALKQVGLEKPFELQPKEGLAIVNGTS 60

Query: 280 VSASMATXXXXXXXXXXXXXXXXXXXXXVEAMVGQQGSFAPFIHDVCRPHPGQVEVARNIR 339
 V A++A+ E M G+ P H + + HPGQ+E A +
 Sbjct: 61 VGAALASIVCFDANVLAVLSEVMSAMFCEVMNGKPEFTDPLTHRL-KHHPGQMEAAAIME 119

Query: 340 TLLSGSSFAXXXXXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTT 399
 +L GSS+ +QDRY LRTSPQ+LGP VE + A + E N+
 Sbjct: 120 YVLDGSSYMKQAAMLQELNPLQKP-KQDRYALRTSPQWLGPQVEVIRAATHMIEREINSV 178

Query: 400 TDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRLGPS 459
 DNP++DV + HGGNFQ + + +SM+ RL++A IGKL F Q +EL+N N GLPS
 Sbjct: 179 NDNPVIDVSRDKALHGGNFQGTPIGVSMNLRSLIAAIGKLMFAQFSELVNDYYNGGLPS 238

Query: 460 CLA-AEDPSLNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAV 507
 L+ +PSL+Y KG +I +A+Y SEL +LANPVT VQ AE NQ V
 Sbjct: 239 NLSGGPNPSLDYGLKGAEIAMASYTSELEYLANPVTNHVQSAEQHNQDV 287

☐ >gi|51246205|ref|YP_066089.1| ☒ histidine ammonia-lyase [Desulfotalea psychrophila]
☒ gi|50877242|emb|CAG37082.1| ☒ probable histidine ammonia-lyase [Desulfotalea psychrophila]
 Length = 512

Score = 194 bits (492), Expect = 1e-47
 Identities = 141/456 (30%), Positives = 214/456 (46%), Gaps = 35/456 (7%)

Query: 93 DDEIRARVDKSVDFLKAQLQNS--VYGVTTGFGGSADT--RTEDAVSLQKALIEHQLCGV 148
 +++ + +++ SV + ++ +YG+ TGFG A+T E+ LQ++LI GV
 Sbjct: 30 EEKCKGKINASVQTVGEVIRQGRVIYGINTEGFGLLANTIIPNEEHLQRLSLILSHAAGV 89

Query: 149 TPTSVSFSVGRGLENTLPLEVVRGAMVIRVNSLTRGHSVRLVLEALTNFLNHRITPI 208
 S VR MV+++NSL RG+S +RL V+EAL LN + P

Sbjct: 90 GAFMADS-----TVRLMMVLKINSLARGYSGIRLEVIEALVQLLNAEVYPS 135

Query: 209 VPLRGSISASGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEAVVLGP 268
VP +GS+ ASGDL+PL++++ + G + + G + RE + L GL + LGP

Sbjct: 136 VPQKGSVGASGDLAPLAHMSIVLLGEGEAS----YRGQR--LSGREGLELAGLSPITLGP 189

Query: 269 KEGLGLVNGTAVSASMATXXXXXXXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPH 328
KEGL L+NGT S + A ++A +G + F P IH V R H

Sbjct: 190 KEGLALLNGTQASTAFALQGLFAAEELFATAMVSGSLSLDAALGSRRPFNPLIHAV-RGH 248

Query: 329 PGQVEVARNIRTLLSGSSFAXXXXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHA 388
Q++VA + R LL S QD Y LR PQ +G + + +A

Sbjct: 249 KSQIDVAASRQLLEHSEIERSHKFCEAV-----QDPYSLRCQPQVMGACLNQIRNA 300

Query: 389 YSTLSLENNTTTDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTEL 448
+ E N +DNPL+ + GGNF A +++ + LA+A IG L + L

Sbjct: 301 AEVIGTEANAVSDNPLVFCCKENDIISGGNFHAEPIAMVADNLALAIIEIGALPERRTALL 360

Query: 449 LNAAMNRGLPSCLAEDPSLNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVN 508
+++ M+ GLP L + LN + AA ASE LA+P + P +

Sbjct: 361 IDSHMS-GLPPFL-VDKGGLSNGFMIAQVTAAALASENKS LAHPASVDSLPTSANQEDHV 418

Query: 509 SLALISARRTAEANDVLSLLLASHLYCTLQAVDLRA 544
S+A +ARR E D + +LA L Q +D RA

Sbjct: 419 SMATFAARRLLEMADNTAGILAIELLAACQGIDFRA 454

☐ >gi|37522635|ref|NP_926012.1| **G** histidine ammonia-lyase [Gloeobacter violaceus I
gi|35213636|dbj|BAC91007.1| **G** histidine ammonia-lyase [Gloeobacter violaceus PCC
Length = 514

Score = 193 bits (491), Expect = 1e-47

Identities = 139/448 (31%), Positives = 214/448 (47%), Gaps = 34/448 (7%)

Query: 100 VDKSVDFLKAQLQNS--VYGVTTGFGGSADTRTEDAV--SLQKALIEHQLCGVTPTSVSS 155
V +S F++A L+ VYG+TTGFG + R + LQ+ L+

Sbjct: 40 VRRSRAFVEALLEGDEIVYGITTFGFGYFKNRRI PRSAVEQLQQNLL----- 85

Query: 156 FSVGRGLENLTPLEVVRGAMVIRVNSLTRGHSVRLVLEALTNFLNHRITPIVPLRGS 215
S GL EVVR ++R N+L +G+S VR L+ L LN + P+VP RGS+

Sbjct: 86 MSSAAGLGEPFGREVVRLMLLRANTLAQGYSGVRPETLQLLVAMLRGVHPVPCRGSV 145

Query: 216 SASGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEAVVLGPKEGLGLV 275
ASGDL+PL+++A +TG + +V G E ++ A++ GLE + LG KEGL L+

Sbjct: 146 GASGDLAPLAHLALVLTGEGEAEV-----GGE-VLPGAAALARAGLEPIRLGAKEGLALI 199

Query: 276 NGTAVSASMATXXXXXXXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQVEVA 335
NGT +++ +EA +G + +F P H + RPHPGQ A

Sbjct: 200 NGTQAMSALGALTVHRAQRLAKLADLACAMTLEATLGSRS AFLPHFHLR-RPHPGQQSSA 258

Query: 336 RNIRTLLSGSSFAXXXXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLE 395
RN+ L S+ QD Y LR +PQ G ++ + +A +++E

Sbjct: 259 RNLLVLTEDSALIASHAGCDRV-----QDAYSLRCAPQVHGASLDAISYAAGVIAIE 310

Query: 396 NNTTTDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNR 455
N+ TDNPL+ + Q GG+F V+++ + +ALA + ++ + L+NA +

Sbjct: 311 INSVTDNPLIFADTGQVVTGGHFHGGPQVAMASDVLAIALAELADISERRTERLVNADYSN 370

Query: 456 GLPSCLAEDPSLNYHGKGLDIHIAAYASELGHLANPVTTFFVQPAEMGNQAVNSLALISA 515
 GLP L E L+ A+ SE LA+P P G + S+ L +A
 Sbjct: 371 GLPMFL-TEAGGLHSGYMVAQYTAASLVSENKVLAPACVDSIPTASAGQEDHVSMLTAA 429

Query: 516 RRTAEANDVLSLLLASHLYCTLQAVDLR 543
 R+ D ++A L C QA+DLR
 Sbjct: 430 RKAFTVCDNCERVIAIELMCAAQALDLR 457

☐ >gi|9655681|gb|AAF94361.1| **G** histidine ammonia-lyase [Vibrio cholerae 01 biovar N16961]
 gi|15641215|ref|NP_230847.1| **G** histidine ammonia-lyase [Vibrio cholerae 01 biovar N16961]
 gi|11269677|pir|E82228 histidine ammonia-lyase (EC 4.3.1.3) [similarity] - Vibri (strain N16961 serogroup 01)
 gi|14194869|sp|Q9KSQ4|HUTH_VIBCH Histidine ammonia-lyase (Histidase)
 Length = 511

Score = 193 bits (490), Expect = 2e-47
 Identities = 137/433 (31%), Positives = 214/433 (49%), Gaps = 32/433 (7%)

Query: 114 SVYGVTTGFGGSADTRT--EDAVSLQKALIEHQLCGVTPTSVSSFSVGRGLENLPLEVV 171
 +VYG+ TGFG A+T+ +D +LQK+++ S G+ + E V
 Sbjct: 52 TVYGINTGFGLLANTKIAPQDLETLQKSIV-----LSHAAGIGELMSDETV 97

Query: 172 RGAMVIRVNSLTRGHSVRLVLEALTNFLNHRITPIVPLRGSISASGDLSPLSYIAGAI 231
 R M+++NSL RG+S +RL V++AL +N++I P VP +GS+ ASGDL+PL++++ +
 Sbjct: 98 RLMLLLKINSLARGYSIRLEVIQALIELVNNQIYPCVPKKGSGASGDLAPLAHMSTVL 157

Query: 232 TGHPDVKVHVLHEGTEKIMFAREAISLFGLEAVVLGPKEGLGLVNGTAVSASMATXXXXX 291
 G + + KI+ EA+ + GLE + L PKEGL L+NGT S + A
 Sbjct: 158 LGEGQARYN-----GKIISGLEAMKIAGLEPITLAPKEGLALLNGTQASTAFALEGLFV 211

Query: 292 XXXXXXXXXXXXXXXXVEAMVGQQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGSSFAXXX 351
 VEA +G + F P IH V R H Q++ A R LL SS
 Sbjct: 212 AEDLFASATVCGAMSVEAALGSRPFDPRIHRV-RGHRTQMDAATAYRHLLDVSSEIGQS 270

Query: 352 XXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTNDNPLLDVENKQ 411
 QD Y LR PQ +G ++ + A L +E N+ +DNPL+ E+
 Sbjct: 271 HSNCEKV-----QDPYSLRCQPQVMGACLQQIRSAAEVLEVEANSVSDNPLVFAEDGD 323

Query: 412 TAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCLAEDPSLNYH 471
 GGNF A V+++ + LA+A IG L+ + L+++A+++ LP L ++ +N
 Sbjct: 324 IISGGNFHAEPVAMAADNLALAEIGSLSERMALLIDSALSK-LPPFL-VDNGGVNSG 381

Query: 472 GKGLDIHIAAYASELGHLANPVTTFFVQPAEMGNQAVNSLALISARRTAEANDVLSLLLAS 531
 + AA ASE LA+P + P + S+A +ARR + + +LA
 Sbjct: 382 FMIAQVTAAALASENKTALHPASVDSLPTSANQEDHVSMAATFAARRLRDMGENTRGILAV 441

Query: 532 HLYCTLQAVDLRA 544
 Q +D RA
 Sbjct: 442 EYLAAAQGLDFRA 454

☐ >gi|60326352|gb|AAx18752.1| phenylalanine ammonia-lyase [Styphnolobium japonicum]
 Length = 289

Score = 192 bits (489), Expect = 2e-47

Identities = 122/294 (41%), Positives = 160/294 (54%), Gaps = 8/294 (2%)

Query: 217 ASGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEA--VVLGPKEGLGL 274
 ASGDL PLSY+AG + G P+ K + G +++ A+EA L ++ L PKEGL L
 Sbjct: 1 ASGDLVPLSYVAGILIGRPNSK-SIGPNG--QVLNAKEAFELAEIDGGFFELQPKEGLAL 57

Query: 275 VNGTAVSASMATXXXXXXXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQVEV 334
 VNGTAV + +A+ E M G+ F + + HPGQ+E
 Sbjct: 58 VNGTAVGSGLASIVLFEANTLAVLSEILSAIFAEVMQGKP-EFTDHLTHKLKHHPGQIEA 116

Query: 335 ARNIRTLLSGSSFAXXXXXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSL 394
 A + GSS+ +QDRY LRTSPQ+LGP +E + A T+
 Sbjct: 117 AARTEYIYDGSSYVKAQKLHEIDPLQKP-KQDRYALRTSPQWLGPQIEVLRQATKTIER 175

Query: 395 ENNTTTDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMN 454
 E + DNPL+DV + HGGNFQ + + +SM+ TRLA A IGKL F Q +EL N N
 Sbjct: 176 EIYSGNDNPLVDVSRNKALHGGNFQGTPIGVSMDNTRLARASIGKLMFAQFSELENDNFYN 235

Query: 455 RGLPS-CLAAEDPSLNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAV 507
 GLPS A+ +PSL+Y KG +I +A+Y SEL LANPVT VQ AE NQ V
 Sbjct: 236 NGLPSNRTASRNPSLDYGFKAIEAMASYCSELQFLANPVTNHVQSAEQHNQDV 289

☐ >gi|60299941|gb|AA18624.1| phenylalanine ammonia-lyase [Juglans regia]
 Length = 289

Score = 191 bits (484), Expect = 9e-47

Identities = 122/294 (41%), Positives = 160/294 (54%), Gaps = 8/294 (2%)

Query: 217 ASGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEA--VVLGPKEGLGL 274
 ASGDL PLSYIAG + G P+ K V G + A +A + G+ L PKEGL L
 Sbjct: 1 ASGDLVPLSYIAGLLIGRPNSKA-VGPNGES--LDATKAFQVAGINGGFFELQPKEGLAL 57

Query: 275 VNGTAVSASMATXXXXXXXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQVEV 334
 VNGTAV + +A+ E M G+ F + + HPGQ+E
 Sbjct: 58 VNGTAVGSGLASIVLFEANIQAAILSEILSAIFAEVMQGKP-EFTDHLTHKLEHHPGQIEA 116

Query: 335 ARNIRTLLSGSSFAXXXXXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSL 394
 A + +L GS++ +QDRY LRTSPQ+LGP +E + A +
 Sbjct: 117 AAIMEHILDGSAYVKAQKLHDIDPLQKP-KQDRYALRTSPQWLGPQIEVIRTATKMIER 175

Query: 395 ENNTTTDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMN 454
 E N+ DNPL+DV + HGGNFQ + + +SM+ TRLA+A IGKL F Q +EL++ N
 Sbjct: 176 EINSVNDNPLIDVSRNKALHGGNFQGTPIGVSMDNTRLAIAAIGKLMFAQFSELVSDNFYN 235

Query: 455 RGLPSCL-AAEDPSLNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAV 507
 LPS L A+ +PSL+Y KG +I +A+Y SEL LANPVT VQ AE NQ V
 Sbjct: 236 NRLPSNLTASRNPSLDYGFKAIEAMASYCSELQFLANPVTNHVQSAEQHNQDV 289

☐ >gi|28898047|ref|NP_797652.1| ☒ histidine ammonia-lyase [Vibrio parahaemolyticus
 gi|28806261|dbj|BAC59536.1| ☒ histidine ammonia-lyase [Vibrio parahaemolyticus RI
 gi|33301165|sp|Q87Q77|HUTH_VIBPA Histidine ammonia-lyase (Histidase)
 Length = 511

Score = 190 bits (483), Expect = 1e-46

Identities = 137/433 (31%), Positives = 214/433 (49%), Gaps = 32/433 (7%)

Query: 114 SVYGVTTGFGGSADTRT--EDAVSLQKALIEHQLCGVTPTSVSSFSVGRGLENLPLEVV 171
 +VYG+ TGFG A+TR ED +LQ++++ G+ G+ + + E V
 Sbjct: 52 TVYGINTGFGLLANTRIAPEDLETQRSIVLSHAAGI-----GKFMSD----ETV 97

Query: 172 RGAMVIRVNSLTRGHSVRLVLEALTNFLNHRITPIVPLRGSISASGDLSPSYIAGAI 231
 R MV+++NSL RG S +RL V+ L + +N ++ P VP +GS+ ASGDL+PL++++ +
 Sbjct: 98 RLMMVLKINSLARGFSGIRLKVINMLIDLVAQVPCVPQKGSVGASGDLAPLAHMSTVL 157

Query: 232 TGHPDVKVHVLHEGTEKIMFAREAISLFGLEAVVLGPKEGLGLVNGTAVSASMATXXXXX 291
 G + H G +I+ EA+ + GLE + L PKEGL L+NGT S + A
 Sbjct: 158 LGEGQAR-----HNG--QIVSGYEALKIAGLEPITLAPKEGLALLNGTQASTAFALEGLFI 211

Query: 292 XXXXXXXXXXXXXXXXVEAMVGQQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGSSFAXXX 351
 VEA +G + F P IH V R H ++ A R LL SS
 Sbjct: 212 AEDLFASATVCGAMSVEAALGSRRPFDPRHRV-RGHRSTMDAAMAYRHLLDTSSEIGES 270

Query: 352 XXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTNDNPLLDVENKQ 411
 QD Y LR PQ +G ++ + ++ L +E N+ +DNPL+ E+
 Sbjct: 271 HTNCEKV-----QDPYSLRCQPQVMGACLQQIRNSAEVLQVEANSVSDNPLVFAEDND 323

Query: 412 TAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCLAEDPSLNYH 471
 GGNF A V+++ + LA+A IG L+ + L+++A+++ LP L ++ +N
 Sbjct: 324 IISGGNFHAEPVAMAADNLALAIIEIGSLSERMALLIDSALSK-LPPFL-VDNGGVNSG 381

Query: 472 GKGLDIHIAAYASELGHLANPVTTTFVQPAEMGNQAVNSLALISARRTAEANDVLSLLLAS 531
 + AA ASE LA+P + P + S+A +ARR E + +LA
 Sbjct: 382 FMIAQVTSAAASENKTLAHPASVDSLPTSANQEDHVSMAATFAARRLKEMGENTRGILAV 441

Query: 532 HLYCTLQAVDLRA 544
 Q +D RA
 Sbjct: 442 EYLSAAQGLDFRA 454

☐ >gi|46323992|ref|ZP_00224354.1| COG2986: Histidine ammonia-lyase [Burkholderia c
 Length = 540

Score = 189 bits (481), Expect = 2e-46

Identities = 147/468 (31%), Positives = 215/468 (45%), Gaps = 41/468 (8%)

Query: 97 RARVDKSVDFLKAQLQN--SVYGVTTGFGGSA--DTRTEDAVSLQKALIEHQLCGVTPTS 152
 RAR+++ +L+ L N +VYGVTTG+G + D +L L + CG+
 Sbjct: 57 RARIERGAAWLRDHLANGGTVYGVTTGYGDACVVDVPPSLVEALPLQLTRYHGCGM---- 112

Query: 153 VSSFSVGRGLENLPLEVVRGAMVIRVNSLTRGHSVRLVLEALTNFLNHRITPIVPLR 212
 G + T L +V V R+NSL G+S VR +LE L + +NHRI P +P
 Sbjct: 113 -----GDWFDATQTLISIV----VARLNSLAFGYSGVRFLLERLADMVNHRILPRIPSE 162

Query: 213 GSISASGDLSPSYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEAVVLGPKEGL 272
 GS+ ASGDL+PLSY+A A+ G V G E AR+A + L PKEGL
 Sbjct: 163 GSVGASGDLTPLSYVAAALVGERSVG----FAGGE--CDARDAWRAIDRTLTLAPKEGL 216

Query: 273 GLVNGTAVSASMATXXXXXXXXXXXXXXXXXXXXXVEAMVGQQGSFAPFIHDVCRPHPGQV 332
 L+NGTAV +A A+ G+ G F + D +PH GQ
 Sbjct: 217 ALMNGTAVMTGLACLAFAARADHLTRVAARLTALTITIALDGRAGHFDARLFD-AKPHAGQA 275

Query: 333 EVARNIRTLLSGSSFAXXXXXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTL 392
 E A IR L+G G QDRY +R +P +G + + +

Sbjct: 276 EAAAWIRADLAGRD-----ELPGCRLQDRYSVRCAPHVIGVARDALSWMRDI 323

Query: 393 SLENNTTTDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAA 452
 E N+ DNPL+D + HGGNF ++ +M+ + A+A + L Q L++

Sbjct: 324 EENELNSANDNPLIDPDEGCVLHGGNFYGGHIAFAMDALKTAVANLADLMDRQLALLVDDK 383

Query: 453 MNRGLP---SCLAAEDPSLNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVNS 509
 + GLP S A E ++N+ K + I +A+ +E P + F + E NQ S

Sbjct: 384 FSNGLPRLNSGAAPERAAINHGFKAQVISSAWTAEALKHTMPASVFSRSTESHNQDKVS 443

Query: 510 LALISARRTAEANDVLSLLLASHLYCTLQAVDLRAMELDFKKQFDPLL 557
 + I+AR + + A+H+ T+QAV LR + D Q P L

Sbjct: 444 MGTIAARDCLRVLALTEQVAAAHVLATVQAVRLRLRD-DPHAQLTPAL 490

☐ >gi|54301792|ref|YP_131785.1| ☒ putative histidine ammonia-lyase protein [Photobact SS9]

gi|46915212|emb|CAG21985.1| ☒ putative histidine ammonia-lyase protein [Photobact Length = 518]

Score = 189 bits (479), Expect = 3e-46

Identities = 141/476 (29%), Positives = 226/476 (47%), Gaps = 38/476 (7%)

Query: 92 NDDEIRARVDKSVDFLKAQLQNS--VYGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVT 149
 N E A++D+SV FL+ L+ +YGVTTG+G S V++ L++

Sbjct: 38 NTPEYTAKIDRSVAFLERLKKEGVIVGVTTGYGDSC-----TVAIPPNLVDE-----L 86

Query: 150 PTSVSSFSVGRGLENLTPLEVVRGAMVIRVNSLTRGHSVRLVLEALTNFLNHRITPIV 209
 P ++ F G GL L + R + R+ SL++G S V +L L +NH I+P +

Sbjct: 87 PLHLTRFH-GCGLGENLDHQQARAVLATRLCSLSQGFSGVSHDLLNQLVTLINHDISPRI 145

Query: 210 PLRGSISASGDLSPSYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEAVVLGPK 269
 P GS+ ASGDL+PLSY+A + G +V +++G +I + + G+ + L PK

Sbjct: 146 PQEGSVGASGDLTPLSYVAAVLIGEREV----IYKG--EIRPTADVFAELGITPIKLPK 199

Query: 270 EGLGLVNGTAVSASMATXXXXXXXXXXXXXXXXXXXXVEAMVGQQGSFAPFIHDVCRPHP 329
 EGL L+NGT+V ++A M G F + V +PHP

Sbjct: 200 EGLALMNGTSVMTALACIAYKRAEYLAQLATRITAMVSLGMHGNDHFHDEALFAV-KPHP 258

Query: 330 GQVEVARNIRTLLSGSSFAXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAY 389
 GQ E+A +R+ L + QDRY LR +P +G L + +

Sbjct: 259 GQQEIASWLRSDLQADTPPRNSDRL-----QDRYSLRCAPHVIGVLQDTLPWLR 307

Query: 390 STLLENNTTTDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELL 449
 + E N+ DNP++D EN++ HGG+F ++++M+ + A+A I L Q +L+

Sbjct: 308 QMIENELNSANDNPIIDGENERVLHGGHFGYGGHIAAMDTLKTAVANIADLLDRQMAQLM 367

Query: 450 NAAMNRGLPSCLA---AEDPSLNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQA 506
 + N GLP L E +N+ K + I I+A+ +E P + F + E NQ

Sbjct: 368 DYKFNNGLPFNLTGAEGERKPINHGFKAVQIGISAWTAEALKNTMPASVFSRSTECHNQD 427

Query: 507 VNSLALISARRTAEANDVLSLLLASHLYCTLQAVDLRAM--ELDFKKQFDPLLPTL 560
 S+ IS+R + + A+ L QA+++R ELD + F P L ++

Sbjct: 428 KVSMGTISSRDCLRVLQLTEQVTAASLLAATQALEIRKRHNELD-ENHFSPALKSM 482

☐ >gi|56678792|gb|AAV95458.1| ☒ histidine ammonia-lyase [Silicibacter pomeroyi DS9]

gi|56697055|ref|YP_167417.1| **G** histidine ammonia-lyase [Silicibacter pomeroyi DSS]
Length = 512

Score = 188 bits (478), Expect = 4e-46

Identities = 133/432 (30%), Positives = 195/432 (45%), Gaps = 31/432 (7%)

Query: 115 VYGVTTGFGGSADTRT--EDAVSLQKALIEHQLCGVTPTSVSSFSVGRGLENLTPLEVVR 172
VYGV TGFG A + +D +LQ+ LI CGV +P + R
Sbjct: 53 VYGVNTGFGKLASLKVAPQDTATLQRNLILSHCCGVGAP-----IPRRMAR 98

Query: 173 GAMVIRVNSLTRGHSVRLVVLEALTNFLNHRITPIVPLRGSISASGDLSPLSYIAGAIT 232
MV+++ SL RG S VR ++ L L +TP++P++GS+ ASGDL+PL+++ I
Sbjct: 99 LMMVLKLLSLGRGASGVRWELITLLQEMLARDVTPVIPVQGSVGASGDLAPLAHMTAVII 158

Query: 233 GHDPVKVHVLHEGTEKIMFAREAISLFGLEAVVLGPKEGLGLVNGTAVSASMATXXXXXX 292
G + + ++G + EA++ GL + LGPKEGL +NGT S + A
Sbjct: 159 GAGEAE----YQGQR--LPGAELARAGLTPIALGPKEGLAFINGTQFSTAFALAGLFGA 212

Query: 293 XXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGSSFAXXXX 352
+A++G P IH R H GQ++ A +R LL GS
Sbjct: 213 WRAATSSLVTAALSTDAIMGSTAPLQPEIH-ALRGHRGQIDAAARMRALLDGSEIRESHR 271

Query: 353 XXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTNDNPLLDVENKQT 412
QD Y +R PQ G ++ + A TL +E N TDNPL+ E
Sbjct: 272 EGDTRV-----QDPYCIRCQPQVTGAAMDVLRQAAQTLEIEANAATDNPLVLAEADMI 324

Query: 413 AHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCLAEDPSLNYHG 472
GGNF A V + + LAL+ IG + + +++ ++ LP L + P LN
Sbjct: 325 VSGGNFHAEPVGFAADLIALALSEIGAIAQRRVALMVDPTLSFDLPPLTPK-PGLNSGL 383

Query: 473 KGLDIHIAAYASELGHLANPVTTTFVQPAEMGNQAVNSLALISARRTAEANDVLSLLASH 532
++ AA SE HLANP T P + S+A A R + L +L
Sbjct: 384 MIAEVTTAALMSENKHLANPCVTDSTPTSANQEDHVSMAAHGAVRLGRMVENLHYILGVE 443

Query: 533 LYCTLQAVDLRA 544
L C Q ++ RA
Sbjct: 444 LLCAAQGIEFRA 455

>gi|27359656|gb|AA008595.1| **G** Histidine ammonia-lyase [Vibrio vulnificus CMCP6]
gi|27363540|ref|NP_759068.1| **G** Histidine ammonia-lyase [Vibrio vulnificus CMCP6]
Length = 512

Score = 187 bits (476), Expect = 8e-46

Identities = 137/472 (29%), Positives = 222/472 (47%), Gaps = 37/472 (7%)

Query: 92 NDDEIRARVDKSVDFLKAQLQNS--VYGVTTGFGGSADTRTEDAVSLQKALIEHQLCGV 149
N E A++D+ V FL+ L+ +YGVTTG+G S V++ L+E
Sbjct: 32 NSVEFTAKIDRGVAFLERLKKEGVIVGVTTGYGDSC-----TVAIPPQLVEE-----L 80

Query: 150 PTSVSSFSVGRGLENLTPLEVVRGAMVIRVNSLTRGHSVRLVVLEALTNFLNHRITPIV 209
P ++ F G GL L E R + R+ SL++G S V +L + +NH I+P +
Sbjct: 81 PLHLTRFH-GCGLGKILTHEQARAVLATRLCSLSQGVSGVSHDLLNQIVTLINHDISPRI 139

Query: 210 PLRGSISASGDLSPLSYIAGAITGHDPVKVHVLHEGTEKIMFAREAISLFGLEAVVLGPK 269
P GS+ ASGDL+PLSY+A A+ G + V+++G E+ E + G++ + L PK
Sbjct: 140 PEEGSVGASGDLTPLSYLAAALVGERE---VIYQGEERA--TAEVYAEGLGIQPIKLRPK 193

Query: 270 EGLGLVNGTAVSASMATXXXXXXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHP 329
 EGL L+NGT+V ++A AM G F + V +PHP
 Sbjct: 194 EGLALMNGTSVMTALACLAYKRAEYLAQLSTKITAM/SVAMHGNDHFHDEALFAV-KPHP 252

Query: 330 GQVEVARNIRTLLSGSSFAXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAY 389
 GQ ++A +R L QDRY LR +P +G + + +
 Sbjct: 253 GQQQIAAWLRDDLKADKPPRNSDRL-----QDRYSLRCAPHVIGVVQDSLFWLR 301

Query: 390 STLSLENNTTTDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELL 449
 + E N+ DNP++D +N++ HGG+F +++M+ + +A + L Q +L+
 Sbjct: 302 QMIENELNSANDNPIIDGDNERNVLHGGHFGYGGHIAMAMDTLKTGIANLADLLDRQMAQLM 361

Query: 450 NAAMNRGLPSCLA---AEDPSLNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQA 506
 + N GLP L+ E +N+ K + I I+A+ +E P + F + E NQ
 Sbjct: 362 DYKFNNGLPFNLGAEGERKPINHGFKAVQIGISAWTAEALKHTMPASVFSRSTECHNQD 421

Query: 507 VNSLALISARRTAEANDVLSLLASHLYCTLQAVDLRAM--ELDFKKQFDPL 556
 S+ I+AR ++ + A+ L Q ++R ELD D L
 Sbjct: 422 KVMGTIAARDCLRVLELTEQVAAASLLAATQGIEIRRRRGELDENHMSDRL 473

☐ >gi|27381353|ref|NP_772882.1| **G** histidine ammonia-lyase [Bradyrhizobium japonicum]
☐ gi|27354520|dbj|BAC51507.1| **G** histidine ammonia-lyase [Bradyrhizobium japonicum U
 Length = 519

Score = 187 bits (476), Expect = 8e-46

Identities = 139/438 (31%), Positives = 196/438 (44%), Gaps = 31/438 (7%)

Query: 109 AQLQNSVYGVTTGFGGSADTRT--EDAVSLQKALIEHQLCGVTPTSVSSFSVGRGLENTL 166
 AQ VYG+ TGFG A R + LQ+ LI CGV P +
 Sbjct: 50 AQADTPVYGINTGFGKLASKRIPPDQTALLQRNLIVSHCCGVGPAT----- 95

Query: 167 PLEVVRGAMVIRVNSLTRGHSVRLVLEALTNFLNHRITPIVPLRGSISASGDLSPLSY 226
 P +VR M +++ SL RG S VR V+E L L R+ P+VP +GS+ ASGDL+PL++
 Sbjct: 96 PEPVIRLMMALKIISLGRGASGVRRVIEQLQGMARRVCPLVPQQGSVGASGDLAPLAH 155

Query: 227 IAGAITGHPDVKVHVLHEGTEKIMFAEAISLFGLEAVVLGPKEGLGLVNGTAVSASMAT 286
 + + G V K + EA++ GL + LGPKEGL L+NGT S + A
 Sbjct: 156 MTAVMIGEGQAIVD-----GKTVSGGEALAAAGLAPLTLGPKEGLALINGTQFSTAYAI 209

Query: 287 XXXXXXXXXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGSS 346
 V+A + F P I + R H GQ+ A + LL GS
 Sbjct: 210 SGVLRGFHLARAALVTGALSVDAAAMASTAPFRPEIQAL-RGHAGQIAAAATLTALDGS 268

Query: 347 FAXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTDNPLLD 406
 QD Y LR PQ G ++ + L +E N TDNPL+
 Sbjct: 269 IRLSHLEGDERV-----QDPYCLRCQPQVAGAALDLITQTARALIVEANAVTDNPLVL 321

Query: 407 VENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCLAEDP 466
 VE + GGNF A V+ + + LAL+ IG ++ + L++ A+N GLP L DP
 Sbjct: 322 VETGEIVSGGNFHAEPVAFADTIALALSEIGAISERRIATLVDPALNFGLPPFL-TPDP 380

Query: 467 SLNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVNSLALISARRTAEANDVLS 526
 +N ++ AA +E A + P + S+A +ARR A+ D L+
 Sbjct: 381 GVNSGFMIAEVTAAALYAENKQRAAACSIDSTPTSANQEDHVSMAAHAARRLADMADNLA 440

Query: 527 LLLASHLYCTLQAVDLRA 544
 +L L Q + LRA

Sbjct: 441 AILGIELLVAAQGITLRA 458

☐ >gi|48787881|ref|ZP_00283860.1| COG2986: Histidine ammonia-lyase [Burkholderia f
Length = 510

Score = 187 bits (474), Expect = 1e-45

Identities = 148/457 (32%), Positives = 221/457 (48%), Gaps = 40/457 (8%)

Query: 99 RVDKSVDFLKAQLQNS--VYGVTTGFGGSADTRTEDA--VSLQKALIEHQLCGVTPTSVS 154
RV+KS D + + + VYGV TGFG A+T LQK L V

Sbjct: 39 RVEKSKDIVSRIVADGKIVYGVNTGFGRLANTTIPAGRIAEQKNL-----VL 86

Query: 155 SFSVGRGLENLTPLEVVIRGAMVIRVNSLTRGHSAVRLVVLEALTNFLNHRITPIVPLRGS 214
S SVG G + VV M ++ SL RGHS VR V+ A+ + LN + P +P +GS

Sbjct: 87 SHSVGTG--ELMEDRVVGLIMALKAISLARGHSGVRPQVVLAIISMLNAGVYPCIPSKGS 144

Query: 215 ISASGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEAVVLGPKEGLGL 274
+ ASGDL+PL+++A A+ G V++ K + A E +S+ GLEA+ LGPKEGL L

Sbjct: 145 VGASGDLAPLAHLAAAMLGVGHVRI-----DGKRVPAEGLSVAGLEALKLGPKEGLAL 198

Query: 275 VNGTAVSASMATXXXXXXXXXXXXXXXXXXXXVEAMVGQQGSFAPFIHDVCRPHPGQVEV 334
+NGT S ++A +EA+ G F P IH V R GQ++V

Sbjct: 199 LNGTQASTALALSGLFAAERVFASAMVTGALSLEAVKGSTVPFDPRIH-VARGQRGQIDV 257

Query: 335 ARNIRTLTSGSSFAXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSL 394
A + LL GS G QD Y +R PQ +G ++ + + L++

Sbjct: 258 AGRLAALLDGSGI-----IASHGNGTRVQDPYSIRCQPQVMGACLDHIRYVAGILTI 309

Query: 395 ENNTTTDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMN 454
E N +DNPL+ +N GGNF A V+++ + +A++ IG ++ + LL++ M+

Sbjct: 310 EANAASDNPLV-FDNGDVLSGGNFHAEPVALAADALAVASEIGAISERRTALLLDSHMS 368

Query: 455 RGLPSCLAEDPSLNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVNSLALIS 514
GLP+ L E +N + AA ASE LA+P + P + S+A +

Sbjct: 369 -GLPAFLVKES-GINSGFMAIQVTSAAALASENKSALHPASVDSLPTSANQEDHVSMTATFA 426

Query: 515 ARRTAEANDVLSLLASHLYCTLQAVD----LRAMEL 547

ARR + D ++++ Q +D LR+ EL

Sbjct: 427 ARRLKDMADNTAVIVGIEGMAAAQGMDFHRPLRSSEL 463

☐ >gi|48782814|ref|ZP_00279294.1| COG2986: Histidine ammonia-lyase [Burkholderia f
Length = 507

Score = 187 bits (474), Expect = 1e-45

Identities = 139/429 (32%), Positives = 210/429 (48%), Gaps = 29/429 (6%)

Query: 116 YGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPTSVSSFSVGRGLENLTPLEVVIRGAM 175
YG+ TGFG A T Q L++ L V S +VG G + P VVR +

Sbjct: 52 YGINTGFGRLASTHIPHD---QLELLQRNL-----VLHAVGVGEPMSRP--VVRLLI 99

Query: 176 VIRVNSLTRGHSAVRLVVLEALTNFLNHRITPIVPLRGSISASGDLSPLSYIAGAITGHP 235
++++SL RGHS +R V++AL N + P++P++GS+ ASGDL+PL++++ A+ G

Sbjct: 100 ALKLSSLGRGHSGIRREVMDALITLYNADVLPVIPVKGSVGASGDLAPLAHMSAALLGVG 159

Query: 236 DVKVHVLHEGTEKIMFAREAISLFGLEAVVLGPKEGLGLVNGTAVSASMATXXXXXXXXXX 295

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      +   V   +G   M A E ++L GL+ + L   KEGL L+NGT   S   ++A
Sbjct: 160 E-----VFAKGER--MPATEGLALVGLKPLTLQAKEGLALLNGTQASTALALYNMFAIEDL 213

Query: 296 XXXXXXXXXXXXXVEAMVGQQGSFAPFIHDCRPHPGQVEVARNIRTLLSGSSFAXXXXXXXX 355
      V+A +G   F   IH++ R H GQ++ A   R+LL GS+
Sbjct: 214 YRTALVSGALSVDAAAMGSVKPFDARIHEL-RGHQGGIDAAAAYRSLEGSAINVSHADCD 272

Query: 356 XXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTNDNPLLDVENKQTAHG 415
      QD Y LR   PQ +G   ++ M HA + L LE N   +DNPL+   +   +   G
Sbjct: 273 KV-----QDPYSLRCQPQVMGACLDQMRHAANVLLLEANAVSDNPLIFPDTGEVLSG 324

Query: 416 GNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCLAEDPSLNYHGKGL 475
      GNF A V+ + +   LA A IG L   +   L++A ++ GLP L   D   +N
Sbjct: 325 GNFHAEPVAFADNLALAAAEIGALAERRIALLDATLS-GLPPFL-VRDGGVNSGFMIA 382

Query: 476 DIHIAAYASELGHLANPVTTFVQPAEMGNQAVNSLALISARRTAEANDVLSLLLASHLYC 535
      + AA ASE   LA+P +   P   +   S+A +AR+   +   +   +L+ L
Sbjct: 383 HVTAAALASENKTLAHPASVDSLPTSANQEDHVSMTAARKLGDIAENTANILSIELLA 442

Query: 536 TLQAVDLRA 544
      Q VDLRA
Sbjct: 443 AAQGVDLRA 451

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☐ >gi|6563308|gb|AAF17247.1| phenylalanine ammonia lyase [Prunus persica]
Length = 356

Score = 187 bits (474), Expect = 1e-45

Identities = 135/363 (37%), Positives = 187/363 (51%), Gaps = 22/363 (6%)

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Query: 331 QVEVARNIRTLLSGSSFAXXXXXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYS 390
      Q+E A   +   +L+GS +   +QDRY LRTSPQ+L P +E + A
Sbjct: 1   QIEAAAIMEHILAGSDYVKAEEKVHDLDPKQP-KQDRYALRTSPQWLSPQIEVIRAATK 59

Query: 391 TLSLENNTTTNDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLN 450
      + E N+   DNPL+DV   + HGGNFQ + + ++M+ TRLA+A IGKL F Q +EL+N
Sbjct: 60 MIEREINSVNDNPLIDVSRNKALHGGNFQGTPIGVAMDNTRLAIAAIGKLMFAQFSELVN 119

Query: 451 AAMNRGLPSC-L-AAEDPSLNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVNS 509
      N GLPS L   + +PSL+Y KG +I +A+Y SEL L NPVT VQ AE NQ VNS
Sbjct: 120 DFYNNGLPSNLTGSSNPSLDYGFKGAEIAMASYCSELQFLGNPVTNHVQSAEQHNQDVNS 179

Query: 510 LALISARRTAEANDVLSLLLASHLYCTLQAVDLRAMELDFKKQFDPLLPTLLQQHLGTGL 569
      L LIS+R+TAEA DVL L+ +++L   QAVDLR +E + K   +   + ++ L G
Sbjct: 180 LGLISSRKTAEAVDVLKLMSSSTYLVALCQAVDLRHLEENLKSTVKSTVSQVAKRVLTGVF 239

Query: 570 DVNALALE-VKKALNKRLEQ-----TTTYDLEPRW-HDAFSYATGTVVELLSSS 616
      +   +K L K +++   + TY L + H   +A   + SSS
Sbjct: 240 NGELHPSRFCEKDLLKVVDREYVFAYIDDPSCSATYPLMQKL RHVLVEHALNNGEKEKSSS 299

Query: 617 PSANVTLTAVNAWKVASAEKAISLTR-EVRNRFWQTPSSQAPAHAYLSPRTRVLYSFVRE 675
      S   +TA   K +   R E N   TP+   +Y   LY FVRE
Sbjct: 300 TSIFQKITAFEEELKTLLPKEVESARLEYDNGKSATPNRIKDCRSY-----PLYKFVRE 353

Query: 676 ELG 678
      ELG
Sbjct: 354 ELG 356

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☐ >gi|48732075|ref|ZP_00265818.1| COG2986: Histidine ammonia-lyase [Pseudomonas fl
Length = 514

Score = 186 bits (473), Expect = 2e-45

Identities = 152/509 (29%), Positives = 229/509 (44%), Gaps = 45/509 (8%)

Query: 91 QNDDEIRARVDKSVDFLKAQLQNS--VYGVTTGFGGSADTRTEDAVSLQKALIEHQLCGV 148
Q+D R R+ K FL + L +YGVTTG+G S V++ +E
Sbjct: 34 QSDAPYRERIAGARFLDSDLKEGVYGVTTGYGDSC-----VVAVPLHHVE-----A 82

Query: 149 TPTSVSSFSVGRGLENLTPLEVVRGAMVIRVNSLTRGHSVRLVLEALTNFLNHRITPI 208
P + +F G GL L + R + R+ SL G S VR+ +LE L FL H I P+
Sbjct: 83 LPRHLYTFH-GCGLGKLLDAQATRAVLAARLQSLCHGVSGVRIELLERLHAFLEHDILPL 141

Query: 209 VPLRGSISASGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEAVVLGP 268
+P GS+ ASGDL+PLSY+A ++G + V+ G + A + G +VL P
Sbjct: 142 IPEEGSVGASGDLTPLSYVAATLSGERE-----VMFRGERR--QAADVHRELGWTPVLRLP 195

Query: 269 KEGLGLVNGTAVSASMATXXXXXXXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPH 328
KE L L+NGTAV +A V A+ G F + +PH
Sbjct: 196 KEALALMNGTAVMTGLACLAYARADYLLQLATRITALNVVALQGNPEHFDERLF-AAKPH 254

Query: 329 PGQVEVARNIRTLLSGSSFAXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHA 388
PGQ++VA +R L+ + QDRY LR +P LG L + +
Sbjct: 255 PGQMQVAAWLRKDLAIDAPTAPLHRL-----QDRYSLRCAPHVLGVLADSLNWL 303

Query: 389 YSTLSLENNTTTDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTEL 448
S + E N+ DNP++D E ++ HGG+F ++ +M+ + +A + L Q L
Sbjct: 304 RSFIETELNSANDNPIIDAEAEVLHGGHFYGGHIAFAMDSLKNLVANVADLLDRQLALL 363

Query: 449 LNAAMNRGLPSCS---AAEDPSLNHYHGKGLDIHIAAYASELGHLANPVTTTFVQPAEMGNQ 505
++ N GLPS L +A+ LN+ K + I +A+ +E P + F + E NQ
Sbjct: 364 VDERYNHGLPSNLSGASADRAMLNHGFKAVQIGASAWTAEALKNTMPASVFSRSTECHNQ 423

Query: 506 AVNSLALISARRTAEANDVLSLLLASHLYCTLQAVDLRAMELDFKKQFDPLLPTLLQQHL 565
S+ I+AR ++ + A+ L Q V LR + D + PL P+L H
Sbjct: 424 DKVSMGTIAARDAIRVLELTEQVAAATLLAANQGVWLRGRDEDAR----PLPPSLAAMHE 479

Query: 566 GTGLDV-----NALALEVKKALNKRLEQ 588
D AL E++ L + EQ
Sbjct: 480 QLAQDFPPVIEDRALEGELRLCLQRIAEQ 508

☐ >gi|56418920|ref|YP_146238.1| ☒ histidine ammonia-lyase (histidase) [Geobacillus
HTA426]

gi|56378762|dbj|BAD74670.1| ☒ histidine ammonia-lyase (histidase) [Geobacillus ka
HTA426]

Length = 504

Score = 186 bits (472), Expect = 2e-45

Identities = 141/458 (30%), Positives = 214/458 (46%), Gaps = 36/458 (7%)

Query: 93 DDEIRARVDKSVDFLKAQLQN--SVYGVTTGFGGSADTRTE--DAVSLQKALIEHQLCGV 148
D+E V+KS ++ + N ++YGV TGFG AD R E D LQ L+ C V
Sbjct: 27 DEESMRAVEKSRAAVEQAISNGRTIYGVNTGFGKLADVRIEGSDLEQLQINLLRSHACAV 86

Query: 149 TPTSVSSFSVGRGLENLTPLEVVRGAMVIRVNSLTRGHSVRLVLEALTNFLNHRITPI 208

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                                +VVR  +++R N+L +G+S VR  V+E L  FLN  I  PI
Sbjct: 87  GEPFAE-----DVVRAMLLLRANALLKGYSGVRPAVIEQLLAFLNTGIHPI 132

Query: 209  VPLRGSISASGDLSPSYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEAVVLGP 268
            VP +GS+ ASGDL+PL+++A A  G  +      +++G  + M A +A+S  G+  + L
Sbjct: 133  VPQQGSLGASGDLAPLAHLALAFAGEGE----AMYQG--RRMPAAQALSQAGISPLSLQE 186

Query: 269  KEGLGLVNGTAVSASMATXXXXXXXXXXXXXXXXXXXXVEAMVGQQGSFAPFIHDVCRPH 328
            KEGL L+NGT V  ++                      +EA+ G  +F  IH  R
Sbjct: 187  KEGLALINGTQVMTAVGALAYLEAEQLAYDSEWIAALTIEALYGIVDAFDARIH-AARGF 245

Query: 329  PGQVEVARNIRTLLSGSSFAXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHA 388
            QVEVA  +R  L+GS                      QD Y +R  PQ  G  +  +  +
Sbjct: 246  QEQVEVAERLRRYLAGSQLTTRQGERRV-----QDAYSIRCLPQVHGASLRALRYV 296

Query: 389  YSTLSLENNTTTDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTEL 448
            TL +E N  TDNPL+  +      + GGNF  V+I+M+  ++A+A  +  ++  +  L
Sbjct: 297  KETLEIEMNAATDNPLIFADGTALS-GGNFHGQPVAIAMDLLKIAVAELANISERRIERL 355

Query: 449  LNAAMNRGLPSCLAEDPSLNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVN 508
            +N  ++ GLP  L+  + P L      +      A+  SE  LA+P  +  P+  +
Sbjct: 356  VNPQLSEGLPPFLSPQ-PGLQSGAMIMQYVAASLVSENKTLAHPASVDSIPSSANQEDHV 414

Query: 509  SLALISARRTAEANDVLSLLASHLYCTLQAVDLRAME 546
            S+  +AR                      +LA  L C LQAV+ R +E
Sbjct: 415  SMGTTAARHAYMIVQNARKVLAIELICALQAVEARGIE 452

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☐ >gi|53719954|ref|YP_108940.1| ☒ histidine ammonia-lyase [Burkholderia pseudomall]
gi|52210368|emb|CAH36347.1| ☒ histidine ammonia-lyase [Burkholderia pseudomallei]
Length = 507

Score = 186 bits (472), Expect = 2e-45
Identities = 137/429 (31%), Positives = 207/429 (48%), Gaps = 29/429 (6%)

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Query: 116  YGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPPTSVSSFSVGRGLENTLPLEVVRGAM 175
            YG+ TGFG  A T      Q  L++  L      V S +VG G      P  VVR  M
Sbjct: 52  YGINTGFGRLASTHIPHD---QLELLQKNL-----VLHAVGVGEPMARP--VVRLLM 99

Query: 176  VIRVNSLTRGHSVRLVLEALTNFLNHRITPIVPLRGSISASGDLSPSYIAGAITGHP 235
            ++++SL RGHS +R VV++AL  N  + P++P++GS+ ASGDL+PL++++  + G
Sbjct: 100  ALKLSSLGRGHS GIRRVMDALVTLFNADVLPLIPVKGSVGASGDLAPLAHMSAVLLGIG 159

Query: 236  DVKVHVLHEGTEKIMFAREAISLFGLEAVVLGPKEGLGLVNGTAVSASMATXXXXXXXXXX 295
            DV +      +  A E + + GL  + L  KEGL L+NGT  S ++A
Sbjct: 160  DVFIR-----GERASAAEGLRVAGLAPLTLEAKEGLALLNGTQASTALALDNLFAIEDL 213

Query: 296  XXXXXXXXXXXXVEAMVGQQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGSSFAXXXXXXX 355
            V+A  G      F  IH++ R H GQ++ A      R+LL GS+
Sbjct: 214  YRTALVSGALSVDAAGSVKPFDAIRHEL-RGHRGQIDAAAAYRSLDGSAINVSHRDCD 272

Query: 356  XXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTDNPLLDVENKQTAHG 415
            QD Y LR  PQ +G  ++  + HA  L +E N  +DNPL+  +  +  G
Sbjct: 273  KV-----QDPYSLRCQPQVMGACLDQIRHAAGVLLIEANAVSDNPLIFPDTGEVLSG 324

Query: 416  GNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCLAEDPSLNYHGKGL 475
            GNF A  V+  +  +  +A A IG L  +  L++A ++ GLP  L  +D  +N
Sbjct: 325  GNFAEPVFAADNLAIAAAEIGALAERRIALLDATLS-GLPPFL-VKDGGVNSGFMIA 382

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Query: 476 DIHIAAYASELGHLANPVTTFVQPAEMGNQAVNSLALISARRTAEANDVLSLLLASHLYC 535
 + AA ASE LA+P + P + S+A +AR+ A+ + ++ +LA L
 Sbjct: 383 HVTAAALASENKTLAHPASVDSLPTSANQEDHVSMATFAARKLADIAENVANILAIELLA 442

Query: 536 TLQAVDLRA 544
 Q VDLRA
 Sbjct: 443 AAQGVDLRA 451

☐ >gi|37679258|ref|NP_933867.1| ☒ histidine ammonia-lyase [Vibrio vulnificus YJ016]
☐ gi|37198001|dbj|BAC93838.1| ☒ histidine ammonia-lyase [Vibrio vulnificus YJ016]
 Length = 514

Score = 185 bits (469), Expect = 5e-45
 Identities = 136/472 (28%), Positives = 221/472 (46%), Gaps = 37/472 (7%)

Query: 92 NDDEIRARVDKSVDFLKAQLQNS--VYGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVT 149
 N E A++D+ V FL+ L+ +YGVTTG+G S V++ L+E
 Sbjct: 34 NSVEFTAKIDRGVAFLERLKKEGVYIYGVTTGYGDSC-----TVAIPPQLVEE-----L 82

Query: 150 PTSVSSFSVGRGLENLPLEVVIRVNSLTRGHSVRLVVLEALTNFLNHRITPIV 209
 P ++ F G GL L E R + R+ SL++G S V +L + +NH I+P +
 Sbjct: 83 PLHLTRFH-GCGLGKILTHEQARAVLATRLCSLSQGVSGVSHDLLNQIVTLINHDISPRI 141

Query: 210 PLRGSISASGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIMFAEAISLFGLEAVVLGPK 269
 P GS+ ASGDL+PLSY+A A+ G + V+++G E+ E + ++ + L PK
 Sbjct: 142 PEEGSGASGDLTPLSYLAAALVGERE----VIYQGEERA--TAEVYAELSIKPIKLRPK 195

Query: 270 EGLGLVNGTAVSASMATXXXXXXXXXXXXXXXXXXXXVEAMVGQQGSFAPFIHDVCRPHP 329
 EGL L+NGT+V ++A AM G F + V +PHP
 Sbjct: 196 EGLALMNGTSVMTALACLAYKRAEYLAQLSTKITAMVSVAMHGNDFFHFDEALFAV-KPHP 254

Query: 330 GQVEVARNIRTLLSGSSFAXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAY 389
 GQ ++A +R L QDRY LR +P +G + + +
 Sbjct: 255 GQQQIAAWLRDDLKADKPPRNSDRL-----QDRYSLRCAPHVIGVVQDSLPLWLR 303

Query: 390 STLLENNTTTDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELL 449
 + E N+ DNP++D +N++ HGG+F ++++M+ + +A + L Q +L+
 Sbjct: 304 QMIENELNSANDNPIIDGDNERVHGGHFGYGGHIAMADTLKTGIANLADLLDRQMAQLM 363

Query: 450 NAAMNRGLPSCLA---AEDPSLNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQA 506
 + N GLP L+ E +N+ K + I I+A+ +E P + F + E NQ
 Sbjct: 364 DYKFNNGLPFNLGAEGERKPINHGFKAVQIGISAWTAEALKHTMPASVFSRSTECHNQD 423

Query: 507 VNSLALISARRTAEANDVLSLLLASHLYCTLQAVDLRAM--ELDFKKQFDPL 556
 S+ I+AR ++ + A+ L Q +++R ELD D L
 Sbjct: 424 KVSMGTIAARDCLRVLELTEQVAAASLLAATQGIEIRRRRGELDENHMSDRL 475

☐ >gi|48770373|ref|ZP_00274716.1| COG2986: Histidine ammonia-lyase [Ralstonia meta]
 Length = 533

Score = 184 bits (468), Expect = 6e-45
 Identities = 134/439 (30%), Positives = 198/439 (45%), Gaps = 31/439 (7%)

Query: 115 VYGVTTGFGGSADTRT--EDAVSLQKALIEHQLCGVTPTSVSSFSVGRGLENLPLEVVR 172

Sbjct: 56 +YGV+TGFG E +LQ+ L+ GV P + VR
IYGVSTGFGELVHNWVDIEHGRALQENLLRSHCAGVGPL-----FSRDEV 101

Query: 173 GAMVIRVNSLTRGHSVRLVLEALTNFLNHRITPIVPLRGSISASGDLSPLSYIAGAIT 232
MV R N+L RG+SAVR V+E L +L ITP VP GS+ ASGDL+PLS++A +

Sbjct: 102 AMMVARANALARGYSAVRPAVIEQLLKYLEAGITPAVPQVGSGLGASGDLAPLSHVAITLI 161

Query: 233 GHPDVKVHVLHEGTEKIMFAREAISLFGLEAVVLGPKEGLGLVNGTAVSASMATXXXXXX 292
G + KV GT E + G+ + L KEGL L+NGT+ ++

Sbjct: 162 G--EGKVLTEDGGTAP---TAEVLRERGITPLALAYKEGLALINGTSAMTGVSCLLLETL 216

Query: 293 XXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGS----- 345
+E + +F HD+ +PHPGQ+ A N+R LL+ S

Sbjct: 217 RAQVQQAETIAALALEGLSASADAFMAHGHDIAKPHPGQIRSAANMRALLADSARLSGHG 276

Query: 346 --SFAXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTDNP 403
S G+ Q Y LR PQ LG + + + H + + E N++ DNP

Sbjct: 277 ELSAEMKTRAGEAKNTGTGVFIQKAYTLRCIPQVLGAVRDTLDHCATVVERELNSSNDNP 336

Query: 404 LLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRLGPSCLAA 463
L E+ + HGGNF V+ +M+ +A +G ++ + LL+ +N LP+ LAA

Sbjct: 337 LF-FEDGELFHGGNFHGQQVAFAMDFLAIAATQLGVVSERRLNRLLSPHLNNNLPAFLAA 395

Query: 464 EDPSLNYHGKGLDIHIAAYASELGHLANPVTTTFVQPAEMGNQAVNSLALISARRTAEAND 523
+ L+ G A +E + +P + P+ NQ V S+ LI+AR D

Sbjct: 396 ANEGLSCGFAGAQYPATALIAENRTICSPASIQSVPSNGDNQDVVSMGLIAARNARRILD 455

Query: 524 VLSLLLASHLYCTLQAVDL 542
+LA L + QA +L

Sbjct: 456 NNQYILALELLASCQAAEL 474

☐ >gi|50083810|ref|YP_045320.1| ☒ histidine ammonia-lyase protein (Histidase) [Acidobacterium] ADP1]

gi|49529786|emb|CAG67498.1| ☒ histidine ammonia-lyase protein (Histidase) [Acinetobacter] ADP1]

Length = 527

Score = 184 bits (468), Expect = 6e-45
Identities = 138/457 (30%), Positives = 214/457 (46%), Gaps = 40/457 (8%)

Query: 97 RARVDKSVDFLKAQLQNS--VYGVTTGFGGSADTRTEDAVSLQKALIE---HQLCGVTPT 151
R + K DFL LQ +YGVTTG+G S L+E HQ+ + P

Sbjct: 44 RDLIQKGADFLDTLLQEEGVYGVTTGYGDSC-----LVEVPTHQVHEL-PL 89

Query: 152 SVSSFSVGRGLENLTPLEVVRGAMVIRVNSLTRGHSVRLVLEALTNFLNHRITPIVPL 211
+S F G GL L L R ++ R+ SL RG+S V L +LE L LN + P++P

Sbjct: 90 QLSRFH-GCGLGQNLDLVTARAVVITRLCSLARGYSGVSLALLERLVWLLNENVIPVIPS 148

Query: 212 RGSISASGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEAVVLGPKEG 271
GS+ ASGDL+PLSYIAG + G + V ++G KI+ ++ ++ + L PKEG

Sbjct: 149 EGSVGASGDLTPLSYIAGVLGERE----VYYQG--KIIPVQQVYQQKAIQPLTLRPKEG 202

Query: 272 LGLVNGTAVSASMATXXXXXXXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQ 331
L L+NGTAV ++A V A+ G F + +PH GQ

Sbjct: 203 LALMNGTAVMTAIACLNYKRAEQIAQTATLVTAINVLALEGNPTHFDEVLF-AQKPHGTGQ 261

Query: 332 VEVARNIRTLLSGSSFAXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYST 391

++A +R L+ QDRY LR +P +G + +
 Sbjct: 262 QKIAAQLRDWLNSE-----VQTAHQSPRLQDRYSLRCAPHVIGVFEDSKVWLRQF 311
 Query: 392 LSLNNNTTTDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNA 451
 + E N++ DNPL+D N + HGG+F ++ +M+ ++ +A I L Q +L++
 Sbjct: 312 IENELNSSNDNPLIDPVNLRVLHGGHFYGGHIAQAMDSLKIMIANIADLMRQLAQLVDH 371
 Query: 452 AMNRGLPSCSCL---AAEDPSLNYHGKGLDIHIAAYASELGHLANPVTTTFVQPAEMGNQAVN 508
 MN GLP L AE LN+ K + I ++A+ +E + F + E NQ
 Sbjct: 372 KMNHGLPRNLTGATAERLPLNHGFKAVQIGVSAWTAEALKQTLASIFSRSTECHNQDKV 431
 Query: 509 SLALISARRTAEANDVLSLLLASHLYCTLQAVDLRAM 545
 S+ I+AR + ++A+ ++QA+ L+ +
 Sbjct: 432 SMGTIAARDATRIIVLTEQVMAALCCASIQAIHLKQL 468





☐ >gi|53725657|ref|YP_102423.1| ☒ histidine ammonia-lyase [Burkholderia mallei ATCC
 gi|52429080|gb|AAU49673.1| ☒ histidine ammonia-lyase [Burkholderia mallei ATCC 23
 Length = 529

Score = 184 bits (468), Expect = 6e-45

Identities = 136/429 (31%), Positives = 206/429 (48%), Gaps = 29/429 (6%)

Query: 116 YGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPTSVSSFSVGRGLENLPLEVVRGAM 175
 YG+ TGFG A T Q L++ L V S +VG G P VVR M
 Sbjct: 74 YGINTGFGRLASTHIPHD---QLELLQKNL-----VLHAVGVGEPMARP--VVRLLM 121
 Query: 176 VIRVNSLTRGHSVRLVVLEALTNFLNHRITPIVPLRGSISASGDLSPSYIAGAITGHP 235
 ++++SL RGHS +R VV++AL N + P++P++GS+ ASGDL+PL++++ + G
 Sbjct: 122 ALKLSSLGRGHSGIRRVMDALVTLFNADVLPKGVSGASGDLAPLAHMSAVLLGIG 181
 Query: 236 DVKVHVLHEGTEKIMFAREAISLFGLEAVVLGPKEGLGLVNGTAVSASMATXXXXXXXXXX 295
 DV + + A E + + GL + L KEGL L+NGT S ++A
 Sbjct: 182 DVFIR-----GERASAAEGLRVAGLAPLTLEAKEGLALLNGTQASTALALDNLFAIEDL 235
 Query: 296 XXXXXXXXXXXXVEAMVGQQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGSSFAXXXXXXXX 355
 V+A G F IH++ R H GQ++ A R+LL GS+
 Sbjct: 236 YRTALVSGALSVDAAAGSVKPFDAIRHEL-RGHRGQIDAAAAYRSLLDGSAINVSHRDCD 294
 Query: 356 XXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNNTTTDNPLLDVENKQTAHG 415
 QD Y LR PQ +G ++ + HA L +E N +DNPL+ + + G
 Sbjct: 295 KV-----QDPYSLRCQPQVMGACLDQIRHAAGVLLIEANAVSDNPLIFPDTGEVLSG 346
 Query: 416 GNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCSCLAAEDPSLNYHGKGL 475
 GNF A V+ + + +A A IG L + L++A ++ GLP L +D +N
 Sbjct: 347 GNFAEPVAFADNLIAAAEIGALAERRIALLLIDATLS-GLPPFL-VKDGGVNSGFMIA 404
 Query: 476 DIHIAAYASELGHLANPVTTTFVQPAEMGNQAVNSLALISARRTAEANDVLSLLLASHLYC 535
 + AA ASE LA+P + P + S+A +AR+ + + ++ +LA L
 Sbjct: 405 HVTAAALASENKTLAHPASVDSLPTSANQEDHVSMAFARKLTDIAENVANILAIELLA 464
 Query: 536 TLQAVDLRA 544
 Q VDLRA
 Sbjct: 465 AAQGVDLRA 473

☐ >gi|17937636|ref|NP_534425.1| ☒ histidine ammonia-lyase [Agrobacterium tumefaciens]

gi|17742375|gb|AAL44741.1|  histidine ammonia-lyase [Agrobacterium tumefaciens s
gi|15159358|gb|AAK89487.1|  AGR_L_1825p [Agrobacterium tumefaciens str. C58]
gi|25292176|pir|E98245 hutH gene homolog [imported] - Agrobacterium tumefaciens
C58, Cereon)
gi|25292178|pir|AG3040 histidine ammonia-lyase hutH [imported] - Agrobacterium t
(strain C58, Dupont)
gi|24211817|sp|Q8U8Z7|HUTH_AGRT5  Histidine ammonia-lyase (Histidase)
gi|15891030|ref|NP_356702.1|  hypothetical protein AGR_L_1825 [Agrobacterium tum
C58]
Length = 514

Score = 184 bits (468), Expect = 6e-45

Identities = 134/431 (31%), Positives = 201/431 (46%), Gaps = 32/431 (7%)

Query: 115 VYGVTTGFGGSADTRTE--DAVSLQKALIEHQLCGVTPTSVSSFSVGRGLENLTPLEVVR 172
VYG+ TGFG A + + D +LQ+ LI CGV LP VVR
Sbjct: 55 VYGINTGFGKLASIKIDAADVATLQRNLILSHCCGVGVP-----LPENVVR 100

Query: 173 GAMVIRVNSLTRGHSVRLVLEALTNFLNHRITPIVPLRGSISASGDLSPLSYIAGAIT 232
M +++ SL RG S VRL ++ + L + P++P +GS+ ASGDL+PL+++A +
Sbjct: 101 LIMALKLVSLGRGASGVRLVRLIEAMLEKGVIPVPIPEKGSVGASGDLAPLAHMAAVMM 160

Query: 233 GHPDVKVHVLHEGTEKIMFAREAISLFGLEAVVLGPKEGLGLVNGTAVSASMATXXXXXX 292
G + +EG + A EA++ GL VVL KEGL L+NGT S ++A
Sbjct: 161 GEGE----AFYEGAP--LPAGEALAKAGLTPVVLAAKEGLALINGTQTSTALALAGLFRA 214




Query: 293 XXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGSSFAXXXX 352
+A +G F P IH + R H GQ++ +R LL GS
Sbjct: 215 HRAAQAALITGALSTDAAMGSSAPFHPDIHSL-RGHKGQIDAGAALRNLEGSEIRVSHI 273

Query: 353 XXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTNDNPLLDVENKQT 412
QD Y +R PQ G ++ + TL +E N TDNPL+ + +
Sbjct: 274 EGDERV-----QDPYCIRCQPQVDGACLDLLRQVARTLEIEANAVTDNPLV-LSDNSV 325

Query: 413 AHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCLAEDPSLNYHG 472
GGNF A V+ + ++T LA+ IG + + L++ A++ GLP+ L ++ P LN
Sbjct: 326 VSGGNFHAEPVAFADQTAALICEIGAIAQRRVALLVDPALSYGLPAFL-SKKPGLNSGL 384

Query: 473 KGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVNSLALISARRTAEANDVLSLLASH 532
++ AA SE +A+P + P + S+A ARR D L +L
Sbjct: 385 MIAEVTSAALMSENQMAHPASVDSTPTSANQEDHVSMAHGARRLLPMTDNLFILGIE 444

Query: 533 LYCTLQAVDLR 543
+Q V+LR
Sbjct: 445 ALSAVQGVLR 455

 >gi|54309352|ref|YP_130372.1|  putative histidine ammonia-lyase [Photobacterium
gi|46913788|emb|CAG20570.1|  putative histidine ammonia-lyase [Photobacterium pr
Length = 510

Score = 184 bits (467), Expect = 8e-45

Identities = 128/432 (29%), Positives = 216/432 (50%), Gaps = 32/432 (7%)

Query: 115 VYGVTTGFGGSADTR--TEDAVSLQKALIEHQLCGVTPTSVSSFSVGRGLENLTPLEVVR 172
VYG+ TGFG A+TR ED +LQ++++ G+ G +++ VR
Sbjct: 53 VYGINTGFGLLANTRIAAEDLETQRSIVLSHAAGI-----GTFMDDA----TVR 98

Query: 173 GAMVIRVNSLTRGHSAVRLVVLEALTNFLNHRITPIVPLRGSISASGDLSPYSIAGAIT 232
 +V++VNSL+RG+S +R +V+ AL +N + P +P +GS+ ASGDL+PL++++ +
 Sbjct: 99 MMIVLKVNSLSRGYSGRPLVVNALMQLVNTTEVYPCIPKKGSVGASGDLAPLAHMSTVLL 158

Query: 233 GHPDVKVHVLHEGTEKIMFAREAISLFGLEAVVLGPKEGLGLVNGTAVSASMATXXXXXX 292
 G + + ++G +++ +A+ + GLE + L PKEGL L+NGT S + A
 Sbjct: 159 GEGEAR----YQG--EVITGAQALEIAGLEPITLAPKEGLALLNGTQASTAFALGFFAA 212

Query: 293 XXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGSSFAXXXX 352
 V+A +G + F P IH V R H Q++ A R +L +S
 Sbjct: 213 EDLYAAATVCGAMSVDAALGSRRPFDPRIHRV-RGHRSQLDAAMGYRHMLGQNSEIGLSH 271

Query: 353 XXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTNDNPLLDVENKQT 412
 QD Y LR PQ +G ++ + ++ TL +E N +DNPL+ ++
 Sbjct: 272 QQCEKV-----QDPYSLRCQPQVMGACLQQIRNSAVTLEVEANAVSDNPLVFAADDGDI 324

Query: 413 AHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCLAAEDPSLNYHG 472
 GGNF A V+++ + LA+A IG L+ + L+++ +++ LP L ++ +N
 Sbjct: 325 ISGGNFHAEPVAMAADNLALAI AEIGLSERRMALLIDSGLSK-LPPFL-VDNGGVNSGF 382

Query: 473 KGLDIHIAAYASELGHLANPVTTTFVQPAEMGNQAVNSLALISARRTAEANDVLSLLASH 532
 + AA ASE LA+P + P + S+A +ARR + + +LA
 Sbjct: 383 MIAQVTAAALASENKS LAHPASVDSLPTSANQEDHVS MATFAARRLTDMAENTRGILAVE 442

Query: 533 LYCTLQAVDLRA 544
 L Q +D R+
 Sbjct: 443 LLAAQGLDFRS 454

☐ >gi|53762553|ref|ZP_00168547.2| COG2986: Histidine ammonia-lyase [Ralstonia eutropha]
 Length = 526

Score = 184 bits (467), Expect = 8e-45

Identities = 137/408 (33%), Positives = 195/408 (47%), Gaps = 33/408 (8%)

Query: 115 VYGVTTGFGGSADTR--TEDAVSLQKALIEHQLCGVTPTSVSSFSVGRGLENTLPLEVVR 172
 VYG+ TGFG A TR + +LQ+ L V S SVG G + L +VVR
 Sbjct: 63 VYGINTGFGKLAQTRIPNDKLATLQRNL-----VLSHSVGTGPD--LAEDVVR 108

Query: 173 GAMVIRVNSLTRGHSAVRLVVLEALTNFLNHRITPIVPLRGSISASGDLSPYSIAGAIT 232
 + I+ SL RGHS VR ++EAL NH +TP +P +GS+ ASGDL+PL++++ +
 Sbjct: 109 VILAIKAVSLARGHSGVRPEIIEALLALANHGVTPCIPAKGSVGASGDLAPLAHMSTCTLI 168

Query: 233 GHPDVKVHVLHEGTEKIMFAREAISLFGLEAVVLGPKEGLGLVNGTAVSASMATXXXXXX 292
 G DV V + + A E ++ GL A LGPKEGL L+NGT VS ++A
 Sbjct: 169 GVGDIV-----DGRRVPAAEGLAHAGLSAFELGPKEGLALLNGTQVSTALALAGLFAA 222

Query: 293 XXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGSSFAXXXX 352
 +EA+ G F IH+ R GQ+ VA +R +L GS
 Sbjct: 223 EDTFAAGLVAGALSLEAIKGSVKPFDARIHE-ARGQAGQI AVAGAVRAMLDGSEIVDSHK 281

Query: 353 XXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTNDNPLLDVENKQT 412
 QD Y +R PQ +G ++++ HA L +E N +DNPL+
 Sbjct: 282 ACGRV-----QDPYSIRCQPQVMGACLDNLQHAARILRIEANAASDNPLVFS AQGDV 333

Query: 413 AHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCLAAEDPSLNYHG 472
 GGNF A V+ + + LA+A IG ++ + LL+ ++ GLP L D LN
 Sbjct: 334 ISGGNFHAEPVAFADIIALAI AEIGAISERRLALLLD TGLS-GLPPFL-VRDGGVNSGF 391

Query: 473 KGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVNSLALISARRTAE 520
 + AA ASE LA+P + P + S+A ARR +
 Sbjct: 392 MIAQVTAAALASENKS LAHPSSVDSLPTSANQEDHVS MATYGARRLGD 439

☐ >gi|17429668|emb|CAD16353.1| **G** PROBABLE HISTIDINE AMMONIA-LYASE (HISTIDASE) PRO
 solanacearum]
 gi|17547365|ref|NP_520767.1| **G** PROBABLE HISTIDINE AMMONIA-LYASE (HISTIDASE) PROTE
 solanacearum GMI1000]
 Length = 518

Score = 184 bits (466), Expect = 1e-44
 Identities = 134/426 (31%), Positives = 202/426 (47%), Gaps = 28/426 (6%)

Query: 116 YGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPTSVSSFSVGRGLENLPLEVVRGAM 175
 YG+ TGFG A T+ + H+L + + S +VG G + L V R +
 Sbjct: 60 YGINTGFGKLARTQ-----IATHELEHLQRNLILSHAVGTGQD--LDDNVARLVL 107

Query: 176 VIRVNSLTRGHSVRLVLEALTNFLNHRITPIVPLRGSISASGDLSPLSYIAGAITGHP 235
 +++ SL RG+S VR VV++ L LN I P +P +GS+ ASGDL+PL+++ A+ G
 Sbjct: 108 LMKAAASLARGYSVRRVVIDTLLAMLNAGIVPCIPSKGSVGASGDLAPLAHMTLAMLGEG 167

Query: 236 DVKVHVLHEGTEKIMFAREAI SLFGL EAVLGPKEGLGLVNGTAVSASMATXXXXXXXXXX 295
 D +V+ + + AREA++ G+ + L KEGL L+NGT VS ++A
 Sbjct: 168 DARVNGVRKP-----AREALAAAGIAPIALAAKEGLALINGTQVSTALALNGLFLAERL 221

Query: 296 XXXXXXXXXXXXVEAMVGQQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGSSFAXXXXXXXX 355
 V+A G F P +H V R GQ+ A R LL+GS+
 Sbjct: 222 LQAATVAGALSVDAAKGSDAPFDPVHTV-RGQAGQIATAAVYRGLLAGSAIRRSHLVGD 280

Query: 356 XXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTNDNPLLDVENKQTAHG 415
 QD Y LR PQ +G ++ + A +TL E N TDNPL+ + + G
 Sbjct: 281 TRV-----QDPYSLRCQPQVMGACLDLIRQAGATLLTEANAVTDNPLVYADAGEVISG 333

Query: 416 GNFAQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCLAEDPSLNYHGKGL 475
 GN F A V+ + + LA+A IG L+ + L+++ ++ GLP L E P LN
 Sbjct: 334 GNFAEPVAFADMLALALAEIGALSERRIALLDSTLS-GLPPFL-VEQPGLNSGFMIA 391

Query: 476 DIHIAAYASELGHLANPVTTFVQPAEMGNQAVNSLALISARRTAEANDVLSLLLASHLYC 535
 + AA ASE LA+P + P + S+A + RR AE + ++
 Sbjct: 392 HVTAAALASENKS LAHPASVDSLPTSANQEDHVS MATFAGRR LAEMAGNTATIVGIEALA 451

Query: 536 TLQAVD 541
 Q +D
 Sbjct: 452 AAQGID 457

☐ >gi|24211821|sp|Q8XW29|HUTH_RALSO Histidine ammonia-lyase (Histidase)
 Length = 515

Score = 184 bits (466), Expect = 1e-44
 Identities = 134/426 (31%), Positives = 202/426 (47%), Gaps = 28/426 (6%)

Query: 116 YGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPTSVSSFSVGRGLENLPLEVVRGAM 175
 YG+ TGFG A T+ + H+L + + S +VG G + L V R +
 Sbjct: 57 YGINTGFGKLARTQ-----IATHELEHLQRNLILSHAVGTGQD--LDDNVARLVL 104

Query: 176 VIRVNSLTRGHSVRLVLEALTNFLNHRITPIVPLRGSISASGDLSPLSYIAGAITGHP 235
 +++ SL RG+S VR VV++ L LN I P +P +GS+ ASGDL+PL+++ A+ G
 Sbjct: 105 LMKAAASLARGYSVRRVVIDTLLAMLNAGIVPCIPSKGSVGASGDLAPLAHMTLAMLGEG 164

Query: 236 DVKVHVLHEGTEKIMFAREAISLFGLEAVVLGPKEGLGLVNGTAVSASMATXXXXXXXXXX 295
 D +V+ + + AREA++ G+ + L KEGL L+NGT VS ++A
 Sbjct: 165 DARVNGVRKP-----AREALAAAGIAPIALAAKEGLALINGTQVSTALALNGLFLAERL 218

Query: 296 XXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGSSFAXXXXXXX 355
 V+A G F P +H V R GQ+ A R LL+GS+
 Sbjct: 219 LQAATVAGALSVDAAKGS DAPFDPRVHTV-RGQAGQIATAAVYRGLLAGSAIRRSHLVGD 277

Query: 356 XXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTDNPLLDVENKQTAHG 415
 QD Y LR PQ +G ++ + A +TL E N TDNPL+ + + G
 Sbjct: 278 TRV-----QDPYSLRCQPQVMGACLDLIRQAGATLLTEANAVTDNPLVYADAGEVISG 330

Query: 416 GNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCLAEDPSLNYHGKGL 475
 GNF A V+ + + LA+A IG L+ + L+++ ++ GLP L E P LN
 Sbjct: 331 GNFHAEPVAFADMLALAIIEIGALSERRIALLLIDSTLS-GLPPFL-VEQPGLNSGFMIA 388

Query: 476 DIHIAAYASELGHLANPVTTTFVQPAEMGNQAVNSLALISARRTAEANDVLSLLLASHLYC 535
 + AA ASE LA+P + P + S+A + RR AE + ++
 Sbjct: 389 HVTAAALASENKS LAHPASVDSLPTSANQEDHVS MATFAGRR LAEMAGNTATIVGIEALA 448

Query: 536 TLQAVD 541
 Q +D
 Sbjct: 449 AAQGID 454

☐ >gi|58039620|ref|YP_191584.1| ☒ Histidine ammonia-lyase [Gluconobacter oxydans (gi|58002034|gb|AAW60928.1| ☒ Histidine ammonia-lyase [Gluconobacter oxydans 621H]
 Length = 515

Score = 183 bits (465), Expect = 1e-44
 Identities = 141/476 (29%), Positives = 220/476 (46%), Gaps = 38/476 (7%)

Query: 115 VYGVTTGFGGSADTRTED--AVSLQKALIEHQLCGVTPTSVSSFSVGRGLENTLPLEVVR 172
 VYGV TGFG A TR D LQ+ L+ S G+ +P VVR
 Sbjct: 55 VYGVNTGFGKLAKTRIPDDRRLRDLQRNLV-----LSHAAGIGQPMPEVVR 100

Query: 173 GAMVIRVNSLTRGHSVRLVLEALTNFLNHRITPIVPLRGSISASGDLSPLSYIAGAIT 232
 ++++ N L RG+S VR +++ L + LN + P++P +GS+ ASGDL+PL++++ +
 Sbjct: 101 LILLKLANGLARGYSVVRPQIVQLLLDMLNQGVVPVPIPEKGSVGASGDLAPLAHMSAVVI 160

Query: 233 GHPDVKVHVLHEGTEKIMFAREAISLFGLEAVVLGPKEGLGLVNGTAVSASMATXXXXXX 292
 G + ++G K + EA+ GLE +VLG KEGL L+NGT S ++A
 Sbjct: 161 GEGE----AFYQG--KRLKGDEALKAAGLEPLVLGAKEGLALLNGTQASTALAIAALLDA 214

Query: 293 XXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGSSFAXXXX 352
 ++A G F P +H++ R GQ+E A R L+ GS+
 Sbjct: 215 ERLFHAALITGGLTLDAARGTDAPFDPRLHEL-RGQKGQIECAAVYRALMQGS AIRASHL 273

Query: 353 XXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTDNPLLDVENKQT 412
 QD Y LR PQ +G ++++ A L +E N +DNP+ + +
 Sbjct: 274 EDDERV-----QDPYCLRCQPQVMGACLDNLRQAARVLVIEANAVSDNPIHFPDPTDEM 326

Query: 413 AHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCLAEDPSLNYHG 472

GGNF A V+I+ + +A++ +G + + L++A M+ GLP L +D LN
 Sbjct: 327 ISGGNFHAEPVAIAADLMAIAVSEVGAIAERRALLLVDAQMS-GLPPFL-VQDSGLNSGF 384

Query: 473 KGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVNSLALISARRTAEANDVLSLLASH 532
 + AA ASE LA+P + P + S+A +ARR + D + ++A
 Sbjct: 385 MIAQVTAALASENKTLAHPASVDSLPTSANQEDHVSMTFAARRVGDIVDNVRTIIAVE 444

Query: 533 LYCTLQAVDL-----RAMELDFKKQFDPLLPTLLQQHLGTGLDVNALALEVKKAL 582
 +Q +D A L+ K +P Q L T A AL + AL
 Sbjct: 445 YLAAVQGLDFLAPLETSAPLLEVAKTLRKTVPFPAQDRLFTPDMEARALIIDGAL 500

☐ >gi|56478698|ref|YP_160287.1| ☒ histidine ammonia-lyase, predicted methylene imi
 cofactor [Azoarcus sp. EbN1]
 gi|56314741|emb|CAI09386.1| ☒ Histidine ammonia-lyase, predicted methylene imidaz
 cofactor [Azoarcus sp. EbN1]
 Length = 526

Score = 183 bits (464), Expect = 2e-44
 Identities = 138/429 (32%), Positives = 200/429 (46%), Gaps = 29/429 (6%)

Query: 116 YGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPTSVSSFSVGRGLENLPLEVVRGAM 175
 YG+ TGFG A T D Q L++ L V S +VG G + P VR +
 Sbjct: 54 YGINTGFGRLAQTHIPDD---QLELLQKNL-----VLSHAVGVGEPLSAP--TVRLVL 101

Query: 176 VIRVNSLTRGHSVRLVVLEALTNFLNHRITPIVPLRGSISASGDLSPLSYIAGAITGHP 235
 +++ SL RGHS VR+ ++ AL N + P VP +GS+ ASGDL+PL++++ + G
 Sbjct: 102 ALKIASLARGHSGVRMELINALLGLFNAGVIPRVPSKGSVGASGDLAPLAHLSALLLGIG 161

Query: 236 DVKVHVLHEGTEKIMFAREAISLFGLEAVVLGPK EGLVLNGTAVSASMATXXXXXXXXXX 295
 + V H + A EA+++ GL + L KEGL L+NGT VS ++A
 Sbjct: 162 EAYVDGRH-----VPATEALAIAGLAPMTLAAKEGLALLNGTQVSTALALVNLFAIETV 215

Query: 296 XXXXXXXXXXXXVEAMVGQQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGSSFAXXXXXXXX 355
 V+A G F IH R PGQ++ A R LL GS
 Sbjct: 216 FRTALVAGALSVDAAAGSFKPFDAIRH-ALRGQPGQIDAAATYRQLLEGSGINLAHRDCG 274

Query: 356 XXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTDNPLLDVENKQTAHG 415
 QD Y LR PQ +G ++ M HA L +E N +DNPL+ ++ + G
 Sbjct: 275 KV-----QDPYSLRCQPQVMGACLDQMRHAARVLLIEANAVSDNPLVFPDSGEVLSG 326

Query: 416 GNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCLAEDPSLNYHGKGL 475
 GNF V+ + + LA A IG L + L++A ++ GLP L E +N
 Sbjct: 327 GNFHGEPAFAADALALAAAEIGALAERRIALLDATLS-GLPPFLVTEG-GVNSGFMIA 384

Query: 476 DIHIAAYASELGHLANPVTTFVQPAEMGNQAVNSLALISARRTAEANDVLSLLASHLYC 535
 + AA ASE LA+P + P + S++ +AR+ E D + +LA L
 Sbjct: 385 HVTAAALASENKL LAHPASVDSLPTSANQEDHVSMTFAARKLGELADNTATILAIELLA 444

Query: 536 TLQAVDLRA 544
 Q V+LRA
 Sbjct: 445 AAQGVELRA 453

☐ >gi|48768557|ref|ZP_00272906.1| COG2986: Histidine ammonia-lyase [Ralstonia meta
 Length = 522

Score = 182 bits (462), Expect = 3e-44

Identities = 136/427 (31%), Positives = 200/427 (46%), Gaps = 29/427 (6%)

Query: 115 VYGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPTSVSSFSVGRGLENTLPLEVVRGA 174
 VYG+ TGFG A +R + +L + V S SVG G + L ++ VR

Sbjct: 60 VYGIN TGFGKLAQSR-----IAHDKLAELQRNLVLSHVS VGTGSD--LSVDTVRLI 107

Query: 175 MVIRVNSLTRGHSVRLVLEALTNFLNHRITPIVPLRGSISASGDLSPLSYIAGAITGH 234
 + I+ SL RGHS VR ++EAL NH +TP +P +GS+ ASGDL+PL++++ + G

Sbjct: 108 LAIKAVSLARGHSGVRPELIEALLALANHGVTIPCIPAKGSVGASGDLAPLAHMSCTLIGV 167

Query: 235 PDVKVHVLHEGTEKIMFAREAI SLFGLEAVVLGPKEGLGLVNGTAVSASMATXXXXXXXXX 294
 DV V +G + A + + GL A LGPKEGL L+NGT VS ++A

Sbjct: 168 GDVYV---DGQR--VPAAQGLVHAGLAAFTLGPKEGLALLNGTQVSTALALAGLFAAED 221

Query: 295 XXXXXXXXXXXXXVEAMVGQQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGSSFAXXXXXX 354
 +EA+ G F IH R GQ+ VA R +L GS

Sbjct: 222 AFAAGLVAGALSLEAIKGSVKPFDARIH-AARGQAGQIAVAGAARAMLDGSEIVDSHKMC 280

Query: 355 XXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTDNPLLDVENKQTAH 414
 QD Y +R PQ +G ++++ HA L +E N +DNPL+ E

Sbjct: 281 GRV-----QDPYSIRCQPQVMGACLDNLTHAARILRIEANAASDNPLVFSEQGDVVS 332

Query: 415 GGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCLAEDPSLNYHGKG 474
 GGNF A +V+ + + LA+A IG ++ + LL+ ++ GLP L D LN

Sbjct: 333 GGNFHAESVAFADIIALAEIGAISERRLALLLDLTGLS-GLPPFL-VRDGLNSGFMI 390

Query: 475 LDIHIAAYASELGHLANPVTTFVQPAEMGNQAVNSLALISARRTAEANDVLSLLLASHLY 534
 + AA ASE LA+P + P + S+A ARR E ++++

Sbjct: 391 AQVTAAALASENKS LAHPSSVDSLPTSANQEDHVS MATY GARRLGEMAANTAVIVGIEAM 450

Query: 535 CTLQAVD 541
 Q ++

Sbjct: 451 AAAQGIE 457

☐ >gi|15807816|ref|NP_285471.1| ☒ histidine ammonia-lyase [Deinococcus radiodurans]
☒ gi|6460510|gb|AAF12216.1| ☒ histidine ammonia-lyase [Deinococcus radiodurans]
☒ gi|7472012|pir|F75610 histidine ammonia-lyase (EC 4.3.1.3) [similarity] - Deinoc
 radiodurans (strain R1)
☒ gi|9910729|sp|Q9RZ06|HUTH_DEIRA Histidine ammonia-lyase (Histidase)
 Length = 524

Score = 182 bits (462), Expect = 3e-44

Identities = 134/433 (30%), Positives = 213/433 (49%), Gaps = 32/433 (7%)

Query: 115 VYGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPTSVSSFSVGRGLENTLPLEVVRGA 174
 +YGV TGFG + + + + Q A ++H L + S ++G G LP EVVRG

Sbjct: 49 IYGVNTGFGKFENVQIDRS---QLAQLQHNL-----IVSHAIGMG--EPLPAEVVRGM 96

Query: 175 MVIRVNSLTRGHSVRLVLEALTNFLNHRITPIVPLRGSISASGDLSPLSYIAGAITGH 234
 +++R SL+ GHS VR+ V+E L LN P+VP +GS+ ASGDL+PL+++A + G

Sbjct: 97 LLLRAQSLSLGHSGVRVEVELLLALLNADALPVVPSQGSVGASGDLAPLAHLALGLIGL 156

Query: 235 PDVKVHVLHEGTEKIMFAREAI SLFGLEAVVLGPKEGLGLVNGTAVSASMATXXXXXXXXX 294
 D++ ++G ++ A + ++ GL V L KEGL L+NGT + S+

Sbjct: 157 GDIE----YQG--QVRPAADVLAELGLSPVQLQAKEGLALINGTQLMGSLALALHDAQV 210

Query: 295 XXXXXXXXXXXXXVEAMVGQGSFAPFIHDV--CRPHPGQVEVARNIRTLLSGSSFAXXXX 352
 VEA + GS PF DV RPHPG + VA +R L+GS A
 Sbjct: 211 LLGTANLAAAMTVEA---RYGSHRPFQPDVVGLRPHPGALAVAAELREFLAGSEIAPSHL 267

Query: 353 XXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTNDNPLLDVENKQT 412
 QD Y LR PQ G + + A L++E + TDNPL+ E +
 Sbjct: 268 TGDGKV-----QDAYSLRAVPQVHGATWDALAQAEVLAVEFASVTDNPLIFPETGEV 320

Query: 413 AHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCLAEDPSLNYHG 472
 GGNF +++++ ++A+A +G ++ + +LLN A++ GLP+ L + LN
 Sbjct: 321 VSGGNFHGQPLAVTIDALKVAVAEGLSISERRTEQLLNPAALS-GLPAFL-TPNGGLNSGF 378

Query: 473 KGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVNSLALISARRTAEANDVLSLLASH 532
 AA SE L++P + P + S+ +AR+ + + +L+
 Sbjct: 379 MIAQYTSAAALVSENKVLSPASVDSIPTSANQEDHVSMDGAHAARQLRQIVANVQTVLSIE 438

Query: 533 LYCTLQAVDLRAM 545
 L C Q +D + +
 Sbjct: 439 LLCAAQGLDFQQL 451

☐ >gi|28897663|ref|NP_797268.1| ☒ putative histidine ammonia-lyase protein [Vibrio
 RIMD 2210633]
☒ gi|28805876|dbj|BAC59152.1| ☒ putative histidine ammonia-lyase protein [Vibrio pa
 RIMD 2210633]
 Length = 517

Score = 182 bits (462), Expect = 3e-44

Identities = 132/454 (29%), Positives = 217/454 (47%), Gaps = 35/454 (7%)

Query: 95 EIRARVDKSVDFLKAQLQNS--VYGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPPTS 152
 E A++D+ V FL+ L+ +YGVTTG+G S V++ AL++ P
 Sbjct: 37 EFTAKIDRGVAFLELLKEEGVIYGVTTGYGDSC-----TVAIPPALVDE-----LPLH 85

Query: 153 VSSFSVGRGLENLTPLEVVVRGAMVIRVNSLTRGHSVAVRLVVLEALTNFLNHRITPIVPLR 212
 ++ F G GL L E R + R+ SL++G S V +L + +NH I P +P
 Sbjct: 86 LTRFH-GCGLGQILSHEQARAVLATRLCSLSQGVSGVSHDLLNQIVTLINHDIAPRIPQE 144

Query: 213 GSISASGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIMFAEAISLFGLEAVVLGPKEGL 272
 GS+ ASGDL+PLSY+A + G +V L++G + +E + +E + L PKEGL
 Sbjct: 145 GSVGASGDLTPLSYLAATLIGEREV----LYKGD--VRPTQEVFAELDIEPIRLKPKEGL 198

Query: 273 GLVNGTAVSASMATXXXXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQV 332
 L+NGT+V ++A M G F + V +PHPGQ
 Sbjct: 199 ALMNGTSVMTALACLAYKRAEYLAQLCTKITAMVSVGMQGNDFHFDEALFAV-KPHPGQQ 257

Query: 333 EVARNIRTLLSGSSFAXXXXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTL 392
 +VA +R L+ QDRY LR +P +G + + + +
 Sbjct: 258 QVAAWLRDDLNAERPPRNSDRL-----QDRYSLRCAPHVIGMVQDSLPLWLRQLI 306

Query: 393 SLENNTTTNDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAA 452
 E N+ DNP++D +N++ HGG+F ++++M+ ++ +A + L Q +L++
 Sbjct: 307 ENELNSANDNPIIDGDNERNVLHGGHFYGGHIAMAMDTLKVNIANLADLLDRQMAQLMDYK 366

Query: 453 MNRGLPSCLA---AEDPSLNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVNS 509
 N GLP L E +N+ K + I I+A+ +E P + F + E NQ S
 Sbjct: 367 FNNGLPFNLTGAEGERKPINHGFKAVQIGISAWTAEALKNTPASVFSRSTECHNQDKVS 426

Query: 510 LALISARRTAEANDVLSLLLASHLYCTLQAVDLR 543
 + I+AR ++ + A+ L ++QAV++R
 Sbjct: 427 MGTIAARDCLRVLELTEQVAAASLLASVQAVEIR 460

☐ >gi|22959589|ref|ZP_00007239.1| COG2986: Histidine ammonia-lyase [Rhodobacter sp.]
 Length = 507

Score = 182 bits (461), Expect = 4e-44
 Identities = 134/432 (31%), Positives = 197/432 (45%), Gaps = 32/432 (7%)

Query: 115 VYGVTTGFGGSADTRTE--DAVSLQKALIEHQLCGVTPTSVSSFSVGRGLENTLPLEVVR 172
 VYGV TFGG A + D LQ+ LI CGV +P R
 Sbjct: 51 VYGVNTGFGKLASLKIAPADTAQLQRNLILSHCCGVG-----EPMPPSTAR 96

Query: 173 GAMVIRVNSLTRGHSVRLVLEALTNFLNHRITPIVPLRGSISASGDLSPLSYIAGAIT 232
 + +++ SL RG S VR ++ L L +TP++P +GS+ ASGDL+PL+++A +
 Sbjct: 97 LMIALKLLSLGRGASGVRWEIVALLEGMLAAGVTPVIPAQGSVGASGDLAPLAHMAAVMI 156

Query: 233 GHPDVKVHVLHEGTEKIMFAREAIISFLGLEAVLGPKEGLGLVNGTAVSASMATXXXXXX 292
 G + +V G ++ A A++ GL V LGPKEGL L+NGT S + A
 Sbjct: 157 GEGEAEV-----GRRRLPGA-AALAEAGLAPVALGPKEGLALINGTQFSTAYALAGLFEG 210

Query: 293 XXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGSSFAXXXX 352
 +A++G P IH R H GQ+E A +R LL GS+
 Sbjct: 211 WRAAQAALVISALSTDAIMGSTAPLRPEIH-ALRGHAGQIEAAATMRALLEGSAIRESHR 269

Query: 353 XXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTDNPLLDVENKQT 412
 QD Y +R PQ G ++ + A TL+ E N TDNPL+ + + +
 Sbjct: 270 EGDQRV-----QDPYCIRCQPQVTGAAMDVLRLMAAGTLATEANAATDNPLV-LSDGRI 321

Query: 413 AHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCLAEDPSLNYHG 472
 GGNF A V + + LAL+ IG + + +++ ++ LP L E P LN
 Sbjct: 322 VSGGNFHAEPVGFAADMIALALSEIGAIAQRRVALMVDPTLSFDLPPFLTPE-PGLNSGL 380

Query: 473 KGLDIHIAAYASELGHLANPVTTTFVQPAEMGNQAVNSLALISARRTAEANDVLSLLLASH 532
 ++ AA SE H+A P T P + S+A ARR + L+++L +
 Sbjct: 381 MIAEVTTAALMSENKHMAAPTVDSTPTSANQEDHVSMAAHGARRLGRMVENLAVILGTE 440

Query: 533 LYCTLQAVDLRA 544
 C Q V+ RA
 Sbjct: 441 AICAAQGVEFRA 452

☐ >gi|5690433|gb|AAD47085.1| phenylalanine ammonia lyase [Eucalyptus globulus]
 Length = 398

Score = 182 bits (461), Expect = 4e-44
 Identities = 128/365 (35%), Positives = 190/365 (52%), Gaps = 14/365 (3%)

Query: 365 RQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTDNPLLDVENKQTAHGGNFQASAVS 424
 +QDRY LRTSPQ+LGP +E + A + E N+ DNPL+DV + HGGNFQ + +
 Sbjct: 31 KQDRYALRTSPQWLGPQIEVIRAATKMIEREINSVNDNPLIDVARNKALHGGNFQGTPIG 90

Query: 425 ISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCLA-AEDPSLNYHGKGLDIHIAAYA 483
 +SM+ TRLA+A IGKL F Q +EL+N N GLPS L+ +PSL+Y KG +I +A+Y
 Sbjct: 91 VSMDNTRLAIASIGKLMFAQFSELVNDNFYNNGLPSNLSGGRNPSTDYGFKAIEIAMASYC 150

Query: 484 SELGHLANPVTTFVQPAEMGNQAVNSLALISARRTAEANDVLSLLLASHLYCTLQAVDLR 543
 SEL LANPVT VQ AE NQ VNSL LIS+R+TAEA D+L L+ ++ L QA DLR
 Sbjct: 151 SELQFLANPVTNHVQSAEQHNQDVNSLGLISSRKTAEAIDILKLVSSSTFLVGLCQAGDLR 210

Query: 544 AMELDFKKQFDPLLPTLLQQHLGTGLD-----VNALALEVKKALNKRLEQTTTYDLEPRW 598
 +E + K + + ++ L G + + ++ K ++ T D
 Sbjct: 211 HLEENLKSTVKNTVGRVARKVLMVGANGELHPSHYCERDLLKVVDGEHVFTYADDACSAT 270

Query: 599 HDAFSYATGTVVE--LLSSSPSANVTLTAVNAWKVASAEKAIISLTREVRN-RFWQTPSSQ 655
 + +V+ L++ N + + E L ++V R S
 Sbjct: 271 YPLMQKLRLVDQALVNGESELNPSTSIFQKIVAFEEELKAQLPKDVEGVRVQYETGSL 330

Query: 656 APAHAYLSPRTRVLYSFVREELGVQARRGDVFGVQQETIGSNVSRIYEAIKDGRIHVL 715
 A + R+ LY VREELG G+ + + G + +++ AI G++ L
 Sbjct: 331 AIPNQIKECRSYPLYKLVRRELGTALLTGEQVI-----SPGEDFDKVFITAICAGKLIDPL 385

Query: 716 VKMLA 720
 ++ L+
 Sbjct: 386 LECLS 390

☐ >gi|10567350|dbj|BAB16159.1| ☒ riorf40 [Agrobacterium rhizogenes]
☒ gi|10954686|ref|NP_066621.1| ☒ hypothetical protein [Agrobacterium rhizogenes]
☒ gi|14194870|sp|Q9KWE4|HUTH_AGRH ☒ Histidine ammonia-lyase (Histidase)
☒ gi|8918686|dbj|BAA97751.1| ☒ huth gene homolog [Rhizobium rhizogenes]
 Length = 511

Score = 181 bits (460), Expect = 5e-44
 Identities = 129/431 (29%), Positives = 203/431 (47%), Gaps = 32/431 (7%)

Query: 115 VYGVTTGFGGSADTRTE--DAVSLQKALIEHQLCGVTPTSVSSFSVGRGLENTLPLEVVR 172
 VYG+ TGFG A + + D +LQ+ LI CGV LP VVR
 Sbjct: 52 VYGINTGFGKLASIKIDAADLATLQRNLILSHCCGVGAP-----LPENVVR 97

Query: 173 GAMVIRVNSLTRGHSAVRLVLEALTNFLNHRITPIVPLRGSISASGDLSPLSYIAGAIT 232
 M +++ SL RG S VR+ ++ + L + P++P +GS+ ASGDL+PL++++ +
 Sbjct: 98 LIMALKLISLGRGASGVRIELIRLIEGMLEKGVIPVPIPEKGSVGASGDLAPLAHMSATMM 157

Query: 233 GHPDVKVHVLHEGTEKIMFAREAIISLFGLEAVVLGPKEGLGLVNGTAVSASMATXXXXXX 292
 G + ++G + M +++A++ GL VVL KEGL L+NGT S ++A
 Sbjct: 158 GEGE----AFYQGVQ--MPSKDALAKAGLSPVLAAKEGLALINGTQTSTALALAGLFRA 211

Query: 293 XXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQVEVARNIRTLISGSSSFAXXXX 352
 +A +G F P IH + R H GQ++ +R LL GS
 Sbjct: 212 HRAAQSAVLTGALSTDAAMGSSAPFHPDIHTL-RGHKGQIDAGSALRNLLQGSEIRESHI 270

Query: 353 XXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTDNPLLDVENKQT 412
 QD Y +R PQ G ++ + TL +E N TDNPL+ + +
 Sbjct: 271 EGDERV-----QDPYCIRCQPQVDGACLDLLASVARTLEIEANAVTDNPLV-LSDNSV 322

Query: 413 AHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCLAEDPSLNYHG 472
 GGNF A V+ + ++T LA+ IG + + L++ A++ GLP+ L ++ P LN
 Sbjct: 323 VSGGNFHAEPVAFADQ TALAVCEIGAIAQRRIALLVDPALSYGLPAFL-SKKPGLNSGL 381

Query: 473 KGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVNSLALISARRTAEANDVLSLLLASH 532
 ++ AA SE +++P + P + S+A ARR D L +L
 Sbjct: 382 MIAEVTSAALMSENKQMSHPASVDSTPTSANQEDHVSMAHGARRLLAMTDNLFILGIE 441

Query: 533 LYCTLQAVDLR 543
+Q V+LR
Sbjct: 442 ALAAVQGVELR 452

☐ >gi|56461550|ref|YP_156831.1| ☒ Histidine ammonia-lyase [Idiomarina loihiensis I
gi|56180560|gb|AAV83282.1| ☒ Histidine ammonia-lyase [Idiomarina loihiensis L2TR]
Length = 511

Score = 181 bits (459), Expect = 7e-44
Identities = 133/431 (30%), Positives = 209/431 (48%), Gaps = 32/431 (7%)

Query: 115 VYGVTTGFGGSADTRT--EDAVSLQKALIEHQCGVTPTSVSSFSVGRGLENTLPLEVVR 172
VYG+ TGFG A+TR E LQ+ ++ S G + + VVR
Sbjct: 53 VYGINTGFGLLANTRIPPERLTDLQRRIV-----LSHAAGTGDLMEDSVVR 98

Query: 173 GAMVIRVNSLTRGHSVRLVLEALTNFLNHRITPIVPLRGSISASGDLSPLSYIAGAIT 232
+++++NSL+RG S VR V+++AL LN + P +P +GS+ ASGDL+PL+++ +
Sbjct: 99 LMLLLKINSLSRGFSGVRQVLVDALIKLLNAEVYPCIEKGSVGASGDLAPLAHMLVPLV 158

Query: 233 GHPDVKVHVLHEGTEKIMFAREAIISLFGLEAVVLGPKEGLGLVNGTAVSASMATXXXXXX 292
G V+ H G K++ A E + + G+E L PKEGL L+NGT S ++A
Sbjct: 159 GEGTVR----HNG--KVLNAEEGLKIAGIEPFELAPKEGLALLNGTQASTALALAGLFRI 212

Query: 293 XXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGSSFAXXXX 352
VEA +G + F +H V R PGQ++ A +R +L+ SS
Sbjct: 213 ERNFHAAIVGATSVEAAMGSRAPFDERVHAV-RGQPGQIKAAEMLRHVLTDSSEIAKDH 271

Query: 353 XXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTNDNPLLDVENKQT 412
QD Y LR PQ +G +++ + HA L E N TDNPL+ E +
Sbjct: 272 ENCEKV-----QDPYSLRCQPQVMGAVLDQIEHASGILVREANGVTDNPLVFSEEQDI 324

Query: 413 AHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCLAEDPSLNYHG 472
GGNF A V+++ + +A + IG L+ + L+++ +++ LP+ L D +N
Sbjct: 325 ISGGNFHAEPVAMAADILATAASEIGALSERRSALLIDSHLSK-LPAFL-VNDGGVNSGF 382

Query: 473 KGLDIHIAAYASELGHLANPVTTTFVQPAEMGNQAVNSLALISARRTAEANDVLSLLASH 532
+ AA ASE LA+P + P + S+A +ARR + +S ++A
Sbjct: 383 MLAQVTAALASENKTLAHPASVDSLPTSANQEDHVSMTFAARRLTDIAKNVSDIIAIE 442

Query: 533 LYCTLQAVDLR 543
Q +D R
Sbjct: 443 WLEAAQGLDFR 453

☐ >gi|34101636|gb|AAQ58004.1| ☒ histidine ammonia-lyase [Chromobacterium violaceum
gi|34495780|ref|NP_899995.1| ☒ histidine ammonia-lyase [Chromobacterium violaceum
Length = 510

Score = 181 bits (458), Expect = 9e-44
Identities = 137/458 (29%), Positives = 212/458 (46%), Gaps = 35/458 (7%)

Query: 91 QNDDEIRARVDKSVDFLKAQLQN--SVYGVTTGFGGSADTRT--EDAVSLQKALIEHQLC 146
Q D A +D S + L +VYG+ TGFG A T+ E+ LQ++++
Sbjct: 28 QLDPSSHAAIDASAATVARVLSEGRTVYGINTGFGLLASTKIAPEEELLLQRSIVLSHAA 87

Query: 147 GVTPTSVSSFSVGRGLENLTPLEVVIRGAMVIRVNSLTRGHSAVRLVVLEALTNFLNHRIT 206
 G+ G +++++ VR M +++NSL RG S +R V+EAL N +I
 Sbjct: 88 GI-----GAPMDDS-----TVRLVMALKINSLARGFSGIRRQVIEALVTLFNRQIY 133

Query: 207 PIVPLRGSISASGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEAVVL 266
 P++P +GS+ ASGDL+PLS+++ + G + V + + A+ GLE + L
 Sbjct: 134 PVIPQKGSVGASGDLAPLSHMSAVLIGEAEFVDGVR-----VPGSVAMRSAGLEPITL 187

Query: 267 GPKEGLGLVNGTAVSASMATXXXXXXXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCR 326
 PKEGL L+NGT S + A VEA +G + F IH+V R
 Sbjct: 188 APKEGLALLNGTQASTAFALEGLFAAEDLYVSATVAGSLSVEAALGSRTPFDFARIHEV-R 246

Query: 327 PHPGQVEVARNIRTLLSGSSFAXXXXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMM 386
 H GQ++ AR R LL+ S QD Y LR PQ +G + +
 Sbjct: 247 GHQGGIDAARLYRDLLAHSQIEQSHENCGKV-----QDPYSLRCQPQVMGACLTQIR 298

Query: 387 HAYSTLSLENNTTTDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCT 446
 A L +E N+ +DNPL+ + GGNF A V+ + + LA+A IG L+ +
 Sbjct: 299 QAAEVL RVEANSVSDNPLVFAGDNDILSGGNFHAEPVAFADNLALAI AEIGSLSERMA 358

Query: 447 ELLNAAMNRGLPSCLA AEDPSLN YHGKGLDIHIAAYASELGHLANPVTTTFVQPAEMGNQA 506
 L+++ +++ LP L + +N + AA ASE LA+P + P +
 Sbjct: 359 LLIDSNL SK-LPPFL-VNNGGVNSGFMIAQVTS AALASENKS LAHPASVDSLPTSANQED 416

Query: 507 VNSLALISARRTAEANDVLSLLLASHLYCTLQAVDLRA 544
 S+A + RR + + +LA L Q +D RA
 Sbjct: 417 HVSMATFAGRRRLRDMAGNTAGILAVELLAACQGIDFRA 454

☐ >gi|37527077|ref|NP_930421.1| ☒ Histidine ammonia-lyase (histidase) [Photorhabdus
 subsp. laumondii T101]
☒ gi|36786510|emb|CAE15566.1| ☒ Histidine ammonia-lyase (histidase) [Photorhabdus l
 subsp. laumondii T101]
 Length = 514

Score = 181 bits (458), Expect = 9e-44

Identities = 139/455 (30%), Positives = 220/455 (48%), Gaps = 34/455 (7%)

Query: 93 DDEIRARVDKSVDFLKAQL--QNSVYGVTTGFGGSADTRTED--AVSLQKALIEHQLCGV 148
 D +I +++SV+ + A L + YG+ TGFG A TR E+ LQ++L+ GV
 Sbjct: 29 DSQIFPAIERSVECVNAILAENRTAYGINTGFGLLASTRIEEDNLEKLQSLVSHAAGV 88

Query: 149 TPTS SVSSFSVGRGLENLTPLEVVIRGAMVIRVNSLTRGHSAVRLVVLEALTNFLNHRITPI 208
 G+ L++ + R MV+++NSL+RG+S +RL V++AL +N I P
 Sbjct: 89 -----GKALDDNM-----TRLIMVLKINSLSRGYSGIRLAVIQALIALVNAEIYPH 134

Query: 209 VPLRGSISASGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEAVVLGP 268
 +P +GS+ ASGDL+PL++++ + G + ++G + + A+EA++ L+ + L
 Sbjct: 135 IPCKGSVGASGDLAPLAHMSLLLLGEGQAR----YQG--EWLPAKEALAKANLQIPITLAA 188

Query: 269 KEGLGLVNGTAVSASMATXXXXXXXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPH 328
 KEGL L+NGT VS + A VEA +G + F +H V R
 Sbjct: 189 KEGLALLNGTQVSTAFALRGLFEAEDLLAAIIVCGSLSVEAALGSRKPFDFARVH-VVRGQ 247

Query: 329 PGQVEVARNIRTLLSGSSFAXXXXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHA 388
 GQ++VA R +L SS QD Y LR PQ +G + + HA
 Sbjct: 248 QGQIDVAALYRHVLEESSELSDSHINCPKV-----QDPYSLRCQPQVMGACLTQLRHA 300

Query: 389 YSTLSLENNTTTNDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTEL 448
 + E N +DNPL+ E + GGNF A V+++ + L LA IG L+ + L
 Sbjct: 301 ADVILTEANAVSDNPLVFAEQGEVISGGNFHAEPVAMASDNLALVLAIEIGALSERRIAL 360

Query: 449 LNAAMNRGLPSCLAEDPSLNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVN 508
 +++ M++ LP L E+ +N + AA ASE LA+P + P +
 Sbjct: 361 MDSHMSQ-LPPFL-VENGGVNSGFMIAQVTAALASENKALAHPASVDSLPTSANQEDHV 418

Query: 509 SLALISARRTAEANDVLSLLLASHLYCTLQAVDLR 543
 S+A + RR E + +LA Q +D R
 Sbjct: 419 SMAPAAGRRLWEMAENTRGILAEWLSACQGIDFR 453

☐ >gi|59711459|ref|YP_204235.1| **G** histidine ammonia-lyase [Vibrio fischeri ES114]
 gi|59479560|gb|AAW85347.1| **G** histidine ammonia-lyase [Vibrio fischeri ES114]
 Length = 511

Score = 181 bits (458), Expect = 9e-44

Identities = 129/457 (28%), Positives = 216/457 (47%), Gaps = 35/457 (7%)

Query: 92 NDDEIRARVDKSVDFLKAQLQNS--VYGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVT 149
 N DE A++D+ V+FL+ L+ +YGVTTG+G S V++ L++
 Sbjct: 31 NSDEFTAKIDRGVEFLERLLKEEGVIYGVTTGYGDSC-----TVAIPMDLVDE-----L 79

Query: 150 PTSVSSFSVGRGLENLPLEVVRGAMVIRVNSLTRGHSVAVRLVLEALTNFLNHRITPIV 209
 P ++ F G GL L + R + R+ SL++G S V +L + +NH ++P +
 Sbjct: 80 PLHLTRFH-GCGLGENLDEQQARAVLATRLCSLSQGVSGVTHDLLNQIVTLINHGVS PRI 138

Query: 210 PLRGSISASGDLSPSYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEAVVLGPK 269
 P GS+ ASGDL+PLSY+A A+ G +V +++G +I + + + L PK
 Sbjct: 139 PQEGSVGASGDLTPLSYLAAALIGEREV----IYKG--EIRATADVFKELNITPIKLPK 192

Query: 270 EGLGLVNGTAVSASMATXXXXXXXXXXXXXXXXXXXXVEAMVGQQGSFAPFIHDVCRPHP 329
 EGL L+NGT+V ++A M G F + V +PHP
 Sbjct: 193 EGLALMNGTSVMTALACLAYKRAEYLAQMATKITAMVSVGMQGNDFHFDEALFAV-KPHP 251

Query: 330 GQVEVARNIRTLLSGSSFAXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAY 389
 GQ ++A +R+ L + QDRY LR +P +G L + +
 Sbjct: 252 GQQQIAAWLRSDLHNETPPRNSDRL-----QDRYSLRCAPHVIGVLQDSLPLFLR 300

Query: 390 STLSLENNTTTNDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELL 449
 + E N+ DNP++D +N++ HGG+F ++++M+ + A+A I L Q +L+
 Sbjct: 301 QMIENELNSANDNPIIDGDNERVHGGHFYGGHIAMAMDMLKTAVANIADLLDRQMAQLM 360

Query: 450 NAAMNRGLPSCLAEDPS---LNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQA 506
 + N GLP L + +N+ K + I I+A+ +E P + F + E NQ
 Sbjct: 361 DYKFNNGLPFNLTGSTGARKPINHGFKAVQIGISAWTAEALKGTMPSVFSRSTECHNQD 420

Query: 507 VNSLALISARRTAEANDVLSLLLASHLYCTLQAVDLR 543
 S+ I++R + + ++ L QA+ LR
 Sbjct: 421 KVSMGTIASRDCLRVLQLTEQVTSASLLAATQALVLR 457

☐ >gi|23106296|ref|ZP_00092750.1| COG2986: Histidine ammonia-lyase [Azotobacter vi
 Length = 509

Score = 181 bits (458), Expect = 9e-44

Identities = 144/458 (31%), Positives = 213/458 (46%), Gaps = 39/458 (8%)

Query: 93 DDEIRARVDKSVDFLKAQL--QNSVYGVTTGFGGSADTR--TEDAVSLQKALIEHQLCGV 148
 D R V+ S + A L Q +VYG+ TGFG A T E +LQ+ L+ G
 Sbjct: 30 DPACRTGVEASARSVAAILASQRTVYGINTGFGLLARTSIPAESLTALQRNLVLSHCTG- 88

Query: 149 TPTSVSSFSVGRGLENTLPLEVVRGAMVIRVNSLTRGHSVRLVLEALTNFLNHRITPI 208
 T + SVG + +++ SL RGHS V ++EAL R+ P
 Sbjct: 89 TGALLDDASVGL-----ILALKIASLARGHSGVGWALIEALLRLYRARVYPC 135

Query: 209 VPLRGSISASGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEAVVLGP 268
 +P +GS+ ASGDL+PL+++A + G V+ H G ++ A E ++L GLE + LGP
 Sbjct: 136 IPSQGSVGASGDLAPLAHLAATLLGIGQVR----HRG--HLLAGEGLALAGLEPLTLGP 189

Query: 269 KEGLGLVNGTAVSASMATXXXXXXXXXXXXXXXXXXVEAMVGQQGSFAPFIHDV--CR 326
 KEGL L+NGT VS ++A EA+ +GSF PF + R
 Sbjct: 190 KEGLALLNGTQVSTALALRGLFAAERLFGAAVAGSLSTEAL---KGSFVPFDTRIQA VR 246

Query: 327 PHPGQVEVARNIRTLTLLSGSSFAXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMM 386
 PGQ+ VA R LL S+ QD Y LR PQ +G ++ +
 Sbjct: 247 GQPGQIAVAALYRELLHDSAINRSHARCVR-----QDPYSLRCQPQVMGACLDHLR 298

Query: 387 HAYSTLSLENNTTTNDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCT 446
 A E N +DNPL+ ++ + GGNF A V+++ + LA+A IG L+ +
 Sbjct: 299 FAAGVFLREANAVSDNPLVFADDAEVLSGGNFHAEPVAMAADALALAEIGALSERRIA 358

Query: 447 ELLNAAMNRGLPSCLAAEDPSLNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQA 506
 L++ A++ GLP+ L E LN + A+ ASE LA+P + P G +
 Sbjct: 359 LLIDPALS-GLPAFLVKEG-GLNSGFMIAQVTAASLASENKTLAHPASVDSLPTSAGQED 416

Query: 507 VNSLALISARRTAEANDVLSLLLASHLYCTLQAVDLRA 544
 S+A +ARR + + ++ L Q VD A
 Sbjct: 417 HVSMATFAARRLQDMAGNAAGVVGIELLAAAQGVDFHA 454

☐ >gi|45916326|ref|ZP_00197437.1| COG2986: Histidine ammonia-lyase [Mesorhizobium]
 Length = 511

Score = 180 bits (457), Expect = 1e-43

Identities = 133/432 (30%), Positives = 201/432 (46%), Gaps = 32/432 (7%)

Query: 115 VYGVTTGFGGSADTRTE--DAVSLQKALIEHQLCGVTPPTSVSSFSVGRGLENTLPLEVVR 172
 VYG+ TGFG A + + D +LQ+ L+ CGV LP VVR
 Sbjct: 52 VYGINTGFGKLASIKIDSADVAALQRNLVLSHCCGVG-----EALPENVVR 97

Query: 173 GAMVIRVNSLTRGHSVRLVLEALTNFLNHRITPIVPLRGSISASGDLSPLSYIAGAIT 232
 M +++ SL RG S VRL ++ + L + P++P +GS+ ASGDL+PL+++A +
 Sbjct: 98 LMMALKLVSLGRGASGVRLLELVRLIEAMLARGVIPVIPEKGSVGASGDLAPLAHMAAVMM 157

Query: 233 GHPDVKVHVLHEGTEKIMFAREAISLFGLEAVVLGPKEGLGLVNGTAVSASMATXXXXXX 292
 GH + G E++ A A+ GL+ V L KEGL L+NGT S ++A
 Sbjct: 158 GHGEA-----FFGGERLNGA-TALLKAGLQPVELAAKEGLALINGTQTSTALALAGLFRA 211

Query: 293 XXXXXXXXXXXXXXXXVEAMVGQQGSFAPFIHDVCRPHPGQVEVARNIRTLTLLSGSSFAXXXX 352
 +A +G F P IH + R H GQ++ A +R LL S
 Sbjct: 212 HRAAQSAITGAMSTDAAMGSSAPFHPEIHTL-RGHRGQIDTAEALRALLENSPIRQSHI 270

Query: 353 XXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTNDNPLLDVENKQT 412
 QD Y +R PQ G ++ + TL +E N TDNPL+ +N

Sbjct: 271 EGDERV-----QDPYCIRCQPQVDGACLDLLRSVARTLEIEANAVTDNPLVLSDNSVV 323

Query: 413 AHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCLAEDPSLNYHG 472
A GGNF A V+ + ++ LA+ IG + + L++ A++ GLP+ L A+ P LN

Sbjct: 324 A-GGNFHAEPVAFADQIVLAICEIGAIAQRRIALLVDPALSYGLPAFL-AKKPGLNSGL 381

Query: 473 KGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVNSLALISARRTAEANDVLSLLASH 532
++ AA SE +++P + P + S+A ARR + L ++

Sbjct: 382 MIAEVTSAALMSENKQMSHPASVDSTPTSANQEDHVSMAHGARRLLPMTENLFAIGIE 441

Query: 533 LYCTLQAVDLRA 544
C Q V+LRA

Sbjct: 442 ALCAAQGVLELRA 453

☐ >gi|59713633|ref|YP_206408.1| ☒ histidine ammonia-lyase [Vibrio fischeri ES114]
gi|59481881|gb|AAW87520.1| ☒ histidine ammonia-lyase [Vibrio fischeri ES114]
Length = 510

Score = 180 bits (456), Expect = 2e-43

Identities = 126/433 (29%), Positives = 213/433 (49%), Gaps = 32/433 (7%)

Query: 114 SVYGVTTGFGGSADTRT--EDAVSLQKALIEHQLCGVTPTSVSFSVGRGLENTLPLEVV 171
+VYG+ TGFG A+TR +D +LQ++++ G+ G +++ V

Sbjct: 52 TVYGIN TGFGLLANTRIAEKDLETLQRSIVLSHAAGI-----GEFMDDA----TV 97

Query: 172 RGAMVIRVNSLTRGHSVAVRLVVLEALTNFLNHRITPIVPLRGSISASGDLSPLSYIAGAI 231
R MV+++NSL RG+S +R +V++AL +N + P +P +GS+ ASGDL+PL++++ +

Sbjct: 98 RLMMVLKINSLARGYS GIRPLVIDALIQLVNSEVYPCIPKKGSVGASGDLAPLAHMSTVL 157

Query: 232 TGHDPVKVHVLHEGTEKIMFAREAISLFGLEAVVLGPKEGLGLVNGTAVSASMATXXXXX 291
G + + +++ + A+ + GL + L PKEGL L+NGT S + A

Sbjct: 158 LGEGEARYR-----GEVITGKTALEIAGLTPITLAPKEGLALLNGTQASTAFLEGLFA 211

Query: 292 XXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGSSFAXXX 351
VEA +G + F P IH V R H Q++ A R LL+ SS

Sbjct: 212 AEDLYASATVCGAMSVEAALGSRKPFDPRIHRV-RGHRSQMDAALAYRHLLAQSSDIGLS 270

Query: 352 XXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTDNPLLDVENKQ 411
QD Y LR PQ +G ++ + ++ L +E N+ +DNPL+ ++

Sbjct: 271 HQCCERV-----QDPYSLRCQPQVMGACLQQIRNSADILEIEANSVSDNPLVFADDGD 323

Query: 412 TAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCLAEDPSLNYH 471
GGNF A V+++ + LA++ IG L+ + L+++ +++ LP L ++ +N

Sbjct: 324 IISGGNFHAEPVAMAADNLALAISEIGSLSERRMALLIDSGLSK-LPPFL-VDNGGVNSG 381

Query: 472 GKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVNSLALISARRTAEANDVLSLLLAS 531
+ AA ASE LA+P + P + S+A + RR + + +LA

Sbjct: 382 FMIAQVTAAALASENKT LAHPASIDSLPTSANQEDHVSMAHFAGRRLGDMAENTRGILAV 441

Query: 532 HLYCTLQAVDLRA 544
L Q +D RA

Sbjct: 442 ELLAAQGLDFRA 454

☐ >gi|62321196|dbj|BAD94354.1| phenylalanine ammonia lyase [Arabidopsis thaliana]
Length = 357

Score = 179 bits (455), Expect = 2e-43

Identities = 125/354 (35%), Positives = 189/354 (53%), Gaps = 20/354 (5%)

Query: 378 LGPLVEDMMHAYSTLSLENNTTTDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALI 437
 LGP +E + +A ++ E N+ DNPL+DV + HGGNFQ + + +SM+ TRLA+A I
 Sbjct: 1 LGPQIEVIRYATKSIEREINSVNDNPLIDVSRNKAIHGGNFQGTPIGVSMDNTRLAIAAI 60


Query: 438 GKLNFTQCTELLNAAMNRGLPSCL-AAEDPSLNYHGKGLDIHIAAYASELGHLANPVVTF 496
 GKL F Q +EL+N N GLPS L A+ +PSL+Y KG +I +A+Y SEL +LANPVT+
 Sbjct: 61 GKLMFAQFSELVNDNFYNNGLPSNLTASRNPSLDYGFKGAEIAMASYCSELQYLANPVTSH 120

Query: 497 VQPAEMGNQAVNSLALISARRTAEANDVLSLLLASHLYCTLQAVDLRAMELDFKKQFDPL 556
 VQ AE NQ VNSL LIS+R+T+EA D+L L+ + L QAVDLR +E + ++
 Sbjct: 121 VQSAEQHNQDVNSLGLISSRKTSEAVDILKLMSTTFLVAICQAVDLRHLEENLRQTVKNT 180

Query: 557 LPTLLQQHLGTGLDVNALALEVKKALNKRL-----EQTTTYDLEP--RWHDAFSYATGT 608
 + + ++ L TG++ L + K L EQ TY +P +
 Sbjct: 181 VSQVAKKVLTTGVNGE---LHPSRFCEKDLLKVVDREQVYTYADDPCSATYPLIQKLRQV 237

Query: 609 VVE--LLSSSPSANVTLTAVNAWKVASAEKAIISLTREVR-NRFWQTPSSQAPAHAYLSPR 665
 +V+ L++ N + + E L +EV R + A + R
 Sbjct: 238 IVDHALINGESEKNAVTSIFHKIGAFEEELKAVLPKEVEAARAAYDNGTSAIPNRIKECR 297

Query: 666 TRVLYSFVREELGVQARRGDVFGVQQETIGSNVSRIYEAIKDGRINHVLVKML 719
 + LY FVREELG ++ G + + G +++ AI +G+I +++ L
 Sbjct: 298 SYPLYRFVREELGT-----ELLTGEKVTSPGEEFDKVFTAICEGKIIDPMMECL 346

 >gi|46322661|ref|ZP_00223029.1| COG2986: Histidine ammonia-lyase [Burkholderia c
 Length = 507

Score = 179 bits (455), Expect = 2e-43

Identities = 136/432 (31%), Positives = 201/432 (46%), Gaps = 35/432 (8%)

Query: 116 YGVTTGFGGSADTRT--EDAVSLQKALIEHQLCGV-TPTSVSFSVGRGLENTLPLEVVR 172
 YG+ TGFG A T + LQK L+ GV P + SS VR
 Sbjct: 52 YGINTGFGRLASTHIPHDQLELLQKNLVLHAVGVGEPMARSS-----VR 96

Query: 173 GAMVIRVNSLTRGHSAVRLVVLEALTNFLNHRITPIVPLRGSISASGDLSPLSYIAGAIT 232
 M ++++SL RGHS +R V++AL N + P++P++GS+ ASGDL+PL++++ +
 Sbjct: 97 LLMALKLSSLGRGHSGIRREVM DALITL FNADVLPLIPVKGSVGASGDLAPLAHMSAVLL 156

Query: 233 GHPDVKVHVLHEGTEKIMFAREAI SLFGLEAVVLGPKEGLGLVNGTAVSASMATXXXXXX 292
 G +V + + A + + + GL + L KEGL L+NGT S ++A
 Sbjct: 157 GVGEVFIR-----GERASALDGLRVAGLAPLTLQAKEGLALLNGTQASTALALDNMFAI 210

Query: 293 XXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGSSFAXXXX 352
 V+A G F IH++ R H GQ++ A + R LL GS
 Sbjct: 211 EDLYRTALVAGALSVDAAGSVKPF DARIHEL-RGHRGQIDAAASYRELLEGSPINQSHR 269

Query: 353 XXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTDNPLLDVENKQT 412
 QD Y LR PQ +G ++ M HA L +E N +DNPL+ + +
 Sbjct: 270 DCDKV-----QDPYSLRCQPQVMGACLDQMRHAADVLLVEANAVSDNPLIFPDTEGEV 321

Query: 413 AHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCLAAEDPSLNYHG 472
 GGNF A V+ + + LA A IG L + L++A ++ GLP L D +N
 Sbjct: 322 LSGGNFHAEPVAFADNLALAAAEIGALAERRIALLLIDATLS-GLPPFL-VRDGGVNSGF 379

Query: 473 KGLDIHIAAYASELGHLANPVTTTFVQPAEMGNQAVNSLALISARRTAEANDVLSLLASH 532
 + AA ASE LA+P + P + S+A +AR+ A+ D +LA
 Sbjct: 380 MIAHVTAALASENKTLAHPASVDSLPTSANQEDHVSMTAFAARKLADIADNTKHILAIE 439

Query: 533 LYCTLQAVDLRA 544
 L Q VDLRA
 Sbjct: 440 LLAAAQGVDLRA 451

☐ >gi|16264579|ref|NP_437371.1| **G** putative histidine ammonia-lyase histidase prot
 meliloti 1021]
 gi|25292171|pir|G95945 probable histidine ammonia-lyase (EC 4.3.1.3) [imported]
 Sinorhizobium meliloti (strain 1021) magaplasmid pSymb
 gi|17380365|sp|O31197|HUTH_RHIME Histidine ammonia-lyase (Histidase)
 gi|15140717|emb|CAC49231.1| **G** putative histidine ammonia-lyase histidase protein
 meliloti 1021]
 Length = 511

Score = 179 bits (454), Expect = 3e-43
 Identities = 128/432 (29%), Positives = 203/432 (46%), Gaps = 32/432 (7%)

Query: 115 VYGVTTGFGGSADTRTE--DAVSLQKALIEHQLCGVTPTSVSSFSVGRGLENTLPLEVVR 172
 VYG+ TGFG A + + D +LQ+ LI CGV L ++VR
 Sbjct: 52 VYGINTGFGKLASIKIDSSDVATLQRNLILSHCCGVG-----QPLTEDIVR 97

Query: 173 GAMVIRVNSLTRGHSVRLVLEALTNFLNHRITPIVPLRGSISASGDLSPLSYIAGAIT 232
 M +++ SL RG S VRL ++ + L+ + P++P +GS+ ASGDL+PL+++A +
 Sbjct: 98 LIMALKLISLGRGASGVRLLEVLRIEAMLDKGVIPLIPEKGSVGASGDLAPLAHMAAVMM 157

Query: 233 GHPDVKVHVLHEGTEKIMFAREAISLFGLEAVVLGPKEGLGLVNGTAVSASMATXXXXXX 292
 GH + + M A+ GL V L KEGL L+NGT VS ++A
 Sbjct: 158 GHGEAFF-----AGERMKGDAALKAAGLSPVTLAAKEGLALINGTQVSTALALAGLFRA 211

Query: 293 XXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGSSFAXXXX 352
 +A +G F P IH + R H GQ++ A +R LL+GS
 Sbjct: 212 HRAGQAALITGALSTDAAMGSSAPFHPDIHTL-RGHKGQIDTAAALRQLLTGSPIRQSHI 270

Query: 353 XXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTDNPLLDVENKQT 412
 QD Y +R PQ G ++ + +TL++E N TDNPL+ + +
 Sbjct: 271 EGDERV-----QDPYCIRCQPQVDGACLDLLRSVAATLTIEANAVTDNPLV-LSDNSV 322

Query: 413 AHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCLAAEDPSLNYHG 472
 GGNF A V+ + ++ LA+ IG ++ + L++ A++ GLP+ L A+ P LN
 Sbjct: 323 VSGGNFHAEPVAFADQIALAVCEIGAISQRRIALLVDPALSYGLPAFL-AKKPGLNSGL 381

Query: 473 KGLDIHIAAYASELGHLANPVTTTFVQPAEMGNQAVNSLALISARRTAEANDVLSLLASH 532
 ++ AA SE L++P + P + S+A ARR + + L ++
 Sbjct: 382 MIAEVTSALMSENKQLSHPASVDSTPTSANQEDHVSMAHGARRLLQMTENLFSIIGIE 441

Query: 533 LYCTLQAVDLRA 544
 +Q ++ RA
 Sbjct: 442 ALAAVQGIEFRA 453

☐ >gi|46311453|ref|ZP_00212059.1| COG2986: Histidine ammonia-lyase [Burkholderia c
 Length = 507

Score = 179 bits (454), Expect = 3e-43

Identities = 135/432 (31%), Positives = 202/432 (46%), Gaps = 35/432 (8%)

Query: 116 YGVTTGFGGSADTRT--EDAVSLQKALIEHQLCGV-TPTS SVSSFSVGRGLENLTPLEVVR 172
 YG+ TGFG A T + LQK L+ GV P + SS VR

Sbjct: 52 YGINTGFGRLASTHIPHDQLELLQKNLVLHAVGVGEPMARSS-----VR 96

Query: 173 GAMVIRVNSLTRGHSVRLVLEALTNFLNHRITPIVPLRGSISASGDLSPLSYIAGAIT 232
 M ++++SL RGHS +R V++AL N + P++P++GS+ ASGDL+PL++++ +

Sbjct: 97 LLMALKLSSLGRGHSGRIRREVM DALIKLFNADVLPLIPVKGSVGASGDLAPLAHMSAVLL 156

Query: 233 GHPDVKVHVLHEGTEKIMFAREAI SLFGLEAVVLGPKEGLGLVNGTAVSASMATXXXXXX 292
 G +V + + A + + + GL + L KEGL L+NGT S ++A

Sbjct: 157 GVGEVFIR-----GERASALDGLRVAGLAPLTLQAKEGLALLNGTQASTALALDNMF SI 210

Query: 293 XXXXXXXXXXXXXXXXVEAMVGQQGSFAPFIH DVC RPHPGQVEVARNIRTL LSGSSFAXXXX 352
 V+A G F IH++ R H GQ++ A + R LL+GS

Sbjct: 211 EDLYRTALVAGALSVDAAAGSVKPF DARIHEL-RGHQGQIDAAA SYRDL LAGSPINQSHL 269

Query: 353 XXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTT DNPLLDVENKQT 412
 QD Y LR PQ +G ++ M HA L +E N +DNPL+ + +

Sbjct: 270 DCDKV-----QDPYSLRCQPQVMGACLDQMRHAADVLLVEANAVSDNPLIFPDTGEV 321

Query: 413 AHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSC LAEEDPSLNYHG 472
 GGNF A V+ + + LA + IG L + L++A ++ GLP L D +N

Sbjct: 322 LSGGNFHAEPVAFADNLALAA SEIGALAERRIAL LIDATLS-GLPPFL-VRDGGVNSGF 379

Query: 473 KGLDIHIAAYASELGH LANPVTTTFVQPAEMGNQAVNSLALISARRTAEANDVLSLL LASH 532
 + AA ASE LA+P + P + S+A +AR+ A+ D +LA

Sbjct: 380 MIAHVTAALASENKT LAHPASVDSLPTSANQEDHVS MATFAARKLADIADNTKHILAIE 439

Query: 533 LYCTLQAVDLRA 544
 L Q VDLRA

Sbjct: 440 LLAAAQGVDLRA 451

☐ >gi|28872387|ref|NP_795006.1| ☒ histidine ammonia-lyase [Pseudomonas syringae pv DC3000]

gi|28855642|gb|AA058701.1| ☒ histidine ammonia-lyase [Pseudomonas syringae pv. to DC3000]

gi|38257948|sp|Q87UM1|HUTH_PSESM Histidine ammonia-lyase (Histidase)
 Length = 515

Score = 179 bits (453), Expect = 4e-43

Identities = 140/455 (30%), Positives = 221/455 (48%), Gaps = 34/455 (7%)

Query: 93 DDEIRARVDKSVDFLKAQL--QNSVYGVTTGFGGSADTR--TEDAVSLQKALIEHQLCGV 148
 D ++D SV ++ L + YG+ TGFG A TR +ED +LQ++L+ GV

Sbjct: 34 DSSANQQIDDSVACVERILAENRTAYGINTGFGLLASTRIASEDLNLQRSVLVSHAAGV 93

Query: 149 TPTS SVSSFSVGRGLENLTPLEVVRGAMVIRVNSLTRGHSVRLVLEALTNFLNHRITPI 208
 G+ + + L VR MV++VNSL+RG S +R VV++AL +N + P

Sbjct: 94 -----GQPISDDL-----VRLIMVLKVNLSRGSFSGIRRVVIDALIALINAEVYPH 139

Query: 209 VPLRGSISASGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIMFAREAI SLFGLEAVVLGP 268
 +PL+GS+ ASGDL+PL++++ + G + H+G + + A +A+++ GL+ + L

Sbjct: 140 IPLKGSVGASGDLAPLAHMSLVLLGEGKAR----HKG--EWLNAVDALAVAGLKPLTLAA 193

Query: 269 KEGGLGVNGTAVSASMATXXXXXXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPH 328
 KEGL L+NGT VS + A VEA++G + F IH R
 Sbjct: 194 KEGLALLNGTQVSTAYALRGLFEGEDLFAAALTTCGSLTVEAVLGSRSFPDARIH-AARGQ 252

Query: 329 PGQVEVARNIRTLLSGSSFAXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHA 388
 GQ++ A R LL SS QD Y LR PQ +G + + A
 Sbjct: 253 RGQIDAAACYRELLGESSGVSESHRNCDKV-----QDPYSLRCQPQVMGACLTQLRQA 305

Query: 389 YSTLSLENNTTTDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTEL 448
 L +E+N +DNPL+ GGNF A V+++ + LA+A IG L+ + + +
 Sbjct: 306 AEVLEVESNAVSDNPLVFAAENDVISGGNFHAEPVAMAADNLALAEIGSLSERRISLM 365

Query: 449 LNAAMNRGLPSCLAEDPSLNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVN 508
 ++ M++ LP L A + +N + AA ASE LA+P + P +
 Sbjct: 366 MDKHSQ-LPPFLVA-NGGVNSGFMIAQVTAALASENKALAHPHSVDSLPTSANQEDHV 423

Query: 509 SLALISARRTAEANDVLSLLLASHLYCTLQAVDLR 543
 S+A + +R E + + +LA Q +DLR
 Sbjct: 424 SMAPAAGKRLWEMAENVRGILAVEWLAACQGLDLR 458

☐ >gi|53762102|ref|ZP_00350913.1| COG2986: Histidine ammonia-lyase [Ralstonia eutropha]
 Length = 522

Score = 179 bits (453), Expect = 4e-43

Identities = 138/455 (30%), Positives = 221/455 (48%), Gaps = 34/455 (7%)

Query: 93 DDEIRARVDKSVDFLKAQLQN--SVYGVTTGFGGSADTRT--EDAVSLQKALIEHQLCGV 148
 D+ A +D+SV +++ + + YG+ TGFG A TR ED SLQ++L+ GV
 Sbjct: 41 DERAFAAIDQSVACVESVISEGRTAYGINTGFGLLAQTRIAREDLQSLVLSHAAGV 100

Query: 149 TPTSVSFSVSGRGLENTLPLEVVRGAMVIRVNSLTRGHSVRLVLEALTNFLNHRITPI 208
 G +++ L VR MV+++NSL RG S +R V++ALT +N + P
 Sbjct: 101 -----GEPIDDAL----VRLIMVLKINSLARGLSGIRRKVIDALTTLVNAAEVYPR 146

Query: 209 VPLRGSISASGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEAVVLGP 268
 +PL+GS+ ASGDL+PL++++ + G + + + AREA++L L+ + L
 Sbjct: 147 IPLKGSVGASGDLAPLAHMSLLLLGEGQARYR-----GEWLPAREALALADLQPLTLAA 200

Query: 269 KEGGLGVNGTAVSASMATXXXXXXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPH 328
 KEGL L+NGT VS + A VEA +G + F P IH R
 Sbjct: 201 KEGLALLNGTQVSTAYALQGLFQAEDLFAAASVCGALTVEASLGSRAPFDPRIH-AARGQ 259

Query: 329 PGQVEVARNIRTLLSGSSFAXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHA 388
 GQ++ A R LL +S QD Y LR PQ +G + + +A
 Sbjct: 260 RGQIDSAAVYRHLLGPTSEVGQSHASCEKV-----QDPYSLRCQPQVMGACLTQIRNA 312

Query: 389 YSTLSLENNTTTDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTEL 448
 L++E N+ +DNPL+ + GGNF A V+++ + LALA IG L+ + + +
 Sbjct: 313 ADVLAVEANSVSDNPLVFAQEGDIISGGNFHAEPVAMAADNLALALAEIGALSERRISLM 372

Query: 449 LNAAMNRGLPSCLAEDPSLNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVN 508
 ++ M++ LP+ L A + +N + AA AS+ LA+P + P +
 Sbjct: 373 MDKHSQ-LPAFLVA-NGGVNSGFMIAQVTAALASDNKALAHPASVDSLPTSANQEDHV 430

Query: 509 SLALISARRTAEANDVLSLLLASHLYCTLQAVDLR 543
 S+A + +R E + ++A Q +D R
 Sbjct: 431 SMAPNAGKRLWEMASNVKGIIEWLAACQGLDFR 465

☐ >gi|51598141|ref|YP_072332.1| ☒ G histidine ammonia-lyase [Yersinia pseudotubercu]
gi|51591423|emb|CAH23089.1| ☒ G histidine ammonia-lyase [Yersinia pseudotuberculosi
Length = 510

Score = 178 bits (451), Expect = 6e-43

Identities = 139/455 (30%), Positives = 219/455 (48%), Gaps = 34/455 (7%)

Query: 93 DDEIRARVDKSVDFLKAQL--QNSVYGVTTGFGGSADTR--TEDAVSLQKALIEHQLCGV 148
D+ + +SVD ++A L Q + YG+ TGFG A TR TED +LQ++++ GV
Sbjct: 29 DESAYVPIQQSVDCVQAILAEQRTAYGINTGFGLLASTRIATEDLENLQRSIVLSHAAGV 88

Query: 149 TPTSVSSFSVGRGLENTLPLEVVRGAMVIRVNSLTRGHSVRLVVLEALTNFLNHRITPI 208
+ + +VR MV+++NSL RG S +RL V++AL +N + P
Sbjct: 89 GEANDDA-----IVRLIMVLKINSLARGFSGIRLEVIQALITLVNAGVYPH 134

Query: 209 VPLRGSISASGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEAVVLGP 268
+PL+GS+ ASGDL+PL++++ + G + ++G + + A A++ GL+ + L
Sbjct: 135 IPLKSGVGASGDLAPLAHMSLLLLGEGKAR----YQG--EWLPAHTALAAQAGLQPLTLAA 188

Query: 269 KEGLGLVNGTAVSASMATXXXXXXXXXXXXXXXXXXXXVEAMVGQQGSFAPFIHDVCRPH 328
KEGL L+NGT VSA+ A V+A +G + F IH V R
Sbjct: 189 KEGLALLNGTQVSAAYALRGLFEAEDLYAAASVFGCLTVDAALGSRSPFDARIHAV-RGQ 247

Query: 329 PGQVEVARNIRTLLSGSSFAXXXXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHA 388
GQ++ A R LL S QD Y LR PQ +G + + A
Sbjct: 248 RGQIDAASTYRHLLGERSEISESHKNCDKV-----QDPYSLRCQPQVMGACLGQIRQA 300

Query: 389 YSTLSLENNTTTDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTEL 448
L++E+N +DNPL+ E GGNF A V+++ + LALA IG L+ + + +
Sbjct: 301 AEVLAIESNAVSDNPLVFAEQGDVLSGGNFHAEPVAMAADNLALALAEIGSLSECRISLM 360

Query: 449 LNAAMNRGLPSCLAEDPSLNYHGKGLDIHIAAYASELGHLANPVTTTFVQPAEMGNQAVN 508
++ M++ LP L E+ +N + AA SE LA P + P +
Sbjct: 361 MDKHMSQ-LPPFL-VENGGVNSGFMIAQVTAALTSSENKGLAAPPASVDSIPTSANQEDHV 418

Query: 509 SLALISARRTAEANDVLSLLLASHLYCTLQAVDLR 543
S+A + +R E + + +LA Q +DLR
Sbjct: 419 SMAPRAGKRLWEMAENVRNILAIEWLAACQGLDLR 453

☐ >gi|54032435|ref|ZP_00364567.1| COG2986: Histidine ammonia-lyase [Polaromonas sp]
Length = 514

Score = 178 bits (451), Expect = 6e-43

Identities = 135/432 (31%), Positives = 203/432 (46%), Gaps = 35/432 (8%)

Query: 115 VYGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPPTSVSSFSVGRGLENTLPLEVVRGA 174
VYG+ TGFG A T+ + ++L + V S SVG G LP VVR
Sbjct: 55 VYGINTEGFGKLASTK-----IAPNRLVELQRNLVLSHVSXGTG--EPLPAAVVRVI 102

Query: 175 MVIRVNSLTRGHSVRLVVLEALTNFLNHRITPIVPLRGSISASGDLSPLSYIAGAITGH 234
+ + SL RGHS VR +++AL N + P +P +GS+ ASGDL+PL+++A + G
Sbjct: 103 LATKAVSLARGHSGVRPELVDALLALANAGVMPRIAPKGSVGASGDLAPLAHLACVLIGE 162

Query: 235 PDVKVHVLHEGTEKIMFAREAISLFGLEAVVLGPKEGLGLVNGTAVSASMATXXXXXXXXX 294
+++ +A+ G+ VLGPKGL L+NGT VS ++A

Sbjct: 163 GQATT-----ADGEVISGAQAMRRIGVAPFVLGPKEGLALLNGTQVSTALALAGLFGAEQ 217

Query: 295 XXXXXXXXXXXXXVEAMVGQGSFAPF---IHDVCRPHPGQVEVARNIRTLLSGSSFAXXX 351
 +EA+ QGS PF +H R PGQ+ VA +RTL L GS

Sbjct: 218 VFAAGLVSGALSLEAV---QGSIKPFDARVH-AARGQPGQMAVAAAVRTLLEGSEIVPSH 273

Query: 352 XXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTNDNPLLDVENKQ 411
 QD Y +R PQ +G ++++ HA L +E N +DNPL+ +N

Sbjct: 274 PDCGRV-----QDPYSIRCVPQVMGACLDNLQHAARVLQIEANAASDNPLV-FDNGD 324

Query: 412 TAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCLAEDPSLNYH 471
 GGNF A V+ + + LA+A IG + + LL+ ++ GLP L D +N

Sbjct: 325 VISGGNFHAEPVFAAADIIALAVAEIGAIAERRLALLLDTGLS-GLPPFL-VRDGGVNSG 382

Query: 472 GKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVNSLALISARRTAEANDVLSLLLAS 531
 + AA ASE LA+P + P + S+A +ARR E + ++++

Sbjct: 383 FMIAQVTAAALASENKS LAHPASVDSLPTSANQEDHVS MATFAARRLGEMVNN TAVVVG I 442

Query: 532 HLYCTLQAVDLR 543
 Q ++L+

Sbjct: 443 EAMGAAQGIELK 454

[gi|22127907|ref|NP_671330.1](#) **G** putative histidine ammonia-lyase [Yersinia pestis biovar Medi
[gi|45437994|gb|AAS63542.1](#) **G** histidine ammonia-lyase [Yersinia pestis biovar Medi
 91001]

[gi|45443126|ref|NP_994665.1](#) **G** histidine ammonia-lyase [Yersinia pestis biovar Me
 91001]

[gi|15981920|emb|CAC93475.1](#) **G** histidine ammonia-lyase [Yersinia pestis CO92]

[gi|21961045|gb|AAM87581.1](#) **G** putative histidine ammonia-lyase [Yersinia pestis KI

[gi|16124139|ref|NP_407452.1](#) **G** histidine ammonia-lyase [Yersinia pestis CO92]

[gi|24211827|sp|Q8ZA10|HUTH_YERPE](#) Histidine ammonia-lyase (Histidase)
 Length = 510

Score = 177 bits (450), Expect = 8e-43

Identities = 138/455 (30%), Positives = 219/455 (48%), Gaps = 34/455 (7%)

Query: 93 DDEIRARVDKSVDFLKAQL--QNSVYGVTTGFGGSADTR--TEDAVSLQKALIEHQLCGV 148
 D+ + +SVD ++A L Q + YG+ TGFG A TR TED +LQ++++ GV

Sbjct: 29 DESAYVPIQQSVDCVQAILAEQRTAYGINTGFGLLASTRIATEDLENLQRSIVLSHAAGV 88

Query: 149 TPTSVSSFSVGRGLENLPLEVVRGAMVIRVNSLTRGHSVRLVLEALTNFLNHRITPI 208
 + + +VR MV+++NSL RG S +RL V++AL +N + P

Sbjct: 89 GEANDDA-----IVRLIMVLKINSLARGFSGIRLEVIQALITLVNAGVYPH 134

Query: 209 VPLRGSISASGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEAVVLGP 268
 +PL+GS+ ASGDL+PL++++ + G + ++G + + A A++ GL+ + L

Sbjct: 135 IPLKGSVGASGDLAPLAHMSLLLLGEGKAR----YQG--EWLPAHTALAQAGLQPLTLAA 188

Query: 269 KEGLGLVNGTAVSASMATXXXXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPH 328
 KEGL L+NGT VSA+ A V+A +G + F IH V R

Sbjct: 189 KEGLALLNGTQVSAAYALRGLFEAEDLYAAASVFGCLTVDAALGSRSPFDARIHAV-RGQ 247

Query: 329 PGQVEVARNIRTLLSGSSFAXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHA 388
 GQ++ A R LL S QD Y LR PQ +G + + A

Sbjct: 248 RGQIDAASTYRHLLGERSEISESHKNCDKV-----QDPYSLRCQPQVMGACLGQIRQA 300

Query: 389 YSTLSLENNNTTDDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTEL 448
 L++E+N +DNPL+ E GGNF A V+++ + LALA +G L+ + + +
 Sbjct: 301 AEVLAIESNAVSDNPLVFAEQGDVLSGGNFHAEPVAMAADNLALALAEVGSLSSECRISLM 360

Query: 449 LNAAMNRGLPSCLAEDPSLNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVN 508
 ++ M++ LP L E+ +N + AA SE LA P + P +
 Sbjct: 361 MDKHMSQ-LPPFL-VENGGVNSGFMIAQVTAALTSSENKGLAFPASVDSIPTSANQEDHV 418

Query: 509 SLALISARRTAEANDVLSLLLASHLYCTLQAVDLR 543
 S+A + +R E + + +LA Q +DLR
 Sbjct: 419 SMAPRAGKRLWEMAENVRNILAEIWLAAACQGLDLR 453

☐ >gi|48782713|ref|ZP_00279219.1| COG2986: Histidine ammonia-lyase [Burkholderia f
 Length = 457

Score = 177 bits (450), Expect = 8e-43
 Identities = 137/431 (31%), Positives = 196/431 (45%), Gaps = 33/431 (7%)

Query: 115 VYGVTTGFGGSADTRT--EDAVSLQKALIEHQLCGVTPTSVSSFSVGRGLENTLPLEVVR 172
 +YGV TGFG A T E LQ+ L V S +VG G + VVR
 Sbjct: 1 MYGVNTGFGRLASTHIPLEQLDLLQRNL-----VLHAVGVG--EPMSRSVVR 46

Query: 173 GAMVIRVNSLTRGHSVRLVLEALTNFLNHRITPIVPLRGSISASGDLSPLSYIAGAIT 232
 +V++V+SL RGHS +R V+ AL LN + P++P++GS+ ASGDL+PL++++ +
 Sbjct: 47 LMIVLVKVVSSLARGHSGIRREVIAALVTLLNADVLPVIPVKGSVGASGDLAPLAHMSAVLL 106

Query: 233 GHPDVKVHVLHEGTEKIMFAREAISLFGLEAVVLGPKEGLGLVNGTAVSASMATXXXXXX 292
 G +V + E+ A E + GLE L KEGL L+NGT S ++A
 Sbjct: 107 GVGVEVTI-----GERRASANEGLHAAGLEPPTLRAKEGLALLNGTQASTALALFNMFAI 160

Query: 293 XXXXXXXXXXXXXXXXVEAMVGQQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGSSFAXXXX 352
 V+A F IH R H GQ++ A R LL GS
 Sbjct: 161 EDLFCTALVAGALSVDAAAASVVPFDARIH-ALRGHQGQIDSAAAYRALLEGSEINLSHS 219

Query: 353 XXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNNTTDDNPLLDVENKQT 412
 QD Y LR PQ +G + M H+ L E N+ +DNPL+ +
 Sbjct: 220 DCDKV-----QDPYSLRCQPQVMGACLHQMRHSAEVLLCEANSVSDNPLIFPDTCDV 271

Query: 413 AHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCLAEDPSLNYHG 472
 GGNF A V+ + + LA+A IG L + L++ ++ GLP L D LN
 Sbjct: 272 LSGGNFHAEPVAFADNLALAVAIEGALAERRIALLLIDTTLS-GLPPFL-VRDSGLNSGF 329

Query: 473 KGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVNSLALISARRTAEANDVLSLLLASH 532
 + AA ASE LA+P + P + S+A +AR+ + + +LA
 Sbjct: 330 MIAHVTAALASENKTLAHPASVDSLPTSANQEDHVSMTFAARKLGDMASNTAHILAIE 389

Query: 533 LYCTLQAVDLR 543
 L Q +DLR
 Sbjct: 390 LLAATQGIDLR 400

☐ >gi|8926197|gb|AAF81735.1| putative phenylalanine ammonia lyase EncP [Streptomyces
 Length = 523

Score = 177 bits (449), Expect = 1e-42
 Identities = 136/463 (29%), Positives = 211/463 (45%), Gaps = 33/463 (7%)

Query: 96 IRARVDKSVDFLKAQLQNS--VYGVTTGFGGSAD--TRTEDAVSLQKALIEHQLCGVTPT 151
 +R+RV S D L +Q+ +YGV T GG D A LQ+ LI
 Sbjct: 32 VRSRVASRDVLVKFVQDERVIYGVNTSMGGFVDHLVPVSQARQLQENLI----- 81

Query: 152 SVSSFSVGRGLENLPLEVVRGAMVIRVNSLTRGHSVRLVVLEALTNFLNHRITPIVPL 211
 + + +VG L++T R M+ R+ SL RG+SA+ L+ L LN I P +P
 Sbjct: 82 NAVATNVGAYLDDT----TARTIMLSRIVSLARGNSAITPANLDKLVAVLNAGIVPCIP 137

Query: 212 RGSISASGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEAVVLGPKEG 271
 +GS+ SGDL PL+ IA G + + +IM R+A+S G+E + L K+G
 Sbjct: 138 KGS LGTSGDLGPLAAIALVCAGQWKARYN-----GQIMPGRQALSEAGVEPMELSYKDG 191

Query: 272 LGLVNGTAVSASMATXXXXXXXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQ 331
 L L+NGT+ + T VE + G F P +H V +PH GQ
 Sbjct: 192 LALINGTSGMVGLGTMVLQAARRLVDRYLQVSALSVEGLAGMTKPFDPRVHGV-KPHRGQ 250

Query: 332 VEARNIRTLLSGSSFA-----XXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVE 383
 +VA + L+ S A + +D Y +R +PQ LGP+V+
 Sbjct: 251 RQVASRLWEGLADSHLAVNELDTEQTLGEMGTVAKAGSLAIEDAYSIRCTPQILGPVVD 310

Query: 384 DMMHAYSTLSLENNTTTNDPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFT 443
 + +TL E N++ DNP++ E + H G+F V+++M+ +ALA + L
 Sbjct: 311 VLDRIGATLQDELNSSNDNPVLP EEA EVFHNGHFHGGYVAMAMDHLNMALATVTNLANR 370

Query: 444 QCTELLNAAMNRGLPSCLAEDPSLNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMG 503
 + L+ + + GLP+ L EDP L G A+ +E L P++ +
 Sbjct: 371 RVDRFLDKSNSNGLPAFLCREDPGLRLGLMGGQFMTASITAETRTLTPMSVQSLTSTAD 430

Query: 504 NQAVNSLALISARRTAEANDVLSLLLASHLYCTLQAVDLRAME 546
 Q + S ++ARR E + ++A L C QA VD+R +
 Sbjct: 431 FQDIVSFGFVAARRAREVLTAAYVVAPELLCACQAVDIRGAD 473

☐ >gi|24375855|ref|NP_719898.1| ☒ histidine ammonia-lyase, putative [Shewanella or
 gi|24350819|gb|AAN57342.1| ☒ histidine ammonia-lyase, putative [Shewanella oneide
 Length = 521

Score = 176 bits (447), Expect = 2e-42

Identities = 138/479 (28%), Positives = 214/479 (44%), Gaps = 38/479 (7%)

Query: 92 NDDEIRARVDKSVDFLKAQLQNS--VYGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVT 149
 +D + + + K F+ + L VYGVTTG+G S VSL + H+L
 Sbjct: 40 DDADYQEYIQKGARFIDSLHEEGVVYGVTTGYGDSCVTN----VSLD---LVHEL---- 88

Query: 150 PTSVSSFSVGRGLENLPLEVVRGAMVIRVNSLTRGHSVRLVVLEALTNFLNHRITPIV 209
 P +S F G GL L + R M R+NSL G S V +L+ + LN I P++
 Sbjct: 89 PLHLSRFH-GCGLGEVLSVMQARAVMACRLNSLAIGKSGVTYELLKRIQTLLNLNIVPVI 147

Query: 210 PLRGSISASGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEAVVLGPK 269
 P GS+ ASGDL+PLSY+A + G + V+++G + +E + VL PK
 Sbjct: 148 PEEGSVGASGDLTPLSYLA AVLGERE----VIYQGERRA--TKEVYHELNITPHVLRPK 201

Query: 270 EGLGLVNGTAVSASMATXXXXXXXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHP 329
 EGL L+NGTAV ++A + G F + +PHP
 Sbjct: 202 EGLALMNGTAVMTALACLAFLDRAQYLARLASRITAMASLT LKGNSNHFD DILF-AAKPHP 260

Query: 330 GQVEARNIRTLLSGSSFAXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAY 389

GQ ++A IR L+ QDRY +R +P +G L + +
 Sbjct: 261 GQNQIATWIREDLNHHVHPRNSDRL-----QDRYSIRCAPHIIGVLQDALPFMR 309
 Query: 390 STLSLENNTTTDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELL 449
 + E N+ DNP++D E + HGG+F ++ +M+ + +A I L Q ++
 Sbjct: 310 QFIETEVNSANDNPIVDAEGEHILHGGHFYGGHIAFAMDSLKNIVANIADLIDRQMALVM 369
 Query: 450 NAAMNRGLPSCLAED---PSLNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQA 506
 + N GLP+ L+ ++N+ K + I ++A+ +E P + F + E NQ
 Sbjct: 370 DPKFNNGLPANLSGSTGPRRAINHGFKAVQIGVSAWTAELKHTMPASVFSRSTECHNQD 429
 Query: 507 VNSLALISARRTAEANDVLSLLLASHLYCTLQAVDLRAM--ELDFKKQFDPLLPTLLQ 563
 S+ I+AR + + A+ L Q +DLR ELD + P L T L Q
 Sbjct: 430 KVSMGTIAARDCMRVLQLTEQVAAAALLAMTQGIDLRITQNELD-EASLTPSLATTLAQ 487

☐ >gi|52141894|ref|YP_084939.1| ☒ histidine ammonia-lyase (histidase) [Bacillus ce
 gi|51975363|gb|AAU16913.1| ☒ histidine ammonia-lyase (histidase) [Bacillus cereus
 Length = 505

Score = 176 bits (447), Expect = 2e-42
 Identities = 135/455 (29%), Positives = 213/455 (46%), Gaps = 41/455 (9%)

Query: 95 EIRARVDKSVDFLKAQLQNSVYGVTTGFGGSADT--RTEDAVSLQKALIEHQLCGVTPTS 152
 E R V+K V+ K VYG+TTGFG +D + ED +LQ LI+ CG+
 Sbjct: 36 ECREVVEKIVEDGKV-----VYGITGFGKFSVDVLIQKEDVKALQHNLIQSHACGIG--- 87
 Query: 153 VSSFSVGRGLENTLPLEVVRGAMVIRVNSLTRGHSVAVRLVVLEALTNFLNHRITPIVPLR 212
 + P EV RG +++R N++ +G S VR +V+ L F+N +I P+VP +
 Sbjct: 88 -----DPFPEEVSRLMLILRANTMLKGVSGVRPLVVNMLLEFVNRKIHPVVPQQ 136
 Query: 213 GSISASGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEAVVLGPKEGL 272
 GS+ ASGDL+PLS++A + G + V ++G K A A++ GLE + L KEGL
 Sbjct: 137 GSLGASGDLAPLSHLALVLLGEGE----VFYKG--KRAHAMVALTEEGLEPIELEAKEGL 190
 Query: 273 GLVNGTAVSASMATXXXXXXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQV 332
 L+NGT + +E + G +F +H R + QV
 Sbjct: 191 ALINGTQAMTAQGVL SYIEAEATAYQAELIASMTIEGLQGIIDAFDENVHK-ARGYKEQV 249
 Query: 333 EVARNIRTLLSGSSFAXXXXXXXXXXXXXXGILR-QDRYPLRTSPQFLGPLVEDMMHAYST 391
 EVA IR +L S G LR QD Y LR PQ G + + +
 Sbjct: 250 EVASRIRDILHDSKL-----TTKQGELRVQDAYSLRCIPQVHGASWQVLNVVKEK 299
 Query: 392 LLENNTTTDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNA 451
 L +E N TDNPL+ ++ GGNF ++ +M+ ++ +A + ++ + L+N
 Sbjct: 300 LEIEMNAATDNPLIFDGGEKVISGGNFHGQPIAFAMDFLKVGMELANISERRIERLVNP 359
 Query: 452 AMNRGLPSCLAEDPSLNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVNSLA 511
 +N LP L+ E P L + A+ SE LA+P + P+ + S+
 Sbjct: 360 QLN-DLPPFLSPE-PGLQSGAMIMQYAAASLVSENKTLAHPASVDSIPSSANQEDHVSMD 417
 Query: 512 LISARRTAEANDVLSLLLASHLYCTLQAVDLRAME 546
 I++R + + +L+ + C +QA + R +E
 Sbjct: 418 TIASRHAHQIIQNVRRLVLSIEMICAMQAAEYRGIE 452

☐ >gi|49478310|ref|YP_037727.1| ☒ histidine ammonia-lyase (histidase) [Bacillus th

konkukian str. 97-27]

gi|49329866|gb|AAT60512.1| **G** histidine ammonia-lyase (histidase) [Bacillus thuringiensis]
konkukian str. 97-27]
Length = 505

Score = 176 bits (447), Expect = 2e-42

Identities = 142/503 (28%), Positives = 233/503 (46%), Gaps = 48/503 (9%)

Query: 95 EIRARVDKSVDFLKAQLQNSVYGVTTGFGGSADT--RTEDAVSLQKALIEHQLCGVTPPTS 152
E R V+K V+ K VYG+TTGFG +D + +D +LQ LI+ CG+
Sbjct: 36 ECREVVEKIVEDGKV-----VYGITTTGFGKFSVDLIQKDDVKALQHNLIQSHACGIG--- 87

Query: 153 VSSFSVGRGLENLTPLEVVIRGAMVIRVNSLTRGHSAVRLVVLEALTNFLNHRITPIVPLR 212
+ P EV RG +++R N++ +G S VR +V+ L F+N +I P+VP +
Sbjct: 88 -----DPFPPEVSRGMLILRANTMLKGVSGVRPLVVNMLLEFVNRKIHPVVPQQ 136

Query: 213 GSISASGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEAVVLGPKKEGL 272
GS+ ASGDL+PLS++A + G + V ++G K + A A++ GLE + L KEGL
Sbjct: 137 GSLGASGDLAPLSHLALVLLGEGE----VFYKG--KRVHAMVALTEEGLEPIELEAKEGL 190

Query: 273 GLVNGTAVSASMATXXXXXXXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQV 332
L+NGT + +E + G +F +H R + QV
Sbjct: 191 ALINGTQAMTAQGVLSYIEAEATAYQAEFIASMTIEGLQGIIDAFDENVHK-ARGYKEQV 249

Query: 333 EVARNIRTLLSGSSFAXXXXXXXXXXXXXXXXXXGILR-QDRYPLRTSPQFLGPLVEDMMHAYST 391
EVA IR +L S G LR QD Y LR PQ G + + +
Sbjct: 250 EVASRIRDILHDSKL-----TTKQGKLRVQDAYSRLCIPQVHGASWQVLNYVKEK 299

Query: 392 LSLENNTTTDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNA 451
L +E N TDNPL+ ++ GGNF ++ +M+ ++ +A + ++ + L+N
Sbjct: 300 LEIEMNAATDNPLIFDGGGEKVISGGNFHGQPIAFAMDFLKVGMELANISERRIERLVNP 359

Query: 452 AMNRGLPSCLAEDPSLNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVNSLA 511
+N LP L+ E P L + A+ SE LA+P + P+ + S+
Sbjct: 360 QLN-DLPPFLSPE-PGLQSGAMIMQYAAASLVSENKTLAHPASVDSIPSSANQEDHVSMS 417

Query: 512 LISARRTAEANDVLSLLLASHLYCTLQAVDLRAME-----LDFKKQFDPLLPTLLQQHL 565
I++R + + +L+ + C +QA + R +E F Q +P++ +
Sbjct: 418 TIASRHAHQIIQNVRRVLSIEMICAMQAAEYRGIEINMSTVTKSFYHQGRQQVPSITNDRI 477

Query: 566 -GTGLDVNALALEVKKALNKRLE 587
T ++ A L+ ++ +RL+
Sbjct: 478 FSTDIEINIAYWLKTNYSIKERLD 500

<gi|47567936|ref|ZP_00238643.1| histidine ammonia-lyase [Bacillus cereus G9241]
gi|47555414|gb|EAL13758.1| histidine ammonia-lyase [Bacillus cereus G9241]
Length = 505

Score = 176 bits (446), Expect = 2e-42

Identities = 134/455 (29%), Positives = 214/455 (47%), Gaps = 41/455 (9%)

Query: 95 EIRARVDKSVDFLKAQLQNSVYGVTTGFGGSADT--RTEDAVSLQKALIEHQLCGVTPPTS 152
E R V+K V+ K VYG+TTGFG +D + +D +LQ LI+ CG+
Sbjct: 36 ECREVVEKIVEDGKV-----VYGITTTGFGKFSVDLIQKDDVKALQHNLIQSHACGIG--- 87

Query: 153 VSSFSVGRGLENLTPLEVVIRGAMVIRVNSLTRGHSAVRLVVLEALTNFLNHRITPIVPLR 212
+ P EV RG +++R N++ +G S VR +V+ L F+N +I P+VP +

Sbjct: 88 -----DPFPPEVSRGMLILLRANTMLKGVSGVRPLVVNMLLEFVNRKIHPVVPQQ 136

Query: 213 GSISASGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEAVVLGPKEGL 272
 GS+ ASGDL+PLS++A + G + V ++G K + A A++ GLE + L KEGL

Sbjct: 137 GSLGASGDLAPLSHLALVLLGE-----VFYKG--KRVHAMVALTEEGLEPIELEAKEGL 190

Query: 273 GLVNGTAVSASMATXXXXXXXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQV 332
 L+NGT + +E + G +F +H R + QV

Sbjct: 191 ALINGTQAMTAQGVLSYIEAEATAYQAEFIASMTIEGLQGIIDAFDENVHK-ARGYKEQV 249

Query: 333 EVARNIRTLLSGSSFAXXXXXXXXXXXXXXGILR-QDRYPLRTSPQFLGPLVEDMMHAYST 391
 EVA IR +L S G LR QD Y LR PQ G + + +

Sbjct: 250 EVASRIRDILHDSKL-----TTKQGELRVQDAYSLRCIPQVHGASWQVLNYVKEK 299

Query: 392 LSLENNTTTDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNA 451
 L +E N TDNPL+ ++ GGNF ++ +M+ ++ +A + ++ + L+N

Sbjct: 300 LEIEMNAATDNPLIFDGGKEKVISGGNFHGQPIAFAMDFLKVGMELANISERRIERLVNP 359

Query: 452 AMNRGLPSCLAAEDPSLNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVNSLA 511
 +N LP L+ E P L + A+ SE LA+P + P+ + S+

Sbjct: 360 QLN-DLPPFLSPE-PGLQSGAMIMQYAAASLVSENKTLAHPASVDSIPSSANQEDHVSMD 417

Query: 512 LISARRTAEANDVLSLLLASHLYCTLQAVDLRAME 546
 I++R + + +L+ + C +QA + R +E

Sbjct: 418 TIASRHAHQIIQNVRRLSIEMICAMQAAEYRGIE 452

☐ >gi|53795015|ref|ZP_00021060.2| COG2986: Histidine ammonia-lyase [Chloroflexus :
 Length = 523

Score = 176 bits (446), Expect = 2e-42

Identities = 135/456 (29%), Positives = 210/456 (46%), Gaps = 33/456 (7%)

Query: 97 RARVDKSVDFLKAQLQNSV--YGVTTGFGGSADTRTEDAVSLQKALIEHQLCGVTPTSVS 154
 R RV+++ ++ L V YG+TTGFG D + + Q+ + +

Sbjct: 38 RQVERAAQAVQDLLARGVVAYGITTFGAFKD-----RVIAPDQVERLQYNILV 87

Query: 155 SFSVGRGLENLTPLEVVVRGAMVIRVNSLTRGHSVRLVVLEALTNFLNHRITPIVPLRGS 214
 S +VG G +P R M+IR N+L RGHS VRL +E L + LN I P +P +GS

Sbjct: 88 SHAVGVGPFVDIP--TTRAIMLIRANTLARGHSGVRLQTVERLLDMLNQGIHPRIPCKGS 145

Query: 215 ISASGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEAVVLGPKEGLGL 274
 + ASGDL+PL+++A + G +V E +++ A A+ G + + L KEGL L

Sbjct: 146 LGASGDLAPLAHMLPLIGLGE-----EWQGEVLPAAATALERLQWQPLHLAAKEGLAL 199

Query: 275 VNGTAVSASMATXXXXXXXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQVEV 334
 NGTAV ++ +EA+ G +F +H RP P Q+E

Sbjct: 200 TNGTAVMCALGVIETARAETLSATADIAGCLSLEALYGTAAFDARLH-ALRPFPRIEC 258

Query: 335 ARNIRTLLSGSSFAXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSL 394
 A ++R LL+GS+F QD Y LR PQ G + + + +A ++

Sbjct: 259 AAHLRRLLAGSTFVRNNDPRHV-----QDAYTLRCIPQVHGAVRDAIAYARWVFAI 309

Query: 395 ENNTTTDNPLLDVE---NKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNA 451
 E N TDNPLL V+ N + GGNF ++I+++ LA+A +G + + L +

Sbjct: 310 ELNAVTDNPLLFDVDDGDNVEVISGGNFHGEPLAIALDYLGLAVAELGNIAERRLMRLTDE 369

Query: 452 AMNRGLPSCLAAEDPSLNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVNSLA 511
 A N + LN + AA A+E LA+P + P + S+

Sbjct: 370 ASNTHVLP AFLTRAGGLNSGFMIVQYTAAALATENKVL AHPASVDSIPTSANVEDHVSMG 429

Query: 512 LISARRTAEANDVLSLLLASHLYCTLQAVDLRAMEL 547

+ + + D +S +LA L+ Q +D R EL

Sbjct: 430 VTAGLKLRSIIDNVSQILALELFAAAQGIDFRRQEL 465

☐ >gi|47528996|ref|YP_020345.1| **G** histidine ammonia-lyase [Bacillus anthracis str. gi|30263598|ref|NP_845975.1| **G** histidine ammonia-lyase [Bacillus anthracis str. A gi|49186446|ref|YP_029698.1| **G** histidine ammonia-lyase [Bacillus anthracis str. S gi|30258233|gb|AAP27461.1| **G** histidine ammonia-lyase [Bacillus anthracis str. Ame gi|47504144|gb|AAT32820.1| **G** histidine ammonia-lyase [Bacillus anthracis str. 'Am gi|49180373|gb|AAT55749.1| **G** histidine ammonia-lyase [Bacillus anthracis str. Ste
Length = 505

Score = 176 bits (445), Expect = 3e-42

Identities = 134/455 (29%), Positives = 214/455 (47%), Gaps = 41/455 (9%)

Query: 95 EIRARVDKSVDFLKAQLQNSVYGVTGFGGSADT--RTEDAVSLQKALIEHQLCGVTPTS 152
E R V+K V+ K VYG+TTGFG +D + +D +LQ LI+ CG+

Sbjct: 36 ECREVVEKIVENGKV-----VYGITGFGKFSDVLIQKDDVKALQHNLIQSHACGIG--- 87

Query: 153 VSSFVSVGRGLENTLPLEVVRGAMVIRVNSLTRGHSVRLVLEALTNFLNHRITPIVPLR 212
+ P EV RG +++R N++ +G S VR +V+ L F+N +I P+VP +

Sbjct: 88 -----DPFPEEVSRLMLILRANTMLKGVSGVRPLVNMMLLEFVNRKIHPVVPQQ 136

Query: 213 GSISASGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIMFAREAI SLFGLAVVLGPKEGL 272
GS+ ASGDL+PLS++A + G + V ++G K + A A++ GLE + L KEGL

Sbjct: 137 GSLGASGDLAPLSHLALILLGEGE----VFYKG--KRVHAMVALTEEGLEPIELEAKEGL 190

Query: 273 GLVNGTAVSASMATXXXXXXXXXXXXXXXXXXXXXVEAMVGQQGSFAPFIHDVCRPHPGQV 332
L+NGT + +E + G +F +H R + QV

Sbjct: 191 ALINGTQAMTAQGVLSYIEAEATAYQAELIASMTIEGLQGIIDAFDENVHK-ARGYKEQV 249

Query: 333 EVARNIRTLLSGSSFAXXXXXXXXXXXXXXGILR-QDRYPLRTSPQFLGPLVEDMMHAYST 391
EVA IR +L S G LR QD Y LR PQ G + + +

Sbjct: 250 EVASRIRDILHDSKL-----TTKQGELRVQDAYSLRCIPQVHGASWQVLNRYVKEK 299

Query: 392 LLENNTTTDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNA 451
L +E N TDNPL+ ++ GGNF ++ +M+ ++ +A + ++ + L+N

Sbjct: 300 LEIEMNAATDNPLIFDGGEKVISGGNFHGGQPIAFAMDFLKVGMALANISERRIERLVNP 359

Query: 452 AMNRGLPSCLAEDPSLNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVNSLA 511
+N LP L+ E P L + A+ SE LA+P+ P+ + S+

Sbjct: 360 QLN-DLPPFLSPE-PGLQSGAMIMQYAAASLVSENKTLAHPASVDSIPSSANQEDHVSMG 417

Query: 512 LISARRTAEANDVLSLLLASHLYCTLQAVDLRAME 546

I++R + + +L+ + C +QA + R +E

Sbjct: 418 TIASRHAHQIIQNVRRVLSIEMICAMQAAEYRGIE 452

☐ >gi|16125211|ref|NP_419775.1| **G** histidine ammonia-lyase [Caulobacter crescentus gi|13422237|gb|AAK22943.1| **G** histidine ammonia-lyase [Caulobacter crescentus CB15 gi|25292168|pir|C87368 histidine ammonia-lyase [imported] - Caulobacter crescent gi|14194847|sp|P58082|HUTH_CAUCR Histidine ammonia-lyase (Histidase)

Length = 509

Score = 176 bits (445), Expect = 3e-42

Identities = 135/432 (31%), Positives = 198/432 (45%), Gaps = 32/432 (7%)

Query: 115 VYGVTTGFGGSADTRTEDA--VSLQKALIEHQLCGVTPTSVSSFSVGRGLENTLPLEVVR 172
 VYG+ TGFG A R DA +LQ+ ++ GV S P+ V+R
 Sbjct: 52 VYGINTGFGKLASVRIGDADLETQLQRNIVLSHAAGVGEPs-----PVPVIR 97

Query: 173 GAMVIRVNSLTRGHSVRLVLEALTNFLNHRITPIVPLRGSISASGDLSPLSYIAGAIT 232
 M +++ SL +G S VR+ + L L +TP+VP +GS+ ASGDL+PLS+++A +
 Sbjct: 98 LMMALKLASLAQGASGVRVETVRMLEEMLVEGLTPVVPVPCQGSVGASGDLAPLSHMAATMI 157

Query: 233 GHPDVKVHVLHEGTEKIMFAREAI SLFGLEAVVLGPKEGLGLVNGTAVSASMATXXXXXX 292
 G ++ V G +++ A +A++ GLE + LGPKEGL L+NGT S + A
 Sbjct: 158 GVGEIFV-----GGQRLP-AAQALAQAGLEPLTLGPKEGLALLNGTQFSTANALAGLFEA 211

Query: 293 XXXXXXXXXXXXXXXXVEAMVGQQGSFAPFIHDCRPHPGQVEVARNIRTLLSGSSFAXXXX 352
 EA G F P IH + R H GQ+E A +R L+S S
 Sbjct: 212 ERLFQSALVTGALSTEAAKGS DTPFDPRIHTL-RRHVQIETAAALRALMSASEIRASHL 270

Query: 353 XXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTNDNPLLDVENKQT 412
 QD Y LR PQ +G ++ + A +TL+ E N +DNPL+ E +
 Sbjct: 271 KEDERV-----QDPYCLRCQPQVMGAALDILRQAATTLATEANCVSDNPLIFPEADEA 323

Query: 413 AHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCLAAEDPSLNYHG 472
 GGNF A V+ + + LA+ IG + + L++ A++ GLP+ L + P LN
 Sbjct: 324 LSGGNFHAEPVAFADMIALAVCEIGSIAERRIAMLVDPALS-GLPAFLTPK-PGLNSGF 381

Query: 473 KGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVNSLALISARRTAEANDVLSLLASH 532
 + AA SE A P + P + S+A ARR + +L
 Sbjct: 382 MIPQVTAALVSENKQRAYPASVDSIPTSANQEDHVSMAAHGARRLLAMVENADAVLGIE 441

Query: 533 LYCTLQAVDLRA 544
 L Q D A
 Sbjct: 442 LLAAAQGCDFHA 453

☐ >gi|42782730|ref|NP_979977.1| ☒ histidine ammonia-lyase [Bacillus cereus ATCC 10987]
☐ gi|42738656|gb|AA542585.1| ☒ histidine ammonia-lyase [Bacillus cereus ATCC 10987]
 Length = 505

Score = 176 bits (445), Expect = 3e-42

Identities = 134/455 (29%), Positives = 213/455 (46%), Gaps = 41/455 (9%)

Query: 95 EIRARVDKSVDFLKAQLQNSVYGVTTGFGGSADT--RTEDAVSLQKALIEHQLCGVTPTS 152
 E R V+K V+ K VYG+TTGFG +D + +D +LQ LI+ CG+
 Sbjct: 36 ECREVVEKIVEDGKV-----VYGITGFGKFSDVLIQKDDVKALQHNLIQSHACGIG--- 87

Query: 153 VSSFSVGRGLENTLPLEVVRGAMVIRVNSLTRGHSVRLVLEALTNFLNHRITPIVPLR 212
 P EV RG +++R N++ +G S VR +V+ L F+N +I P+VP +
 Sbjct: 88 -----EPFPEEVSRLMLILRANTMLKGVSGVRPLVNMMLLEFVNRKIHPVVPQQ 136

Query: 213 GSISASGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIMFAREAI SLFGLEAVVLGPKEGL 272
 GS+ ASGDL+PLS+++A + G + V ++G K + A A++ GLE + L KEGL
 Sbjct: 137 GSLGASGDLAPLSHLALVLLGEGE----VFYKG--KRVHAMVALTEEGLEPIELEAKEGL 190

Query: 273 GLVNGTAVSASMATXXXXXXXXXXXXXXXXXXXXXVEAMVGQQGSFAPFIHDCRPHPGQV 332

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      L+NGT      +      +E + G  +F  +H  R +  QV
Sbjct: 191 ALINGTQAMTAQGVLSYIEAEATAYQAELIASMTIEGLQGIIDAFDENVHK-ARGYKEQV 249

Query: 333 EVARNIRTLLSGSSFAXXXXXXXXXXXXXXGILR-QDRYPLRTSPQFLGPLVEDMMHAYST 391
      EVA  IR +L  S      G LR QD Y LR  PQ  G  + + +
Sbjct: 250 EVASRIRDILHDSKL-----TTKQGELRVQDAYSLRCIPQVHGASWQVLNVVKEK 299

Query: 392 LSLENNTTTDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNA 451
      L +E N  TDNPL+      ++  GGNF      ++ +M+  ++ +A +  ++  +  L+N
Sbjct: 300 LEIEMNAATDNPLIFDGGKEKVISGGNFHGGQPIAFAMDFLKVGMALANISERRIERLVNP 359

Query: 452 AMNRGLPSCLAEDPSLNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVNSLA 511
      +N  LP  L+ E P L      +  A+  SE  LA+P +  P+  +  S+
Sbjct: 360 QLN-DLPPFLSPE-PGLQSGAMIMQYAAASLVSENKTLAHPASVDSIPSSANQEDHVSMSG 417

Query: 512 LISARRTAEANDVLSLLLASHLYCTLQAVDLRAME 546
      I++R  +  +  +L+  + C +QA + R +E
Sbjct: 418 TIASRHAHQIIQNVRRVLSIEMICAMQAAEYRGIE 452

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☐ >gi|14210836|gb|AAK57183.1| putative histidine ammonium lyase [Stigmatella aurar
 gi|32129643|sp|Q93TX3|HUTH_STIAU Histidine ammonia-lyase (Histidase)
 Length = 510

Score = 176 bits (445), Expect = 3e-42

Identities = 132/430 (30%), Positives = 201/430 (46%), Gaps = 33/430 (7%)

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Query: 116 YGVTTGFGGSADTRTE--DAVSLQKALIEHQLCGVTPTSVSSFSVGRGLENTLPLEVVRG 173
      YG+ TGFG  A+ R +  D  LQ+ LI      S  G+ + LPL  R
Sbjct: 56 YGINTGFGTLAEVRIDKKDLRELQRNLI-----LSHAAGVGSPPLPEARV 101

Query: 174 AMVIRVNSLTRGHSAVRLVVLEALTNFLNHRITPIVPLRGSISASGDLSPLSYIAGAITG 233
      +++R N L +G+S +R  L      LN  + P+VP RGS+ ASGDL+PL+++A  G
Sbjct: 102 LLLLRCNVLAKGYSGIRPETLALALEMLNRDVVPVPERGSGVSGDLAPLAHLALVFIG 161

Query: 234 HPDVKVHVLHEGTEKIMFAREAISLFGLEAVVLGPKEGLGLVNGTAVSASMATXXXXXXX 293
      +      ++G  + A +A+  GL+ VVL  KEGL LVNGT  ++ T
Sbjct: 162 EGE----AFYKGER--LPAAQALERAGLKPVVLEAKEGLALVNGTQAMCAVGTLLQLRAE 215

Query: 294 XXXXXXXXXXXXXVEAMVQGQSFAPFIHDVCRPHPGQVEVARNIRTLLSGSSFAXXXXX 353
      +E ++G      F P I DV R H GQ  A ++R LL+ S+
Sbjct: 216 MLADLADLAGAMTLEGLLGSHKPFIPFIQDV-RAHEGQKACAAHLRELLADSALVESHVN 274

Query: 354 XXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTDNPLLDVENKQTA 413
      QD Y LR  PQ  G  E +  A  L +E N+ TDNPL+ VE ++
Sbjct: 275 CSKV-----QDPYSLRCMPQVHGAAAREGLSFARRILEVEINSATDNPLVETERIV 326

Query: 414 HGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCLAEDPSLNYHGK 473
      GGNF      VS++++  +AL  +  ++  +  +L+N A++ GLP  L A++ LN
Sbjct: 327 SGGNFHGGQPVSLALDVAAMALTQLSAISERRVEQLVNPALS-GLPPFL-AKNSGLNSGFM 384

Query: 474 GLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVNSLALISARRTAEANDVLSLLLASHL 533
      +  AA +E  L++P +  P+  G +  S+ + +A +  +  D      LA  L
Sbjct: 385 IAQVTSAAALVAESRVLSPASVDSIPSSAGREDHVSMTAALKGRQVADFTRSCLAIEL 444

Query: 534 YCTLQAVDLR 543
      QA+D R
Sbjct: 445 LVAAQALDYR 454

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☐ >gi|48764895|ref|ZP_00269446.1| COG2986: Histidine ammonia-lyase [Rhodospirillum rubrum]
Length = 514

Score = 175 bits (444), Expect = 4e-42
Identities = 132/432 (30%), Positives = 206/432 (47%), Gaps = 31/432 (7%)

Query: 112 QNSVYGVTTGFGGSADTRTE--DAVSLQKALIEHQLCGVTPTSVSSFSVGRGLENLPLE 169
+++VYG+ TGFG A R D +LQ LI S G+ +
Sbjct: 51 ESAVYGINVTGFGKLAHKRIAPADLEALQTNLI-----LSHATGMGAPIADA 96

Query: 170 VVRGAMVIRVNSLTRGHSVAVRLVLEALTNFLNHRITPIVPLRGSISASGDLSPLSYIAG 229
VR + I+ SL G S +R +++AL N + P++P +GS+ ASGDL+PL+++
Sbjct: 97 TVRLILAIAKASLAVGASGIRAEIVDALLALANADVLPVIPSCKGSGASGDLAPLAHLCC 156

Query: 230 AITGHPDVKVHVLHEGTEKIMFAEAIISLFGLEAVVLGPKEGLGLVNGTAVSASMATXXX 289
A+ G V+ H+G ++ A E +++ GL + L KEGL L+NGT VS ++A
Sbjct: 157 ALLGIGSVR----HKGA--VLPAGEGLAIAGLSPITLRAKEGLALINGTQVSTALALAGL 210

Query: 290 XXXXXXXXXXXXXXXXXXXXVEAMVGQQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGSSFAX 349
VEA++G F P I R GQ++VA R LL GS
Sbjct: 211 FEIERAFAAAILAGALSVEAVMGSHRPFDPRI-SALRGQFGQIDVAALFRLLLDGSPLNA 269

Query: 350 XXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTNDNPLLDVEN 409
QD Y LR PQ +G +++ M A TL++E N TDNPL+ V+
Sbjct: 270 AHQGPSCERV-----QDPYSLRCQPQVMGAVLDQMRFAARTLTIEANGVTDNPLVLVDT 323

Query: 410 KQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCLAEDPSLN 469
+ GGNF A V+++ ++ +A + IG L+ + L+++ ++ GLP L AE P LN
Sbjct: 324 GEVLSGGNFHAEPVAMAADQLAIAASEIGALSERRIAMLIDSTIS-GLPPFLVAE-PGLN 381

Query: 470 YHGKGLDIHIAAYASELGHLANPVTTTFVQPAEMGNQAVNSLALISARRTAEANDVLSLLL 529
+ AA ASE LA+P + P + S+A +ARR + ++ ++
Sbjct: 382 SGFMIAHVTAALASENKSIAHPASVDSLPTSANQEDHVSMAATFAARRLGDIANVTGIV 441

Query: 530 ASHLYCTLQAVD 541
L Q ++
Sbjct: 442 GIELLAAAQGLE 453

☐ >gi|16080986|ref|NP_391814.1| ☒ histidase [Bacillus subtilis subsp. subtilis str. 168]
gi|2636481|emb|CAB15971.1| ☒ histidase [Bacillus subtilis subsp. subtilis str. 168]
gi|68358|pir|UFBSHS histidine ammonia-lyase (EC 4.3.1.3) hutH [similarity] - Bac
subtilis
gi|123758|sp|P10944|HUTH_BACSU Histidine ammonia-lyase (Histidase)
gi|603770|dbj|BAA06644.1| histidase [Bacillus subtilis]
gi|143076|gb|AAA22538.1| histidase
Length = 508

Score = 175 bits (444), Expect = 4e-42
Identities = 137/485 (28%), Positives = 215/485 (44%), Gaps = 36/485 (7%)

Query: 65 VVELSGYSLTXXXXXXXXXXXXXXXXXQNDDEIRARVDKSVDFLKAQLQNSVYGVTTGFGG 124
+V L G SLT + R + ++ + + ++YG+ TGFG
Sbjct: 1 MVTLDGSSLTADVARVLFDFEAAAASESMERVKKSRAAVERIVRDEKTIYGINVTGFGK 60

Query: 125 SADT--RTEDAVSLQKALIEHQLCGVTPTSVSSFSVGRGLENLPLEVVRGAMVIRVNSL 182

+D + ED+ +LQ LI CGV + P V R +++R N+L
 Sbjct: 61 FSDVLIQKEDSAALQLNLILSHACGVG-----DPFPECVSRAMLLLRANAL 106
 Query: 183 TRGHSVRLVLEALTNFLNHRITPIVPLRGSISASGDLSPLSYIAGAITGHPDVKVHVL 242
 +G S VR ++E L FLN R+ P++P +GS+ ASGDL+PLS++A A+ G + V
 Sbjct: 107 LKGFSGVRAELIEQLLAFLNKRVPVIPQQGSLGASGDLAPLSHLALALIGQGE----VF 162
 Query: 243 HEGTEKIMFAREAISLFGLEAVVLGPKEGLGLVNGTAVSASMATXXXXXXXXXXXXXXXXX 302
 EG M A + G++ V L KEGL L+NGT +M
 Sbjct: 163 FEGER--MPAMTGLKKAGIQPVTLSKEGLALINGTQAMTAMGVVAYIEAEKLAYQTERI 220
 Query: 303 XXXXVEAMVGQQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGSSFAXXXXXXXXXXXXXXG 362
 +E + G +F IH + R + Q++VA IR LS S G
 Sbjct: 221 ASLTIEGLQGIIDAFDEDIH-LARGYQEIDVAERIRFYLSDSGL-----TTSQG 269
 Query: 363 ILR-QDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTDNPLLDVENKQTAHGGNFQAS 421
 LR QD Y LR PQ G + + + L +E N TDNPL+ + + GGNF
 Sbjct: 270 ELRVQDAYSLRCIPQVHGATWQTLGYVKEKLEIEMNAATDNPLIFNDGDKVISGGNFHGQ 329
 Query: 422 AVSISMEKTRLALALIGKLNFTQCTELNNAAMNRGLPSCLAEDPSLNYHGKGLDIHIAA 481
 ++ +M+ ++A++ + + + L+N +N LP L+ P L + A+
 Sbjct: 330 PIAFAMDFLKIAISELANIAERRIERLVNPQLN-DLPPFLSPH-PGLQSGAMIMQYAAAS 387
 Query: 482 YASELGHLANPVTTTFVQPAEMGNQAVNSLALISARRTAEANDVLSLLLASHLYCTLQAVD 541
 SE LA+P + P+ + S+ I+AR + ++A C LQAV+
 Sbjct: 388 LVSENKTLAHPASVDSIPSSANQEDHVSMTIARHAYQVIANTRRVIAIEAICALQAVE 447
 Query: 542 LRAME 546
 R +E
 Sbjct: 448 YRGIE 452

☐ >gi|20807326|ref|NP_622497.1| ☒ Histidine ammonia-lyase [Thermoanaerobacter tengcon
 gi|20515840|gb|AAM24101.1| ☒ Histidine ammonia-lyase [Thermoanaerobacter tengcon
 gi|24211809|sp|Q8RBH4|HUTH_THETN Histidine ammonia-lyase (Histidase)
 Length = 508

Score = 175 bits (444), Expect = 4e-42

Identities = 129/431 (29%), Positives = 203/431 (47%), Gaps = 34/431 (7%)

Query: 115 VYGVTTFGFGSADT--RTEDAVSLQKALIEHQLCGVTPTSVSSFSVGRGLENTLPLEVVR 172
 VYG+TTGFG +D ED +LQK LI C V + LP EVVR
 Sbjct: 53 VYGITTFGKFSDVVISKEDTEALQKNLIMSHSCAVG-----DPLPEEVVR 98
 Query: 173 GAMVIRVNSLTRGHSVRLVLEALTNFLNHRITPIVPLRGSISASGDLSPLSYIAGAIT 232
 M++R N+L +G S VRL +E L +N + P++P +GS+ ASGDL+PL+++ +
 Sbjct: 99 AIMLLRANALAKGFSVRLTETVETLIEMINKNVVPVPIPEKGS LGASGDLAPLAHMLVMI 158
 Query: 233 GHPDVKVHVLHEGTEKIMFAREAISLFGLEAVVLGPKEGLGLVNGTAVSASMATXXXXXX 292
 G + + G + EA+ G+ + L KEGL L+NGT V +++
 Sbjct: 159 GRGE----AFYAGER--VSGEAMRRAGIPTITLSSKEGLALINGTQVMSALGCLNVYDA 212
 Query: 293 XXXXXXXXXXXXXXXXVEAMVGQQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGSSFAXXXX 352
 +EA+ G +F + V RPH GQ+ A+N+R ++ GS
 Sbjct: 213 KRIIAVADAVASITLALRGIIDAFDDRQMV-RPHKGQIVSAKNVRKMVEGSELITRQG 271
 Query: 353 XXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTDNPLLDVENKQT 412
 I QD Y LR PQ G + + + + L +E N+ TDNPL+ ++ +

Sbjct: 272 E-----IRVQDAYTLRCIPQVHGAVRDAISYIERVLGVEINSATDNPLIFPDDGEV 322

Query: 413 AHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCLAEDPSLNYHG 472
GGNF V+++M+ +AL+ I ++ + L+N +N LP L E LN

Sbjct: 323 ISGGNFHGPEVALAMDFLSIALSEIANISERRIERLVNYQLN-DLPPFL-TEKGGNLNSGM 380

Query: 473 KGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVNSLALISARRTAEANDVLSLLASH 532
A+ SE L++P + P+ + S+ I+AR+ E ++ +LA

Sbjct: 381 MIAQYTAASLVSENKVLSPASVDSIPSSANQEDHVSMTIAARKAREVLKNVTTVLAIE 440

Query: 533 LYCTLQAVDLR 543
L QA++ R

Sbjct: 441 LLTASQALEFR 451

☐ >gi|30021749|ref|NP_833380.1| ☒ Histidine ammonia-lyase [Bacillus cereus ATCC 14579]
gi|29897304|gb|AAP10581.1| ☒ Histidine ammonia-lyase [Bacillus cereus ATCC 14579]
Length = 506

Score = 175 bits (443), Expect = 5e-42

Identities = 133/455 (29%), Positives = 214/455 (47%), Gaps = 41/455 (9%)

Query: 95 EIRARVDKSVDLKAQLQNSVYGVTTGFGGSADT--RTEDAVSLQKALIEHQLCGVTPPTS 152
E R V+K V+ K VYG+TTGFG +D + +D +LQ LI+ CG+

Sbjct: 37 ECREVVEKIVEDGKV-----VYGI TTGFGKFSVDVLIQKDDVKALQHNLIQSHACGIG--- 88

Query: 153 VSSFVSVGRGLENLTPLEVVVRGAMVIRVNSLTRGHSVRLVVLEALTNFLNHRITPIVPLR 212
+ P EV RG +++R N++ +G S VR +V+ L F+N +I P+VP +

Sbjct: 89 -----DPFPPEEVSRLMLILRANTMLKGVSGVRPLVVNMLLEFVNRIHPVVPQQ 137

Query: 213 GSISASGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEAVVLGPKEGL 272
GS+ ASGDL+PLS++A + G + V ++G K + A A++ GLE + L KEGL

Sbjct: 138 GSLGASGDLAPLSHLALVLLGE-----VFYK--KRVHAMVALTEEGLEPIELEAKEGL 191

Query: 273 GLVNGTAVSASMATXXXXXXXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQV 332
L+NGT + +E + G +F +H R + QV

Sbjct: 192 ALINGTQAMTAQGVLSYIEAEATAYQAEIASMTIEGLQGIIDAFDENVHK-ARGYKEQV 250

Query: 333 EVARNIRTLLSGSSFAXXXXXXXXXXXXXXGILR-QDRYPLRTSPQFLGPLVEDMMHAYST 391
+VA IR +L S G LR QD Y LR PQ G + + +

Sbjct: 251 DVASRIRDILHDSKL-----TTKQGELRVQDAYSLRCIPQVHGASWQVLNVVKEK 300

Query: 392 LSLENNTTTDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNA 451
L +E N TDNPL+ ++ GGNF ++ +M+ ++ +A + ++ + L+N

Sbjct: 301 LEIEMNAATDNPLIFDGGEKVISGGNFHGQPIAFAMDFLKVGMALANISERRIERLVNP 360


Query: 452 AMNRGLPSCLAEDPSLNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVNSLA 511
+N LP L+ E P L + A+ SE LA+P + P+ + S+

Sbjct: 361 QLN-DLPPFLSPE-PGLQSGAMIMQYAAASLVSENKTLAHPASVDSIPSSANQEDHVSMT 418

Query: 512 LISARRTAEANDVLSLLASHLYCTLQAVDLRAME 546
I++R + + +L+ + C +QA + R +E

Sbjct: 419 TIASRHAHQIIQNVRRLVLSIEMICAMQAAEYRGIE 453

☐ >gi|52841610|ref|YP_095409.1| ☒ histidine ammonia lyase [Legionella pneumophila str. Philadelphia 1]

gi|52628721|gb|AAU27462.1|  histidine ammonia lyase [Legionella pneumophila subs
str. Philadelphia 1]
Length = 535

Score = 175 bits (443), Expect = 5e-42

Identities = 129/432 (29%), Positives = 204/432 (47%), Gaps = 33/432 (7%)

Query: 112 QNSVYGVTTGFGGSAD-TRTEDAVS-LQKALIEHQLCGVTPPTS SVSSFSVGRGLENLPLE 169
+ +VYG+ TGFG A+ T + D + LQ+ ++ CG LP +
Sbjct: 80 KKT VYGINTGFGSLANQTISSDCLKELQRNIVLSHACGTG-----KLLPDD 125

Query: 170 VVRGAMVIRVNSLTRGHSVRLVVLEALTNFLNHRITPIVPLRGSISASGDLSPSYIAG 229
VV +++++N+L++G+S VRL ++ AL NH++ P +P +GS+ ASGDL PL++++
Sbjct: 126 VVALILLKINNLSSQGYSGVRLELINALIALFNHKVYPCIPSKGSVGASGDLVPLAHL 185

Query: 230 AITGHPDVKVHVLHEGTEKIMFAREAISLFGLEAVVLGPKEGLGLVNGTAVSASMATXXX 289
+ G +V+ H+G +++ A E + L GL+ + L KEGL L+NG VS ++A
Sbjct: 186 PLLGEGERV-----HQG--QVISAEGLKLAGLKP LELEAKEGLALLNGLQVSTALALSAL 239


Query: 290 XXXXXXXXXXXXXXXXXXXXVEAMVGQQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGSSFAX 349
V+A G F IH + R H Q+ A R LL+GS
Sbjct: 240 FISETLFETAIISGSLSDAASGSDVPFDDRIHQI-RGHQAQISAASMYRNLLAGSQIRE 298

Query: 350 XXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTDNPLLDVEN 409
QD Y LR PQ +G ++ M TL +E N +DNPL+ E
Sbjct: 299 SHRHCNRV-----QDPYSLRCQPQIMGAILHQM QFVGQTLQVEANAISDNPLVFAEQ 350

Query: 410 KQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCLAEDPSLN 469
GGNF +++++ LAL+ IG + L++ + GLP+ L E LN
Sbjct: 351 GDILSGGNFHFGEIIMAAADNLALALSEIGGSAERRIALLDKNFS-GLPAFLVRES-GLN 408

Query: 470 YHGKGLDIHIAAYASELGHLANPVTTTFVQPAEMGNQAVNSLALISARRTAEANDVLSLLL 529
+ A+ AS+ LA+P + P + S+A +ARR E D S +L
Sbjct: 409 SGFMIAHVTAASCASDNKALAHPSVDSLPTSANQEDHVS MATSAARRLHEMIDNTSTIL 468

Query: 530 ASHLYCTLQAVD 541
A L Q ++
Sbjct: 469 AIELLAACQGLE 480

gi|23471376|ref|ZP_00126706.1| COG2986: Histidine ammonia-lyase [Pseudomonas sy
B728a]
Length = 515

Score = 175 bits (443), Expect = 5e-42

Identities = 138/455 (30%), Positives = 219/455 (48%), Gaps = 34/455 (7%)

Query: 93 DDEIRARVDKSVDFLKAQL--QNSVYGVTTGFGGSADTR--TEDAVSLQKALIEHQLCGV 148
D ++D SV ++ L + YG+ TGFG A TR +ED +LQ++L+ GV
Sbjct: 34 DSSANQQIDDSVACVERILAENRTAYGINTGFGLLASTRIASEDENLQRSVLVSHAAGV 93

Query: 149 TPTS SVSSFSVGRGLENLPLEVVRGAMVIRVNSLTRGHSVRLVVLEALTNFLNHRITPI 208
G+ + + E+VR MV++VNSL+RG S +R VV++AL +N + P
Sbjct: 94 -----GQPISD-----ELVRLIMVLKVNLSRGSSGIRRVVIDALIALINAEVYPH 139

Query: 209 VPLRGSISASGDLSPSYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEAVVLGP 268
+PL+GS+ ASGDL+PL++++ + G + ++G + + +A++ GL+ + L
Sbjct: 140 IPLKGSVGASGDLAPLAHMSLVLLGEGKAR----YKG--EWLNGVDALAAAGLQPLTLAA 193

Query: 269 KEGLGLVNGTAVSASMATXXXXXXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPH 328
 KEGL L+NGT VS + A VEA++G + F IH R
 Sbjct: 194 KEGLALLNGTQVSTAYALRGLFEGEDLFAAALTCGSLTVEAVLGSRSFPDARIH-AARGQ 252

Query: 329 PGQVEVARNIRTLLSGSSFAXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHA 388
 GQ++ A R LL SS QD Y LR PQ +G + + A
 Sbjct: 253 RGQIDAAACYRDLLGESSGVSESHRNCDKV-----QDPYSLRCQPQVMGACLTQLRQA 305

Query: 389 YSTLSLENNTTTDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTEL 448
 L +E N +DNPL+ GGNF A V+++ + LA+A IG L+ + + +
 Sbjct: 306 AEVLEIEANAVSDNPLVFAAENDVISGGNFHAEPVAMAADNLALAEIGSLSERRISLM 365

Query: 449 LNAAMNRGLPSCLAEDPSLNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVN 508
 ++ M++ LP L A + +N + AA ASE LA+P + P +
 Sbjct: 366 MDKHSQ-LPPFLVA-NGGVNSGFMIAQVTAALASENKALAHPHSVDSLPTSANQEDHV 423

Query: 509 SLALISARRTAEANDVLSLLLASHLYCTLQAVDLR 543
 S+A + +R E + + +LA Q +DLR
 Sbjct: 424 SMAPAAGKRLWEMAENVRGILAVEWLAACQGLDLR 458

☐ >gi|62317244|ref|YP_223097.1| **G** HutH, histidine ammonia-lyase [Brucella abortus
 9-941]
 gi|62197437|gb|AAX75736.1| HutH, histidine ammonia-lyase [Brucella abortus biovar
 9-941]
 Length = 511

Score = 174 bits (442), Expect = 7e-42
 Identities = 131/431 (30%), Positives = 203/431 (47%), Gaps = 32/431 (7%)

Query: 115 VYGVTTGFGGSADTRTE--DAVSLQKALIEHQLCGVTPTSVSSFSVGRGLENTLPLEVVR 172
 VYG+ TGFG A R D +LQ+ LI CGV L +VR
 Sbjct: 52 VYGINTEGFKLASIRIAAGDVATLQRNLILSHCCGVG-----EPLSENIVR 97

Query: 173 GAMVIRVNSLTRGHSVRLVLEALTNFLNHRITPIVPLRGSISASGDLSPLSYIAGAIT 232
 M +++ SL RG S VRL V+ + L + P++P +GS+ ASGDL+PL+++ A+
 Sbjct: 98 LIMALKLVSLGRGASGVRLEVITLIEAMLEKGVIPMIPEKGSVGASGDLAPLAHMTAAMI 157

Query: 233 GHPDVKVHVLHEGTEKIMFAREAISLFGLEAVVLGPKEGLGLVNGTAVSASMATXXXXXX 292
 G + + G E++ A+ A+ GL+ VVL KEGL L+NGT S ++A
 Sbjct: 158 GEGE----AFYRG-ERLSGAK-ALGKAGLKPVVLAAKEGLALINGTQTSTALALAGLFRA 211

Query: 293 XXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGSSFAXXXX 352
 +A +G F IH + R H GQ++ R +RTL L GS+
 Sbjct: 212 HRAARTALITGALSTDAAMGSDAPFHEEIHQL-RGHKGQIDAGRALRTLLEGSAIRRSHL 270

Query: 353 XXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTDNPLLDVENKQT 412
 QD Y +R PQ G ++ + A TL +E N TDNPL+ + + +
 Sbjct: 271 EGDQRV-----QDPYCIRCQPQVDGACLDILRQAARTLEIEANAVTDNPLV-LSDGRA 322

Query: 413 AHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCLAEDPSLNYHG 472
 GGNF A V+ + ++ LA+ IG ++ + L++ +++ GLP+ LA + P LN
 Sbjct: 323 VSGGNFHAEPVAFADQIALAVCEIGAISQRRIALLVDPSSLFGLPAFLARK-PGLNSGL 381

Query: 473 KGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVNSLALISARRTAEANDVLSLLLASH 532
 ++ AA SE +A+P + P + S+A ARR + L+ ++
 Sbjct: 382 MIAEVTSAALMSENKQMAHPASVDSPTPTSANQEDHVSMAHGARRLLQMTANLNAIIGIE 441

Query: 533 LYCTLQAVDLR 543

V+LR

Sbjct: 442 ALTGALGVELR 452

☐ >gi|28395510|gb|AA039102.1| AdmH [Pantoea agglomerans]
Length = 541

Score = 174 bits (441), Expect = 9e-42

Identities = 131/461 (28%), Positives = 214/461 (46%), Gaps = 31/461 (6%)

Query: 94 DEIRARVDKSVDFLKAQLQNS--VYGVTTGFGGSADTRTEDAVSLQKAL-IEHQLCGVTP 150
DE+ RV +S L++ + + +YGV T GG + V + KA +++ L

Sbjct: 54 DEVVNRVTRSRISILESMVSDERVIYGVNTSMGGFVNY----IVPIAKASELQNNLINAVA 109

Query: 151 TSVSSFSVGRGLENLPLEVVVRGAMVIRVNSLTRGHSAVRLVVLEALTNFLNHRITPIVP 210
T+V G+ ++T VR M+ R+ SL+RG+SA+ +V + L N I P +P

Sbjct: 110 TNV-----GKYFDDT-----TVRATMLARIVSLSRGNSAISIVNFKKLIEIYNQGIVPCIP 160

Query: 211 LRGSISASGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEAVVLGPKE 270
+GS+ SGDL PL+ IA TG + ++G+ M A+ G+ + L KE

Sbjct: 161 EKGSGLTSGDLGPLAAIALVCTGQWKAR----YQGEQ--MSGAMALEKAGISPMELSFKE 214

Query: 271 GLGLVNGTAVSASMATXXXXXXXXXXXXXXXXXXXXVEAMVGQQGSFAPFIHDVCRPHPG 330
GL L+NGT+ + +E + G+ F P +H + +PH G

Sbjct: 215 GLALINGTSAMVGLGVLLYDEVKRLFDTYLTVTSLSIEGLHGKTKPFEPVHRM-KPHQG 273

Query: 331 QVEVARNIRTLLSGSSFAXXXXXXXXXXXXXX--GILR-----QDRYPLRTSPQFLGPLV 382
Q+EVA I L+ SS A G+++ +D Y +R +PQ LGP+

Sbjct: 274 QLEVATTIWETLADSSLAVNEHEVEKLIAEEMDGLVKASNHQIEDAYSIRCTPQILGPVA 333

Query: 383 EDMMHAYSTLSLENNTTTDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLN 442
+ + + TL+ E N++ DNPL+D ++ H G+F VS++M+ +AL + L

Sbjct: 334 DTLKNIKQTLTNELNSSNDNPLIDQTTEEVFHNGHFHGGQYVSMAMDHLNIALVTMMNLN 393

Query: 443 TQCTELLNAAMNRGLPSCLAEDPSLNYHGKGLDIHIAAYASELGHLANPVTTTFVQPAEM 502
+ ++ + + GLP L AE+ L G A+ +E P++

Sbjct: 394 RRIDRFMDKSNSNGLPPFLCAENAGRLGLMGGQFMTASITAESRASCMPMSIQSLSTTG 453

Query: 503 GNQAVNSLALISARRTAEANDVLSLLLASHLYCTLQAVDLR 543

Q + S L++ARR E L + + L C QAVD+R

Sbjct: 454 DFQDIVSFGLVAARRVREQLKNLKYVFSFELLCACQAVDIR 494

☐ >gi|34763414|ref|ZP_00144363.1| Histidine ammonia-lyase [Fusobacterium nucleatum
ATCC 49256]

gi|27886908|gb|EAA24031.1| Histidine ammonia-lyase [Fusobacterium nucleatum subsp
ATCC 49256]

Length = 516

Score = 174 bits (441), Expect = 9e-42

Identities = 130/454 (28%), Positives = 221/454 (48%), Gaps = 41/454 (9%)

Query: 94 DEIRARVDKSVDFLKAQLQNSVYGVTTGFGGSADTRT--EDAVSLQKALIEHQLCGVTPPT 151
D+ RA VDK V+ K YG+TTGFG A+ E LQK ++ C

Sbjct: 41 DKARALVDKYVEEGKVS-----YGITTGFGKFAEVSISKEQTGQLQKNIVMSHSC----- 90

Query: 152 SVSSFSVGRGLENTLPLEVVRGAMVIRVNSLTRGHSVRLVVLEALTNFLNHRITPIVPL 211
 SVG N LP+++ +G +++R +L +G+S R +V+E L LN +TP +P
 Sbjct: 91 -----SVG-----NPLPIDIAKGVVLLRAVNLAAGYSGARRIVIEKLVELLNKDVTWPIE 141

Query: 212 RGSISASGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEAV-VLGPKE 270
 +GS+ +SGDLSPL++++ + G ++G +++ A++A++ G+E + L KE
 Sbjct: 142 KGSVGSSGDLSPLAHMSLVLIG----LGKAYYKG--ELLEAKDALAKAGIEPIPSLSSKE 195

Query: 271 GLGLVNGTAVSASMATXXXXXXXXXXXXXXXXXXXXVEAMVGQQGSFAPFIHDVCRPHPG 330
 GL L NGT S +E++ G ++ I +V R H G
 Sbjct: 196 GLALTNGTQALTSTGAHVLYDAINLSKHLDAASLTMESLHGIIDAYDSRISEV-REHAG 254

Query: 331 QVEVARNIRTLLSGSSFAXXXXXXXXXXXXXXGILR-QDRYPLRTSPQFLGPLVEDMMHAY 389
 Q+ A N+R +L+GS G+ R QD Y LR PQ G + + +
 Sbjct: 255 QINTAENMRKILAGSK-----NVTKQGVVERVQDSYVLCIPQIHGASKDTLEYVK 304

Query: 390 STLLENNTTTDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELL 449
 + +E N TDNPL+ V++ + GGNF +++ + +ALA + ++ + +++
 Sbjct: 305 RKVEIELNAVTDNPLIFVDSDEVISGGNFHGGPMALPFDLGLIALAEMANVSEIRIEKMV 364

Query: 450 NAAMNRGLPSCLAEDPSLNHYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVNS 509
 N A+N GLP+ L E+ LN + AA SE LA+P + P + S
 Sbjct: 365 NPAINHGLPAFL-VENGGGLNSGFMIVQYSAAALVSENKVLAPASVDSIPTSANQEDHVS 423

Query: 510 LALISARRTAEANDVLSLLLASHLYCTLQAVDLR 543
 + I+A+++ + + + ++ L QA++L+
 Sbjct: 424 MGSIAAKKSKDIFENVRKVIGMELITACQAIELK 457

☐ >gi|54297290|ref|YP_123659.1| ☒ hypothetical protein lpp1335 [Legionella pneumophila str. Philadelphia 1]
☐ gi|53751075|emb|CAH12486.1| ☒ hypothetical protein [Legionella pneumophila str. P
 Length = 506

Score = 174 bits (440), Expect = 1e-41

Identities = 129/432 (29%), Positives = 203/432 (46%), Gaps = 33/432 (7%)

Query: 112 QNSVYGVTTGFGGSAD-TRTEDAVS-LQKALIEHQLCGVTPTS SVSSFSVGRGLENTLPLE 169
 + +VYG+ TGFG A+ T + D + LQ+ ++ CG LP
 Sbjct: 51 KKTVYGINVTGFGSLANQTISSDCLKELQRNIVLSHACGTG-----KLLPDS 96

Query: 170 VVRGAMVIRVNSLTRGHSVRLVVLEALTNFLNHRITPIVPLRGSISASGDLSPLSYIAG 229
 VV +++++N+L++G+S VRL ++ AL NH++ P +P +GS+ ASGDL PL++++
 Sbjct: 97 VVALILLKINNLQGYSGVRLELINALIALFNHKVYPCIPSKGSGVSGDLVPLAHL 156

Query: 230 AITGHPDVKVHVLHEGTEKIMFAREAISLFGLEAVVLGPKEGLGLVNGTAVSASMATXXX 289
 + G +V+ H+G +++ A E + L GL+ + L KEGL L+NG VS ++A
 Sbjct: 157 PLLGEGEVR----HQG--QVISAEGLKLAGLKPLELEAKEGLALLNGLQVSTALALSAL 210

Query: 290 XXXXXXXXXXXXXXXXVEAMVGQQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGSSFAX 349
 V+A G F IH + R H Q+ A R LL+GS
 Sbjct: 211 FISETLFETAISGSLSDAASGSDVPFDDRIHQI-RGHAQAISAASMYRNLLAGSQIRE 269

Query: 350 XXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLLENNTTTDNPLLDVEN 409
 QD Y LR PQ +G ++ M TL +E N +DNPL+ E
 Sbjct: 270 SHRHCNRV-----QDPYSLRCQPQIMGAVLHQMVFVGQTLQVEANAISDNPLVFAEQ 321

Query: 410 KQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCLAEDPSLN 469
 GGNF ++++ + LAL+ IG + L++ + GLP+ L E LN


Sbjct: 322 GDILSGGNFHFGEIIMAADNLALALSEIGGSAERRIALLLIDKNFS-GLPAFLVRES-GLN 379

Query: 470 YHGKGLDIHIAAYASELGHLANPVTTFFVQPAEMGNQAVNSLALISARRTAEANDVLSLLL 529
 + A+ AS+ LA+P + P + S+A +ARR E D S +L

Sbjct: 380 SGFMIAHVTAASCASDNKALAHPHSVDSLPTSANQEDHVSMATSAARRLHEMIDNTSTIL 439

Query: 530 ASHLYCTLQAVD 541
 A L Q ++

Sbjct: 440 AIELLAACQGLE 451

 >gi|1666265|emb|CAB04783.1| phenylalanine ammonia-lyase [Agaricus bisporus]
 gi|2499432|sp|Q92195|PALY_AGABI Phenylalanine ammonia-lyase
 Length = 142

Score = 173 bits (439), Expect = 1e-41
 Identities = 90/142 (63%), Positives = 112/142 (78%)

Query: 408 ENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCLAEDPS 467
 E + HGGNFQA AV+ +MEKTRLAL IGK+ F Q TEL+N A NRGLP LAA DPS




Sbjct: 1 ETGRIHHGGNFQAMAVTNAMEKTRLALHHIGKIIFAQSTELINPATNRGLPPSLAASDPS 60

Query: 468 LNYHGKGLDIHIAAYASELGHLANPVTTFFVQPAEMGNQAVNSLALISARRTAEANDVLSL 527
 LNYH KG+DI AAYA+ELG+LA+PV+T +Q AEM NQAVNS+AL+SAR T + DVLS+

Sbjct: 61 LNYHVKGVDIATAAYAAELGYLASPVSTHIQSAEMHNQAVNSMALVSARATINSIDVLSM 120

Query: 528 LLASHLYCTLQAVDLRAMELDF 549
 L+A++LY QA+DLRA++ +F

Sbjct: 121 LVATYLYNLCQALDLRALQAEF 142

 >gi|15600291|ref|NP_253785.1|  histidine ammonia-lyase [Pseudomonas aeruginosa]
 gi|9951393|gb|AAG08483.1|  histidine ammonia-lyase [Pseudomonas aeruginosa PAO1]
 gi|14194858|sp|Q9HU85|HUTH_PSEAE Histidine ammonia-lyase (Histidase)
 Length = 509

Score = 172 bits (437), Expect = 3e-41
 Identities = 134/432 (31%), Positives = 205/432 (47%), Gaps = 32/432 (7%)

Query: 114 SVYGVTTGFGGSADTRTE--DAVSLQKALIEHQLCGVTPTSVSSFSVGRGLENLTPLEV 171
 + YG+ TGFG A TR D LQ++++ GV G L++ + V

Sbjct: 51 TAYGINTGFGLLASTRISPADLEKLQRSIVLSHAAGV-----GEALDDAM----V 96

Query: 172 RGAMVIRVNSLTRGHSVRLVLEALTNFLNHRITPIVPLRGSISASGDLSPLSYIAGAI 231
 R M+++VNSL RG S +R V++AL +N + P +PL+GS+ ASGDL+PL++++ +

Sbjct: 97 RLVMLLKVNSLARGFSGIRRKVIDALIALINAEVYPHIPKGSVGASGDLAPLAHMSLV 156

Query: 232 TGHPDVKVHVLHEGTEKIMFAREAISLFGLEAVVLGPKEGLGLVNGTAVSASMATXXXXX 291
 G + H G + + A EA+++ GLE + L KEGL L+NGT VS + A

Sbjct: 157 IGESRAR----HRG--EWLPAAEALAVAGLEPLTLAAKEGLALLNGTQVSTAYALRGLFE 210

Query: 292 XXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGSSFAXXX 351
 VEAM+G + F IH R GQ++VA R LL+ SS

Sbjct: 211 AEDLFAAATVCGGLSVEAMLGSRAPFDARIH-AARGQRGQIDVAAAYRDLLTASSEVARS 269

Query: 352 XXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTDNPLLDVENKQ 411
 QD Y LR PQ +G + M A L +E N +DNPL+

Sbjct: 270 HEKCDKV-----QDPYSLRCQPQVMGACLQMRQAAEVLEIEANAVSDNPLVFAAEGD 322

Query: 412 TAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCLAEDPSLN 471
 GGNF A V+++ + LALA IG L+ + + +++ M++ LP L A + +N

Sbjct: 323 VISGGNFHAEPVAMAADNLALALAEIGSLSERRISLMDMHMSQ-LPPFLVA-NGGVNSG 380

Query: 472 GKGLDIHIAAYASELGHLANPVTTTFVQPAEMGNQAVNSLALISARRTAEANDVLSLLLAS 531
 + AA AS+ LA+P + P + S+A + +R + + +LA

Sbjct: 381 FMIAQVTAALASDNKALAHPASVDSLPTSANQEDHVSMAFNAGKRLWAMAENVRGILAV 440

Query: 532 HLYCTLQAVDLR 543
 Q +D R

Sbjct: 441 EWLGAACQGLDFR 452

☐ >gi|54294266|ref|YP_126681.1| ☒ hypothetical protein lpl1331 [Legionella pneumophila str. L]
 gi|53754098|emb|CAH15571.1| ☒ hypothetical protein [Legionella pneumophila str. L]
 Length = 506

Score = 172 bits (437), Expect = 3e-41

Identities = 129/432 (29%), Positives = 203/432 (46%), Gaps = 33/432 (7%)

Query: 112 QNSVYGVTTGFGGSAD-TRTEDAVS-LQKALIEHQLCGVTPTSVSSFSVGRGLENLTPLE 169
 + +VYG+ TGFG A+ T + D + LQ+ ++ CG LP +

Sbjct: 51 KKTVYGINVTGFGSLANQTISADCLKELQRNIVLSHACGTG-----KLLPDD 96

Query: 170 VVRGAMVIRVNSLTRGHSVRLVLEALTNFLNHRITPIVPLRGSISASGDLSPLSYIAG 229
 VV +++++N+L++G+S VRL ++ AL NH++ P +P +GS+ ASGDL PL++++

Sbjct: 97 VVALILLKINNLISQGYSGVRLELINALIALFNHKVYPCIPSKGSGVSGDLVPLAHL 156

Query: 230 AITGHPDVKVHVLHEGTEKIMFAREAISLFGLEAVVLGPKEGLGLVNGTAVSASMATXXX 289
 + G +V+ H+G +++ A E + L GL+ + L KEGL L+NG VS ++A

Sbjct: 157 PLLGEGERV----HQG--QLISAEGLKLAGLKPLELEAKEGLALLNGLQVSTALALSAL 210

Query: 290 XXXXXXXXXXXXXXXXXXXXVEAMVGQQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGSSFAX 349
 V+A G F IH R H Q+ A R LL+GS

Sbjct: 211 FISETLFETAIISGSLSVDAASGSDVPFDDRIHQ-T-RGHQAQISAASMYRNLLAGSQIRE 269

Query: 350 XXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTNDNPLLDVEN 409
 QD Y LR PQ +G ++ M TL +E N +DNPL+ E

Sbjct: 270 SHRHCNRV-----QDPYSLRCQPQIMGAVLHQMFVQGTLQVEANAISDNPLVFAEQ 321

Query: 410 KQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCLAEDPSLN 469
 GGNF +++++ + LAL+ IG + L++ + GLP+ L E LN

Sbjct: 322 GDILSGGNFHFGEIIAMAADNLALALSEIGGSAERRIALLLIDKNFS-GLPAFLVRES-GLN 379

Query: 470 YHGKGLDIHIAAYASELGHLANPVTTTFVQPAEMGNQAVNSLALISARRTAEANDVLSLLL 529
 + A+ AS+ LA+P + P + S+A +ARR E D S +L

Sbjct: 380 SGFMIAHVTAASCASDNKALAHPHSVDSLPTSANQEDHVSMAFSAARRLHEMIDNTSTIL 439

Query: 530 ASHLYCTLQAVD 541
 A L Q ++

Sbjct: 440 AIELLAACQGLE 451

☐ >gi|23464302|gb|AAN34102.1| ☒ histidine ammonia-lyase [Brucella suis 1330]
 gi|38258139|sp|Q8FVB4|HUTH_BRUSU Histidine ammonia-lyase (Histidase)

gi|23500657|ref|NP_700097.1| **G** histidine ammonia-lyase [Brucella suis 1330]
Length = 511

Score = 172 bits (437), Expect = 3e-41

Identities = 130/431 (30%), Positives = 202/431 (46%), Gaps = 32/431 (7%)

Query: 115 VYGVTTGFGGSADTRTE--DAVSLQKALIEHQLCGVTPTSVSSFSVGRGLENLTPLEVVR 172
VYG+ TGFG A R D +LQ+ LI CGV L +VR
Sbjct: 52 VYGINTGFGKLASIRIAAGDVATLQRNLILSHCCGVG-----EPLSENIVR 97

Query: 173 GAMVIRVNSLTRGHSVRLVVLEALTNFLNHRITPIVPLRGSISASGDLSPLSYIAGAIT 232
M +++ SL RG S VRL V+ + L + P++P +GS+ ASGDL+PL+++ A+
Sbjct: 98 LIMALKLVSLGRGASGVRLEVITLIEAMLEKGVIPMIPEKGSVGASGDLAPLAHMTAAMI 157

Query: 233 GHPDVKVHVLHEGTEKIMFAREAIISLFGLEAVVLGPKEGLGLVNGTAVSASMATXXXXXX 292
G + + G E++ A+ A+ GL+ VVL KEGL L+NGT S ++A
Sbjct: 158 GEGE----AFYRG-ERLSGAK-ALGKAGLKPVVLAAKEGLALINGTQTSTALALAGLFRA 211

Query: 293 XXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGSSFAXXXX 352
+A +G F IH + R H GQ++ R +RTLL GS+
Sbjct: 212 HRAVRTALITGALSTDAAMGSDAPFHEEIHQL-RGHKGQIDAGRALRTLLEGSAIRRSHL 270

Query: 353 XXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTNDNPLLDVENKQT 412
QD Y +R PQ G ++ + A TL +E N TDNPL+ + + +
Sbjct: 271 EGDQRV-----QDPYCIRCQPQVDGACLDILRQAARTLEIEANAVTDNPLV-LSDGRA 322

Query: 413 AHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCLAAEDPSLNYHG 472
GGNF A V+ + ++ LA+ IG ++ + L++ +++ GLP+ L + P LN
Sbjct: 323 VSGGNFHAEPVAFADQIALAVCEIGAISQRRIALLVDPSSLFGLPAFLTRK-PGLNSGL 381

Query: 473 KGLDIHIAAYASELGHLANPVTTTFVQPAEMGNQAVNSLALISARRTAEANDVLSLLASH 532
++ AA SE +A+P + P + S+A ARR + L+ ++
Sbjct: 382 MIAEVTSAALMSENKQMAHPASVDSTPTSANQEDHVSMAHGARRLLQMTANLNAIIGIE 441

Query: 533 LYCTLQAVDLR 543
V+LR
Sbjct: 442 ALTGALGVELR 452

gi|53726619|ref|ZP_00141570.2| COG2986: Histidine ammonia-lyase [Pseudomonas aeruginosa UCBPP-PA14]
Length = 509

Score = 172 bits (437), Expect = 3e-41

Identities = 134/432 (31%), Positives = 205/432 (47%), Gaps = 32/432 (7%)

Query: 114 SVYGVTTGFGGSADTRTE--DAVSLQKALIEHQLCGVTPTSVSSFSVGRGLENLTPLEVVR 171
+ YG+ TGFG A TR D LQ++++ GV G L++ + V
Sbjct: 51 TAYGINTGFGLLASTRISPADLEKLQRSIVLSHAAGV-----GEALDDAM---V 96

Query: 172 RGAMVIRVNSLTRGHSVRLVVLEALTNFLNHRITPIVPLRGSISASGDLSPLSYIAGAI 231
R M+++VNSL RG S +R V++AL +N + P +PL+GS+ ASGDL+PL++++ +
Sbjct: 97 RLVMLLKVNLSLARGFSGIRRKVIDALIALINAEVYPHIPLKGSVGASGDLAPLAHMSLV 156

Query: 232 TGHDPVKVHVLHEGTEKIMFAREAIISLFGLEAVVLGPKEGLGLVNGTAVSASMATXXXXX 291
G + H G + + A EA+++ GLE + L KEGL L+NGT VS + A
Sbjct: 157 IGESRAR----HRG--EWLPAAEALAVAGLEPLTLAAKEGLALLNGTQVSTAYALRGLFE 210

Query: 292 XXXXXXXXXXXXXXXXVEAMVGQQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGSSFAXXX 351
 VEAM+G + F IH R GQ++VA R LL+ SS
 Sbjct: 211 AEDLFAAATVCGGLSVEAMLGSRAPFDARIH-AARGQRGQIDVAAAYRDLLTASSEVARS 269

Query: 352 XXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLSLENNTTTDNPLLDVENKQ 411
 QD Y LR PQ +G + M A L +E N +DNPL+
 Sbjct: 270 HEKCDKV-----QDPYSLRCQPQVMGACLTQMRQAAEVLEIEANAVSDNPLVFAAEGD 322

Query: 412 TAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRGLPSCLAEDPSLNYH 471
 GGNF A V+++ + LALA IG L+ + + +++ M++ LP L A + +N
 Sbjct: 323 VISGGNFHAEPVMAADNLALALAEIGSLSERISLMMDMHMSQ-LPPFLVA-NGGVNSG 380

Query: 472 GKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVNSLALISARRTAEANDVLSLLLAS 531
 + AA AS+ LA+P + P + S+A + +R + + +LA
 Sbjct: 381 FMIAQVTAAALASDNKALAHPASVDSLPTSANQEDHVSMAFNAGKRLWAMAENVRGILAV 440

Query: 532 HLYCTLQAVDLR 543
 Q +D R
 Sbjct: 441 EWLGACQGLDFR 452

☐ >gi|19714334|gb|AAL94987.1| ☒ Histidine ammonia-lyase [Fusobacterium nucleatum s
 ATCC 25586]
☐ gi|19704126|ref|NP_603688.1| ☒ Histidine ammonia-lyase [Fusobacterium nucleatum s
 ATCC 25586]
☐ gi|24211811|sp|Q8RFC2|HUTH1_FUSNN Histidine ammonia-lyase 1 (Histidase 1)
 Length = 516

Score = 172 bits (435), Expect = 4e-41

Identities = 126/454 (27%), Positives = 217/454 (47%), Gaps = 41/454 (9%)

Query: 94 DEIRARVDKSVDFLKAQLQNSVYGVTTGFGGSADTRT--EDAVSLQKALIEHQLCGVTPPT 151
 D+ RA VDK V+ K YG+TTGFG A+ E LQK ++ C V
 Sbjct: 41 DKARALVDKYVEEGKVS-----YGITTGFGKFAEVSISKEQTGQLQKNIVMSHSCNVG-- 93

Query: 152 SVSSFSVGRGLENLPLEVVRGAMVIRVNSLTRGHSVAVRLVVLEALTNFLNHRITPIVPL 211
 N LP+++ +G +++R +L +G+S R +V+E L LN +TP +P
 Sbjct: 94 -----NPLPIDIAKGIVLLRAVNLAKGYSGARRIVIEKLVELLNKDVTWPIE 141

Query: 212 RGSISASGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEAV-VLGPKE 270
 +GS+ +SGDLSPL++++ + G ++G +++ A++A++ +E + L KE
 Sbjct: 142 KGSVGSSGDLSPLAHMSLVLI-----LGKAYYKG--ELLEAKDALAKADIEPIPALSSKE 195

Query: 271 GLGLVNGTAVSASMATXXXXXXXXXXXXXXXXXXXXXVEAMVGQQGSFAPFIHDVCRPHPG 330
 GL L NGT S +E + G ++ P I +V R H G
 Sbjct: 196 GLALTNGTQALTSTGAHVLYDAINLSKHLDAASLTMEGLHGIIDAYDPRIGEV-RGHLG 254

Query: 331 QVEVARNIRTLLSGSSFAXXXXXXXXXXXXXXGILR-QDRYPLRTSPQFLGPLVEDMMHAY 389
 Q+ A+N+R +L+GS G+ R QD Y LR PQ G + + +
 Sbjct: 255 QINTAKNMRNILAGSK-----NVTKQGVQDSYVLRCPQIHGASKDTLEYVK 304

Query: 390 STLSLENNTTTDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELL 449
 + LE N TDNP++ V+ + GGNF +++ + +AL+ + ++ + +++
 Sbjct: 305 QKVELELNAVTDNPIIFVDTDEVISGGNFHGGPMALPFDFLGIALSEMANVSERRIEKMV 364

Query: 450 NAAMNRGLPSCLAEDPSLNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVNS 509
 N A+N GLP+ L E LN + A+ SE LA+P + P + S
 Sbjct: 365 NPAINNGLPAFL-VEKGGLNSGFMIVQYSAASLVSENKVLAHPASVDSIPTSANQEDHVS 423

Query: 510 LALISARRTAEANDVLSLLLASHLYCTLQAVDLR 543
 + ++A+++ + + + ++ L QA+DL+
 Sbjct: 424 MGSVAAKKS KDIFENVRKVIGMELITACQAIDLK 457

☐ >gi|48769861|ref|ZP_00274205.1| COG2986: Histidine ammonia-lyase [Ralstonia meta
 Length = 518

Score = 170 bits (431), Expect = 1e-40
 Identities = 135/455 (29%), Positives = 217/455 (47%), Gaps = 34/455 (7%)

Query: 93 DDEIRARVDKSVDFLKAQLQN--SVYGVTTGFGGSADTRT--EDAVSLQKALIEHQLCGV 148
 D+ +D+SV ++ + + YG+ TGFG A TR ED +LQ++L+ GV
 Sbjct: 37 DERAFFAIDRSVACVENIIAEGRTAYGINTGFGLLAQTRIAREDLENLQRSVLVLSHAAGV 96

Query: 149 TPTSVSSFSVGRGLENLTPLEVVIRGAMVIRVNSLTRGHSVRLVVLEALTNFLNHRITPI 208
 G +++ L VR MV+++NSL RG S +R V+ AL +N + P
 Sbjct: 97 -----GEPIDDAL----VRLIMVLKINSLARGLSGIRRKVISALIALVNAEVYPC 142

Query: 209 VPLRGSISASGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEAVVLGP 268
 +PL+GS+ ASGDL+PL++++ + G + H G + + AREA+++ L+ + L
 Sbjct: 143 IPLKGSVGASGDLAPLAHMSLLLLGEGRAR----HRG--EWLSAREALAIADLQPLTLAA 196

Query: 269 KEGLGLVNGTAVSASMATXXXXXXXXXXXXXXXXXXXXVEAMVGQQGSFAPFIHDVCRPH 328
 KEGL L+NGT VS + A VEA +G + F P IH R
 Sbjct: 197 KEGLALLNGTQVSTAYALQGLFQAEDLYAAASVCGALTVEATLGSRAPFDPRIH-AARGQ 255

Query: 329 PGQVEVARNIRTLLSGSSFAXXXXXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHA 388
 GQ++ A R LL +S QD Y LR PQ +G + + +A
 Sbjct: 256 RGQIDAAAVYRHLLGETSQLGQSHAHCDKV-----QDPYSLRCQPQVMGACLTQIRNA 308

Query: 389 YSTLSLENNTTTDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTEL 448
 L +E N+ +DNPL+ + GGNF A V+++ + LALA IG L+ + + +
 Sbjct: 309 ADVLGEANSVSDNPLVFAQEGDIISGGNFHAEPVAMAADNLALALAEIGSLSERVSLM 368

Query: 449 LNAAMNRGLPSCLAEDPSLNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVN 508
 ++ +++ LP L A + +N + AA AS+ LA+P + P +
 Sbjct: 369 MDQHLSQ-LPPFLVA-NGGVNSGFMIAQVTAALASDNKALAHPASVDSLPTSANQEDHV 426

Query: 509 SLALISARRTAEANDVLSLLLASHLYCTLQAVDLR 543
 S+A + +R E + ++A Q +D R
 Sbjct: 427 SMAPNAGKRLWEMASNVKGIVAEIWLAAACQGMDFR 461

☐ >gi|24371698|ref|NP_715740.1| ☒ histidine ammonia-lyase [Shewanella oneidensis M
 gi|24345474|gb|AAN53185.1| ☒ histidine ammonia-lyase [Shewanella oneidensis MR-1]
 Length = 513

Score = 170 bits (431), Expect = 1e-40
 Identities = 133/455 (29%), Positives = 216/455 (47%), Gaps = 36/455 (7%)

Query: 92 NDDEIRARVDKSVDFLKAQLQNSVYGVTTGFGGSADTRT--EDAVSLQKALIEHQLCGV 149
 ND I A++ + V +VYG+ TGFG A+T+ ED LQ++++ G
 Sbjct: 37 NDINISAQIVQKV----LDEGRTVYGINTGFGLLANTKIAPEDLQLLQRSIVLSHAAGT- 91

Query: 150 PTVSSFSVGRGLENLTPLEVVIRGAMVIRVNSLTRGHSVRLVVLEALTNFLNHRITPIV 209

G+ +++ VR MV+++NSL+RG S +RL V+ L + +N + P V
 Sbjct: 92 -----GQYMQDA----TVRLMMVLKINSLSRGSFSGIRLEVINFLISLVNAEVYPCV 138

Query: 210 PLRGSISASGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEAVVLGPK 269
 P +GS+ ASGDL+PL+++ + G ++ ++G +I+ A E + + GL+ + L K
 Sbjct: 139 PEKGSVGASGDLAPLAHMCPLPLGEGEMS----YQG--QIISAAEGLEIAGLKPIDLAAK 192

Query: 270 EGLGLVNGTAVSASMATXXXXXXXXXXXXXXXXXXXXVEAMVGQQGSFAPFIHDVCRPHP 329
 EGL L+NGT S ++A VEA +G + F P I H R
 Sbjct: 193 EGLALLNGTQASTALALEGLFHAEDLFAASSVIGAMSVEAMGSRSPFDPRIH-AARGQK 251

Query: 330 GQVEVARNIRTLLSGSSFAXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAY 389
 GQ++ A R LL S QD Y LR PQ LG + + A
 Sbjct: 252 GQIDSAMVFRYLLGEESEISLSHANCEKV-----QDPYSLRCQPQVLGACLTQIRQAA 304

Query: 390 STLLENNTTTDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELL 449
 L+ E N TDNPL+ + GGNF A V+++ + +A+A +G + + L+
 Sbjct: 305 EVLATEANGVTDNPLVFDGTGDIISGGNFHAEPVAMAADNLAIATAELGAIAERRIALLI 364

Query: 450 NAAMNRLPSCLAAEDPSLNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQAVNS 509
 +++++ LP L ++ +N + AA ASE A+P + P + S
 Sbjct: 365 DSSLSK-LPPFL-VKNGGVNSGFMIAQVTAALASENKTYAHPASVDSLPTSANQEDHVS 422

Query: 510 LALISARRTAEANDVLSLLLASHLYCTLQAVDLRA 544
 +A +ARR + ++ +LA L Q +D RA
 Sbjct: 423 MATFAARLRDMSENTRGVLAIELLAAAQGLDFRA 457

[gi|19749213|gb|AAL98596.1|](#) **G** putative histidine ammonia-lyase [Streptococcus py
[gi|19746961|ref|NP_608097.1|](#) **G** putative histidine ammonia-lyase [Streptococcus py
[gi|24211791|sp|Q8NZ46|HUTH_STRP8](#) Histidine ammonia-lyase (Histidase)
 Length = 513

Score = 170 bits (431), Expect = 1e-40

Identities = 129/431 (29%), Positives = 204/431 (47%), Gaps = 35/431 (8%)

Query: 115 VYGVTTGFGG--SADTRTEDAVSLQKALIEHQLCGVTPTSVSSFSVGRGLENTLPLEVVR 172
 VYGVTTGFG + ED V LQ+ LI T S F + LP + VR
 Sbjct: 54 VYGVTTGFGSLCNVSISPEDTVQLQENLIR-----THASGFG-----DLPPEDAVR 99

Query: 173 GAMVIRVNSLTRGHSVRLVLEALTNFLNHRITPIVPLRGSISASGDLSPLSYIAGAIT 232
 M+IR+NSL +G+S +RL +E L LN + P +P +GS+ ASGDL+PL+++ +
 Sbjct: 100 AIMLIRINSLVKGYSGIRLSTIEKLELLNKGVHPYIPEKGSLGASGDLAPLAHMLPML 159

Query: 233 GHPDVKVHVLHEGTEKIMFAREAISLFGLEAVVLGPK EGLGLVNGTAVSASMATXXXXXX 292
 G ++G +++ +EA+ G++ + L KEGL L+NGT V ++
 Sbjct: 160 G----LGKAYYKG--ELLSGQEALDKAGIDKISLAAKEGLALINGTTVLTAIGALATYDA 213

Query: 293 XXXXXXXXXXXXXXXVEAMVGQQGSFAPFIHDVCRPHPGQVEVARNIRTLLSGSSFAXXXX 352
 +E G F +H + RP GQ+ ARNIR LL GS
 Sbjct: 214 IQLLKLSDLAGALSLEVHNGITSPFEENLHTI-RPQSGQLATARNIRNLLEGSQNTTVAT 272

Query: 353 XXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMMHAYSTLLENNTTTDNPLLDVENKQT 412
 QD Y LR PQ G + + + S + +E N+ TDNP++ ++
 Sbjct: 273 QSRV-----QDPYTLRCMPQIHGASKDSIAYVKSVDIEINSVTDNPPII-CKDGHV 322

Query: 413 AHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAMNRLPSCLAAEDPSLNYHG 472
 GGNF ++ S + +A++ IG ++ + L+N+ +++ LPS L + P LN

Sbjct: 323 ISGGNFHGEPMASQSFDFLGIAISEIGNVSERRVERLVNSQLSK-LPSFL-VKYPGLNSGF 380

Query: 473 KGLDIHIAAYASELGHLANPVTTTFVQPAEMGNQAVNSLALISARRTAEANDVLSLLASH 532
 A+ ASE LA+P + P+ + S+ +AR+ E ++A+

Sbjct: 381 MITQYACASLASSENKVLAPASVDSIPSCENQEDFVSMGTTAARKAFEILKNSRRIVATE 440

Query: 533 LYCTLQAVDLR 543
 + QA+DL+

Sbjct: 441 IMAACQALDLK 451

[gi|20663605|pdb|1GKM|A](#) **S** Chain A, Histidine Ammonia-Lyase (Hal) From Pseudomonas
 Inhibited With L-Cysteine

[gi|5107469|pdb|1B8F|A](#) **S** Chain A, Histidine Ammonia-Lyase (Hal) From Pseudomonas P
 Length = 509

Score = 170 bits (430), Expect = 2e-40

Identities = 136/457 (29%), Positives = 217/457 (47%), Gaps = 34/457 (7%)

Query: 91 QNDDEIRARVDKSVDFLKAQL--QNSVYGVTTGFGGSADTR--TEDAVSLQKALIEHQLC 146
 Q D +D SV ++ + + YG+ TGFG A TR + D +LQ++L+

Sbjct: 26 QLDASAAPAIDASVACVEQIIAEDRTAYGINTGFGLLASTRIASHDLENLQRSVLVSHAA 85

Query: 147 GVTPTSVSSFSVGRGLENLPLEVVIRGAMVIRVNSLTRGHSAVRLVVLEALTNFLNHRIT 206
 G+ G L++ L VR MV+++NSL+RG S +R V++AL +N +

Sbjct: 86 GI-----GAPLDDDL----VRLIMVLKINSLSRGFSGIRRKVIDALIALVNAEVY 131

Query: 207 PIVPLRGSISASGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEAVVL 266
 P +PL+GS+ ASGDL+PL++++ + G + ++G + + A EA+++ GLE + L

Sbjct: 132 PHIPLKGSVGASGDLAPLAHMSLVLLGEGKAR----YKG--QWLSATEALAVAGLEPLTL 185

Query: 267 GPKEGLGLVNGTAVSASMATXXXXXXXXXXXXXXXXXXXXXVEAMVGQQGSFAPFIHDVCR 326
 KEGL L+NGT S + A VEA++G + F IH+ R

Sbjct: 186 AAKEGLALLNGTQASTAYALRGLFYAEDLYAAAIACGGLSVEAVLGSRSFPDARIHE-AR 244

Query: 327 PHPGQVEVARNIRTLLSGSSFAXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMM 386
 GQ++ A R LL SS QD Y LR PQ +G + +

Sbjct: 245 GQRGQIDTAACFRDLLGDSSEVSLSHKNADKV-----QDPYSLRCQPQVMGACLTQLR 297

Query: 387 HAYSTLSLENNTTTDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCT 446
 A L +E N +DNPL+ GGNF A V+++ + LA+A IG L+ + +

Sbjct: 298 QAAEVLGIEANAVSDNPLVFAAEGDVISGGNFHAEPVAMAADNLALALAEIGSLSERRIS 357

Query: 447 ELLNAAMNRGLPSCLAAEDPSLNYHGKGLDIHIAAYASELGHLANPVTTTFVQPAEMGNQA 506
 +++ M++ LP L E+ +N + AA ASE L++P + P +

Sbjct: 358 LMMDKHMSQ-LPPFL-VENGGVNSGFMIQVTAALASENKALSHPHSVDSLPTSANQED 415

Query: 507 VNSLALISARRTAEANDVLSLLASHLYCTLQAVDLR 543
 S+A + +R E + +LA Q +DLR

Sbjct: 416 HVSMAPAAGKRLWEMAENTRGVLAIEWLGACQGLDLR 452

[gi|26991708|ref|NP_747133.1|](#) **G** histidine ammonia-lyase [Pseudomonas putida KT24
[gi|24986810|gb|AA70597.1|](#) **G** histidine ammonia-lyase [Pseudomonas putida KT2440]
[gi|38257987|sp|Q88CZ7|HUTH_PSEPK](#) **G** Histidine ammonia-lyase (Histidase)
 Length = 510

Score = 169 bits (428), Expect = 3e-40
 Identities = 136/457 (29%), Positives = 217/457 (47%), Gaps = 34/457 (7%)

Query: 91 QNDDEIRARVDKSVDFLKAQL--QNSVYGVTGFGGSADTR--TEDAVSLQKALIEHQLC 146
 Q D +D SV ++ + + YG+ TGFG A TR + D +LQ++L+

Sbjct: 27 QLDASAAPIDASVACVEQIIAEDRTAYGINTGFGLLASTRIASHDLENLQSLVLSHAA 86

Query: 147 GVTPTSVSFSVGRGLENLPLEVVRGAMVIRVNSLTRGHSVRLVLEALTNFLNHRIT 206
 G+ G L++ L VR MV+++NSL+RG S +R V++AL +N +

Sbjct: 87 GI-----GAPLDDDL----VRLIMVLKINSLSRGFSGIRRKVIDALIALVNAEVY 132

Query: 207 PIVPLRGSISASGDLSPSYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEAVVL 266
 P +PL+GS+ ASGDL+PL++++ + G + ++G + + A EA+++ GLE + L

Sbjct: 133 PHIPLKGSVGASGDLAPLAHMSLVLLGEGKAR----YKG--QWLPATEALAIAGLEPLTL 186

Query: 267 GPKEGLGLVNGTAVSASMATXXXXXXXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCR 326
 KEGL L+NGT S + A VEA +G + F +H+V R

Sbjct: 187 AAKEGLALLNGTQASTAYALRGLFQAEDLYAAAIACGGLSVEAALGSRSPFDARVHEV-R 245

Query: 327 PHPGQVEVARNIRTLLSGSSFAXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMM 386
 GQ++ A R LL SS QD Y LR PQ +G + +

Sbjct: 246 GQRGQIDTAACFRDLLGDSSEVSLSHKNCDKV-----QDPYSLRCQPQVMGACLTQLR 298

Query: 387 HAYSTLSLENNTTTNDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCT 446
 A L +E N +DNPL+ GGNF A V+++ + LA+A IG L+ + +

Sbjct: 299 QAAEVLGIEANAVSDNPLVFAAEGDVISGGNFHAEPVAMAADNLALAEIGSLSERIS 358

Query: 447 ELLNAAMNRGLPSCLAAEDPSLNHYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQA 506
 +++ M++ LP L E+ +N + AA ASE L++P + P +

Sbjct: 359 LMDKHMSQ-LPPFL-VENGGVNSGFMIAQVTAALASENKALSHPHSVDSLPTSANQED 416

Query: 507 VNSLALISARRTAEANDVLSLLLASHLYCTLQAVDLR 543
 S+A + +R E + +LA Q +DLR

Sbjct: 417 HVSMAPAAGKRLWEMAENTRGVLAIEWLGACQGLDLR 453

☐ >gi|9911054|sp|P21310|HUTH_PSEPU Histidine ammonia-lyase (Histidase)
 Length = 510

Score = 169 bits (428), Expect = 3e-40
 Identities = 136/457 (29%), Positives = 217/457 (47%), Gaps = 34/457 (7%)

Query: 91 QNDDEIRARVDKSVDFLKAQL--QNSVYGVTGFGGSADTR--TEDAVSLQKALIEHQLC 146
 Q D +D SV ++ + + YG+ TGFG A TR + D +LQ++L+

Sbjct: 27 QLDASAAPIDASVACVEQIIAEDRTAYGINTGFGLLASTRIASHDLENLQSLVLSHAA 86

Query: 147 GVTPTSVSFSVGRGLENLPLEVVRGAMVIRVNSLTRGHSVRLVLEALTNFLNHRIT 206
 G+ G L++ L VR MV+++NSL+RG S +R V++AL +N +

Sbjct: 87 GI-----GAPLDDDL----VRLIMVLKINSLSRGFSGIRRKVIDALIALVNAEVY 132

Query: 207 PIVPLRGSISASGDLSPSYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEAVVL 266
 P +PL+GS+ ASGDL+PL++++ + G + ++G + + A EA+++ GLE + L

Sbjct: 133 PHIPLKGSVGASGDLAPLAHMSLVLLGEGKAR----YKG--QWLSATEALAVAGLEPLTL 186

Query: 267 GPKEGLGLVNGTAVSASMATXXXXXXXXXXXXXXXXXXXXXVEAMVGQGSFAPFIHDVCR 326
 KEGL L+NGT S + A VEA++G + F IH+ R

Sbjct: 187 AAKEGLALLNGTQASTAYALRGLFYAEDLYAAAIACGGLSVEAVLGSRSPFDARIHE-AR 245

Query: 327 PHPGQVEVARNIRTLTLLSGSSFAXXXXXXXXXXXXXXGILRQDRYPLRTSPQFLGPLVEDMM 386
 GQ++ A R LL SS QD Y LR PQ +G + +
 Sbjct: 246 GQRGQIDTAACFRDLLGDSSEVSLSHKNCDKV-----QDPYSLRCQPQVMGACLTQLR 298

Query: 387 HAYSTLSLENNTTTNDNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCT 446
 A L +E N +DNPL+ GGNF A V+++ + LA+A IG L+ + +
 Sbjct: 299 QAAEVLGIEANAVSDNPLVFAAEGDVISGGNFHAEPVAMAADNLALAEIGSLSERRIS 358

Query: 447 ELLNAAMNRGLPSCLAEDPSLNYHGKGLDIHIAAYASELGHLANPVTTFVQPAEMGNQA 506
 +++ M++ LP L E+ +N + AA ASE L++P + P +
 Sbjct: 359 LMMDKHMSQ-LPPFL-VENGGVNSGFMIAQVTAALASENKALSHPHSVDSLPTSANQED 416

Query: 507 VNLSLALISARRTAEANDVLSLLLASHLYCTLQAVDLR 543
 S+A + +R E + +LA Q +DLR
 Sbjct: 417 HVSMAPAAGKRLWEMAENTRGVLAIEWLGACQGLDLR 453

Get selected sequences

Select all

Deselect all

Database: All non-redundant GenBank CDS
 translations+PDB+SwissProt+PIR+PRF excluding environmental samples
 Posted date: Apr 17, 2005 1:04 AM
 Number of letters in database: 829,394,864
 Number of sequences in database: 2,448,365

Lambda	K	H
0.316	0.131	0.369

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 201,270,679

Number of Sequences: 2448365

Number of extensions: 7419858

Number of successful extensions: 17203

Number of sequences better than 10.0: 73

Number of HSP's better than 10.0 without gapping: 70

Number of HSP's successfully gapped in prelim test: 3

Number of HSP's that attempted gapping in prelim test: 16833

Number of HSP's gapped (non-prelim): 97

length of query: 720

length of database: 829,394,864

effective HSP length: 135

effective length of query: 585

effective length of database: 498,865,589

effective search space: 291836369565

effective search space used: 291836369565

T: 11

A: 40

X1: 16 (7.3 bits)

X2: 38 (14.6 bits)

X3: 64 (24.7 bits)

S1: 41 (21.6 bits)
S2: 79 (35.0 bits)